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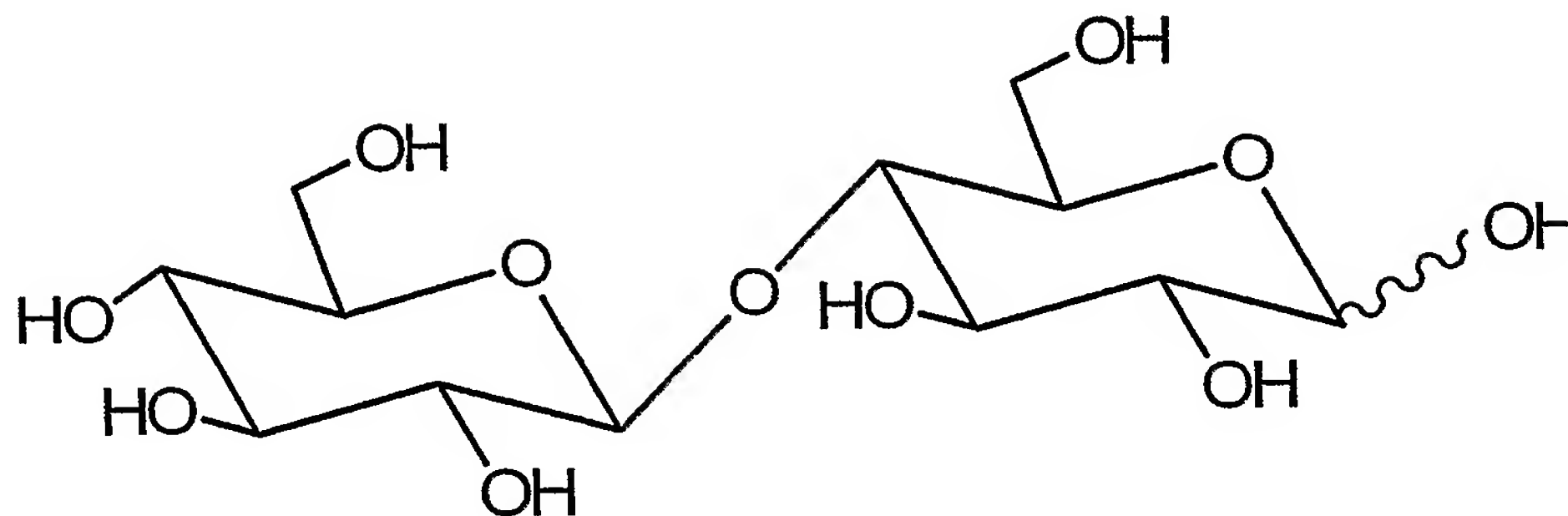
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(54) Title: CELLULASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM



structure of cellobiose

(57) Abstract: This invention relates to molecular and cellular biology and biochemistry. In one aspect, the invention provides polypeptides having cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or β -glucosidase activity, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or β -glucosidase activity, including thermostable and thermotolerant activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural, food and feed processing and industrial contexts.

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CELLULASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

GOVERNMENT SUPPORT

5 This invention was made with United States Government support under Contract Nos. DE-FG03-02ER83395 and DE-FG02-03ER83865, awarded by the Department of Energy. The Government has certain rights in this invention.

FIELD OF THE INVENTION

10 This invention relates to molecular and cellular biology and biochemistry. In one aspect, the invention provides polypeptides having cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or β -glucosidase activity, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides having cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or β -glucosidase activity, 15 including thermostable and thermotolerant activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts.

BACKGROUND

20 Cellulose is the most abundant renewable resource on earth. It is composed of a linear chain of β 1-4 glucose units with the repeating unit being cellobiose, which is a glucose dimer having a structure as shown in Figure 5. The polymer is degraded by a suite of enzymes which include endoglucanases (EG) which randomly hydrolyze the cellulose polymer, and cellobiohydrolases (CBH) which remove terminal cellobiose residues from cellulose. Cellobiose and cello-oligosaccharides are hydrolyzed to glucose 25 by β -glucosidases (BG). All three of these enzymes are necessary for the complete breakdown of cellulose to glucose. For each of these three enzymes different structural variants exist that perform the same function. In addition, fungi and bacteria are known to produce multiple forms of the same structural variants in addition to different structural variants. 30

Further complicating this system is the fact that some anaerobic bacteria and fungi are known to produce these enzymes in multi-enzyme complexes which contain multiple enzymes all attached to an enzyme scaffold with molecular weights above 2 million

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daltons. Why is such a complex system of enzymes necessary for such a simple molecule? Some researchers believe that this complexity is due to the recalcitrant nature of the substrate. The cellulose chains form microfibrils that pack into a crystalline matrix via hydrogen bonding of adjacent chains. This structure is highly resistant to chemical or enzymatic degradation.

CBHs are thought to be the key enzyme in the degradation of this crystalline cellulose because of the nature of their enzymatic attack on cellulose. EGs unlike CBHs have an open cleft that attacks the cellulose chain at a perpendicular angle. CBHs attack the chain directly via a tunnel containing the active site. The current thought is that the cellulose chains enter the tunnel and at the same time, adjacent hydrogen bonding is disrupted. Once the cellobiohydrolases have established this "foothold" on the substrate, the EGs can then come in and more readily attack the substrate.

A major deficiency of known CBHs is their low catalytic activity. Some groups argue that the low activity stems from the fact that energy from hydrolysis is transferred to kinetic energy to disrupt hydrogen bonds and enable the enzyme to move along the substrate. CBHs are exo-acting enzymes and are found in 6 of the 90 families of glycosyl hydrolases. They include families 5, 6, 7, 9, 10 and 48. Family 5 contains many different types of glycosyl hydrolases including cellulases, mannanases and xylanases. Although most cellulases in this family are endoglucanases, there are examples of cellobiohydrolases, most notably CelO from *Clostridium thermocellum*. Family 6 contains only endoglucanases or cellobiohydrolases with more cellobiohydrolase members than endoglucanases. The enzymes have an inverting mechanism and crystallographic studies suggest that the enzyme has a distorted α/β barrel structure containing seven, not eight parallel β -strands. Family 7 enzymes are also composed of both endoglucanases and cellobiohydrolases with more cellobiohydrolases and only known members are from fungi. The enzyme has a retaining mechanism and the crystal structure suggests a β -jellyroll structure. Family 9 contains endoglucanases, cellobiohydrolases and β -glucosidases with a preponderance of endoglucanases. However, *Thermobifida fusca* produces an endo/exo-1,4-glucanase, the crystal structure of which suggests a $(\alpha/\alpha)_6$ barrel fold. The enzyme has characteristics of both endo and exo-glucanases CBHs. Family 10 contains only 2 members described as cellobiohydrolases with mainly the rest described as xylanases. Cellobiohydrolases and xylanases from family 10 have activity on methyl-umbelliferyl cellobioside. Family 48

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contains mainly bacterial and anaerobic fungal cellobiohydrolases and endoglucanases. The structure is a $(\alpha/\alpha)_6$ barrel fold similar to family 9.

There is a need for less expensive and renewable sources of fuel for road vehicles. New fuel sources will be more attractive if they produce nonharmful endproducts after
5 combustion. Ethanol offers an attractive alternative to petroleum based fuels and can be obtained through the fermentation of monomeric sugars derived from starch or lignocellulose. However, current economics do not support the widespread use of ethanol due to the high cost of generating it. One area of research aimed at decreasing costs is enhancement of the technical efficacy of the enzymes that can be used to generate
10 fermentable sugars from lignocellulose. The development of enzymes that more efficiently digest feedstock will translate to decreased ethanol production costs. More efficient processes will decrease the United State's reliance on foreign oil and the price fluctuations that may be related to that reliance. Using cleaner fuels for transportation like bioethanol also may decrease net CO₂ emissions that are believed to be partially
15 responsible for global warming.

SUMMARY

The invention provides cellulases, e.g., endoglucanases, cellobiohydrolases and/or β -glucosidase (beta-glucosidases), and methods for making and using them. In one aspect, the enzymes of the invention have an increased catalytic rate to improve the
20 process of substrate hydrolysis. This increased efficiency in catalytic rate leads to an increased efficiency in producing sugars, which can be useful in industrial applications, e.g., the sugars so produced can be used by microorganisms for ethanol production. In one aspect, the invention provides highly active (e.g., having an increased catalytic rate) cellobiohydrolases, endoglucanases and beta-glucosidase. The invention provides
25 industrial applications (e.g., biomass to ethanol) using enzymes of the invention having decreased enzyme costs, e.g., decreased costs in biomass to ethanol processes. Thus, the invention provides efficient processes for producing bioethanol and bioethanol-comprising compositions, including fuels comprising bioethanol, from any biomass.

In one aspect, the enzymes of the invention have a glucanase, e.g., an
30 endoglucanase, activity, e.g., catalyzing hydrolysis of internal endo- β -1,4- and/or β -1,3-glucanase linkages. In one aspect, the endoglucanase activity (e.g., endo-1,4-beta-D-glucan 4-glucano hydrolase activity) comprises hydrolysis of 1,4- and/or β -1,3- beta-D-glycosidic linkages in cellulose, cellulose derivatives (e.g., carboxy methyl cellulose and

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hydroxy ethyl cellulose) lichenin, beta-1,4 bonds in mixed beta-1,3 glucans, such as cereal beta-D-glucans or xyloglucans and other plant material containing cellulosic parts.

In one aspect, the enzymes of the invention have endoglucanase (e.g., endo-beta-1,4-glucanases, EC 3.2.1.4; endo-beta-1,3(1)-glucanases, EC 3.2.1.6; endo-beta-1,3-
5 glucanases, EC 3.2.1.39) activity and can hydrolyze internal β -1,4- and/or β -1,3-glucosidic linkages in cellulose and glucan to produce smaller molecular weight glucose and glucose oligomers. The invention provides methods for producing smaller molecular weight glucose and glucose oligomers using these enzymes of the invention.

In one aspect, the enzymes of the invention are used to generate glucans, e.g.,
10 polysaccharides formed from 1,4- β - and/or 1,3-glycoside-linked D-glucopyranose. In one aspect, the endoglucanases of the invention are used in the food industry, e.g., for baking and fruit and vegetable processing, breakdown of agricultural waste, in the manufacture of animal feed, in pulp and paper production, textile manufacture and household and industrial cleaning agents. In one aspect, the enzymes, e.g., endoglucanases, of the
15 invention are produced by a microorganism, e.g., by a fungi and/or a bacteria.

In one aspect, the enzymes, e.g., endoglucanases, of the invention are used to hydrolyze beta-glucans (β -glucans) which are major non-starch polysaccharides of cereals. The glucan content of a polysaccharide can vary significantly depending on variety and growth conditions. The physicochemical properties of this polysaccharide are
20 such that it gives rise to viscous solutions or even gels under oxidative conditions. In addition glucans have high water-binding capacity. All of these characteristics present problems for several industries including brewing, baking, animal nutrition. In brewing applications, the presence of glucan results in wort filterability and haze formation issues. In baking applications (especially for cookies and crackers), glucans can create sticky
25 doughs that are difficult to machine and reduce biscuit size. Thus, the enzymes, e.g., endoglucanases, of the invention are used to decrease the amount of β -glucan in a β -glucan-comprising composition, e.g., enzymes of the invention are used in processes to decrease the viscosity of solutions or gels; to decrease the water-binding capacity of a composition, e.g., a β -glucan-comprising composition; in brewing processes (e.g., to
30 increase wort filterability and decrease haze formation), to decrease the stickiness of doughs, e.g., those for making cookies, breads, biscuits and the like.

In addition, carbohydrates (e.g., β -glucan) are implicated in rapid rehydration of baked products resulting in loss of crispiness and reduced shelf-life. Thus, the enzymes, e.g., endoglucanases, of the invention are used to retain crispiness, increase crispiness, or

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reduce the rate of loss of crispiness, and to increase the shelf-life of any carbohydrate-comprising food, feed or drink, e.g., a β -glucan-comprising food, feed or drink.

Enzymes, e.g., endoglucanases, of the invention are used to decrease the viscosity of gut contents (e.g., in animals, such as ruminant animals, or humans), e.g., those with
5 cereal diets. Thus, in alternative aspects, enzymes, e.g., endoglucanases, of the invention are used to positively affect the digestibility of a food or feed and animal (e.g., human or domestic animal) growth rate, and in one aspect, are used to higher generate feed conversion efficiencies. For monogastric animal feed applications with cereal diets, beta-glucan is a contributing factor to viscosity of gut contents and thereby adversely affects
10 the digestibility of the feed and animal growth rate. For ruminant animals, these beta-glucans represent substantial components of fiber intake and more complete digestion of glucans would facilitate higher feed conversion efficiencies. Accordingly, the invention provides animal feeds and foods comprising endoglucanases of the invention, and in one aspect, these enzymes are active in an animal digestive tract, e.g., in a stomach and/or
15 intestine.

Enzymes, e.g., endoglucanases, of the invention are used to digest cellulose or any beta-1,4-linked glucan-comprising synthetic or natural material, including those found in any plant material. Enzymes, e.g., endoglucanases, of the invention are used as commercial enzymes to digest cellulose, e.g., in the wood processing, pulp and/or paper
20 industry, in textile manufacture and in household and industrial cleaning agents, and/or in biomass waste processing.

In one aspect the invention provides compositions (e.g., pharmaceutical compositions, foods, feeds, drugs, dietary supplements) comprising the enzymes, polypeptides or polynucleotides of the invention. These compositions can be formulated
25 in a variety of forms, e.g., as tablets, gels, pills, implants, liquids, sprays, powders, food, feed pellets or as any type of encapsulated form.

The invention provides isolated or recombinant nucleic acids comprising a nucleic acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%,
30 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention, including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ

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5 ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID
NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID
NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID
NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID
NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID
NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID
NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID
NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID
10 NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID
NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID
NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID
NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID
NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID
NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID
15 NO:163 and SEQ ID NO:165; see also Tables 1, 2, and 3, Examples 1 and 4, below, and
Sequence Listing, over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75,
100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950,
1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650,
1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400,
20 2450, 2500, or more residues; and in alternative aspects, these nucleic acids encode at
least one polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase,
mannanase and/or beta-glucosidase activity, or encode a polypeptide capable of
generating an antibody that can specifically bind to a polypeptide of the invention, or,
these nucleic acids can be used as probes for identifying or isolating cellulase-encoding
25 nucleic acids, or to inhibit the expression of cellulase-expressing nucleic acids (all these
aspects referred to as the “nucleic acids of the invention”). In one aspect, the sequence
identities are determined by analysis with a sequence comparison algorithm or by a visual
inspection.

30 Nucleic acids of the invention also include isolated or recombinant nucleic acids
encoding an exemplary enzyme of the invention, including a polypeptide having a
sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,
SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ
ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID
NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID

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NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID
NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID
NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID
NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID
5 NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID
NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID
NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID
NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID
NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID
10 NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID
NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:146, SEQ ID NO:148, SEQ ID
NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID
NO:160, SEQ ID NO:162, SEQ ID NO:164 and SEQ ID NO:166, see also Tables 1, 2,
and 3, Examples 1 and 4, below, and the Sequence Listing, and subsequences thereof and
15 variants thereof. In one aspect, the polypeptide has a cellulase activity, e.g.,
endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

In one aspect, the invention provides cellulase-encoding, e.g., endoglucanase-,
cellobiohydrolase- and/or beta-glucosidase-encoding nucleic acids having a common
novelty in that they are derived from mixed cultures. The invention provides cellulose-
20 degrading enzyme-encoding nucleic acids isolated from mixed cultures comprising a
polynucleotide of the invention, e.g., a sequence having at least about 10%, 15%, 20%,
25%, 30%, 35%, 40%, 45%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%,
60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%,
75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%,
25 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%)
sequence identity to an exemplary nucleic acid of the invention, e.g., SEQ ID NO:1, SEQ
ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13,
SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ
ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID
30 NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID
NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID
NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID
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NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID

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NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID
NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID
NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID
NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID
5 NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID
NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID
NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID
NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 and SEQ
ID NO:165, and see Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing,
10 over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550,
600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, or more.

In one aspect, the invention provides cellulase enzyme-, e.g., endoglucanase
enzyme-, cellobiohydrolase enzyme- and/or beta-glucosidase enzyme-encoding nucleic
acids, including exemplary polynucleotide sequences of the invention, see also Tables 1,
15 2, and 3, Examples 1 and 4, below, and Sequence Listing, and the polypeptides encoded
by them, including enzymes of the invention, e.g., exemplary polypeptides of the
invention, e.g., SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID
NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID
NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID
20 NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID
NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID
NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID
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NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID
25 NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID
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NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID
NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID
NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID
30 NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID
NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:146, SEQ ID NO:148, SEQ ID
NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID
NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ ID NO:166, see also Table 1 and
Sequence Listing, having a common novelty in that they are derived from a common

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source, e.g., an environmental source. In one aspect, the invention also provides cellulase enzyme-, e.g., endoglucanase enzyme-, cellobiohydrolase enzyme- and/or beta-glucosidase enzyme-encoding nucleic acids with a common novelty in that they are derived from environmental sources, e.g., mixed environmental sources.

5 In one aspect, the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

Another aspect of the invention is an isolated or recombinant nucleic acid including at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400,
10 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more consecutive bases of a nucleic acid sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto.

15 In one aspect, the isolated or recombinant nucleic acid encodes a polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, which is thermostable. The polypeptide can retain a cellulase activity under conditions comprising a temperature range of between about 37°C to about 95°C; between about 55°C to about 85°C, between about 70°C to about 95°C, or, between
20 about 90°C to about 95°C. The polypeptide can retain a cellulase activity in temperatures in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, 96°C, 97°C, 98°C or 99°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 99°C, or 95°C, 96°C, 97°C, 98°C or
25 99°C, or more.

In another aspect, the isolated or recombinant nucleic acid encodes a polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, which is thermotolerant. The polypeptide can retain a cellulase activity after exposure to a temperature in the range from greater than 37°C to about 95°C
30 or anywhere in the range from greater than 55°C to about 85°C. The polypeptide can retain a cellulase activity after exposure to a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, 96°C, 97°C, 98°C or 99°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or

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between about 90°C to about 95°C, or more. In one aspect, the polypeptide retains a cellulase activity after exposure to a temperature in the range from greater than 90°C to about 99°C, or 95°C, 96°C, 97°C, 98°C or 99°C, at about pH 4.5, or more.

The invention provides isolated or recombinant nucleic acids comprising a sequence that hybridizes under stringent conditions to a nucleic acid of the invention, including an exemplary sequence of the invention, e.g., a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165 (see also Tables 1, 2, and 3, Examples 1 and 4, below,), or fragments or subsequences thereof. In one aspect, the nucleic acid encodes a polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. The nucleic acid can be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 or more residues in length or the full length of the gene or transcript. In one aspect, the stringent conditions comprise a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

The invention provides a nucleic acid probe for identifying or isolating a nucleic acid encoding a polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, wherein the probe comprises at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90,

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95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more, consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof, wherein the probe identifies the nucleic acid by binding or hybridization. The probe can comprise an oligonucleotide comprising
5 at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof.

The invention provides a nucleic acid probe for identifying or isolating a nucleic acid encoding a polypeptide having a cellulase activity, e.g., endoglucanase,
10 cellobiohydrolase, mannanase and/or beta-glucosidase activity, wherein the probe comprises a nucleic acid comprising a sequence at least about 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more residues of a nucleic acid of the invention, e.g., a polynucleotide having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%,
15 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention. In one aspect, the sequence identities are determined by analysis with a sequence comparison algorithm
20 or by visual inspection. In alternative aspects, the probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a nucleic acid sequence of the invention, or a subsequence thereof.

The invention provides an amplification primer pair for amplifying (e.g., by PCR)
25 a nucleic acid encoding a polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50, or more, consecutive
30 bases of the sequence, or about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more consecutive bases of the sequence. The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more

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residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more residues of the complementary strand of the first member.

5 The invention provides cellulase-encoding, e.g., endoglucanase-, cellobiohydrolase- and/or beta-glucosidase-encoding nucleic acids generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides cellulase-encoding, e.g., endoglucanase-, cellobiohydrolase- and/or beta-glucosidase-encoding nucleic acids generated by
10 amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid
15 from a library, e.g., a gene library, such as an environmental library.

 The invention provides methods of amplifying a nucleic acid encoding a polypeptide having a cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic
20 acid sequence of the invention, or fragments or subsequences thereof.

 The invention provides expression cassettes comprising a nucleic acid of the invention or a subsequence thereof. In one aspect, the expression cassette can comprise the nucleic acid that is operably linked to a promoter. The promoter can be a viral, bacterial, mammalian or plant promoter. In one aspect, the plant promoter can be a
25 potato, rice, corn, wheat, tobacco or barley promoter. The promoter can be a constitutive promoter. The constitutive promoter can comprise CaMV35S. In another aspect, the promoter can be an inducible promoter. In one aspect, the promoter can be a tissue-specific promoter or an environmentally regulated or a developmentally regulated promoter. Thus, the promoter can be, e.g., a seed-specific, a leaf-specific, a root-specific,
30 a stem-specific or an abscission-induced promoter. In one aspect, the expression cassette can further comprise a plant or plant virus expression vector.

 The invention provides cloning vehicles comprising an expression cassette (e.g., a vector) of the invention or a nucleic acid of the invention. The cloning vehicle can be a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an

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artificial chromosome. The viral vector can comprise an adenovirus vector, a retroviral vector or an adeno-associated viral vector. The cloning vehicle can comprise a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

5 The invention provides transformed cell comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention, or a cloning vehicle of the invention. In one aspect, the transformed cell can be a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell. In one aspect, the plant cell can be soybeans, rapeseed, oilseed, tomato, cane sugar, a cereal, a potato, wheat, rice,
10 corn, tobacco or barley cell.

 The invention provides transgenic non-human animals comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. In one aspect, the animal is a mouse, a rat, a pig, a goat or a sheep.

 The invention provides transgenic plants comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic plant
15 can be a cereal plant, a corn plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant or a tobacco plant.

 The invention provides transgenic seeds comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic seed
20 can be a cereal plant, a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a peanut or a tobacco plant seed.

 The invention provides an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides methods of inhibiting the
25 translation of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. In one aspect, the antisense oligonucleotide is between about 10 to 50,
30 about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length, e.g., 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more bases in length. The invention provides methods of inhibiting the translation of a cellulase enzyme, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme message in a cell comprising administering to the cell or expressing in the cell an

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antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention.

The invention provides double-stranded inhibitory RNA (RNAi, or RNA interference) molecules (including small interfering RNA, or siRNAs, for inhibiting transcription, and microRNAs, or miRNAs, for inhibiting translation) comprising a
5 subsequence of a sequence of the invention. In one aspect, the siRNA is between about 21 to 24 residues, or, about at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more duplex nucleotides in length. The invention provides methods of inhibiting the
10 expression of a cellulase enzyme, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (siRNA or miRNA), wherein the RNA comprises a subsequence of a sequence of the invention.

The invention provides isolated or recombinant polypeptides comprising an amino
15 acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary polypeptide or peptide of the invention over a
20 region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350 or more residues, or over the full length of the polypeptide. In one aspect, the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection. Exemplary polypeptide or peptide sequences of the invention include SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID
25 NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID
30 NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID

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NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID
NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID
NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID
NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
5 NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID
NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 and SEQ
ID NO:166 (see also Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing),
and subsequences thereof and variants thereof. Exemplary polypeptides also include
fragments of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 80, 85, 90, 95, 100, 150,
10 200, 250, 300, 350, 400, 450, 500, 550, 600 or more residues in length, or over the full
length of an enzyme. Polypeptide or peptide sequences of the invention include sequence
encoded by a nucleic acid of the invention. Polypeptide or peptide sequences of the
invention include polypeptides or peptides specifically bound by an antibody of the
invention (e.g., epitopes), or polypeptides or peptides that can generate an antibody of the
15 invention (e.g., an immunogen).

In one aspect, a polypeptide of the invention has at least one cellulase enzyme,
e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme
activity. In alternative aspects, a polynucleotide of the invention encodes a polypeptide
that has at least one cellulase enzyme, e.g., endoglucanase, cellobiohydrolase, mannanase
20 and/or beta-glucosidase enzyme activity.

In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase
and/or beta-glucosidase enzyme activity is thermostable. The polypeptide can retain a
cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase
enzyme activity under conditions comprising a temperature range of between about 1°C
25 to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C,
between about 25°C to about 37°C, between about 37°C to about 95°C, between about
55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about
95°C, or more. In another aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase,
mannanase and/or beta-glucosidase enzyme activity can be thermotolerant. The
30 polypeptide can retain a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase
and/or beta-glucosidase enzyme activity after exposure to a temperature in the range from
greater than 37°C to about 95°C, or in the range from greater than 55°C to about 85°C. In
one aspect, the polypeptide can retain a cellulase, e.g., endoglucanase, cellobiohydrolase,

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mannanase and/or beta-glucosidase enzyme activity after exposure to a temperature in the range from greater than 90°C to about 95°C at pH 4.5.

Another aspect of the invention provides an isolated or recombinant polypeptide or peptide comprising at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150 or more consecutive bases of a polypeptide or peptide sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto. The peptide can be, e.g., an immunogenic fragment, a motif (e.g., a binding site), a signal sequence, a prepro sequence or an active site.

The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity and a signal sequence, wherein the nucleic acid comprises a sequence of the invention. The signal sequence can be derived from another cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or a non-cellulase, e.g., non-endoglucanase, non-cellobiohydrolase and/or non-beta-glucosidase enzyme (a heterologous) enzyme. The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence of the invention. In one aspect, the invention provides an isolated or recombinant polypeptide comprising a polypeptide of the invention lacking all or part of a signal sequence. In one aspect, the isolated or recombinant polypeptide can comprise the polypeptide of the invention comprising a heterologous signal sequence, such as a heterologous cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme signal sequence or non-cellulase, e.g., non-endoglucanase, non-cellobiohydrolase and/or non-beta-glucosidase enzyme signal sequence.

In one aspect, the invention provides chimeric proteins comprising a first domain comprising a signal sequence of the invention and at least a second domain. The protein can be a fusion protein. The second domain can comprise an enzyme. The enzyme can be a non-enzyme.

The invention provides chimeric polypeptides comprising at least a first domain comprising signal peptide (SP), a prepro sequence and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal

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peptide (SP), prepro sequence and/ or catalytic domain (CD). In one aspect, the heterologous polypeptide or peptide is not a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. The heterologous polypeptide or peptide can be amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP), prepro sequence and/or catalytic domain (CD).

The invention provides isolated or recombinant nucleic acids encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP), a prepro domain and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro domain and/ or catalytic domain (CD).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of or comprising a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46 or 1 to 47, of a polypeptide of the invention, e.g., the exemplary SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ ID NO:166 (see Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing). In one aspect, the

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invention provides signal sequences comprising the first 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or more amino terminal residues of a polypeptide of the invention.

5 In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprises a specific activity at about 37°C in the range from about 1 to about 1200 units per milligram of protein, or, about 100 to about 1000 units per milligram of protein. In another aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprises a
10 specific activity from about 100 to about 1000 units per milligram of protein, or, from about 500 to about 750 units per milligram of protein. Alternatively, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprises a specific activity at 37°C in the range from about 1 to about 750 units per milligram of protein, or, from about 500 to about 1200 units per milligram of protein. In
15 one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprises a specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein, or, from about 750 to about 1000 units per milligram of protein. In another aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprises a
20 specific activity at 37°C in the range from about 1 to about 250 units per milligram of protein. Alternatively, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprises a specific activity at 37°C in the range from about 1 to about 100 units per milligram of protein.

 In another aspect, the thermotolerance comprises retention of at least half of the
25 specific activity of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme at 37°C after being heated to the elevated temperature. Alternatively, the thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 1200 units per milligram of protein, or, from about 500 to about 1000 units per milligram of protein, after being heated to the elevated temperature.
30 In another aspect, the thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein after being heated to the elevated temperature.

 The invention provides the isolated or recombinant polypeptide of the invention, wherein the polypeptide comprises at least one glycosylation site. In one aspect,

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glycosylation can be an N-linked glycosylation. In one aspect, the polypeptide can be glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

In one aspect, the polypeptide can retain cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity under conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4 or more acidic. In another aspect, the polypeptide can retain a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity under conditions comprising about pH 7, pH 7.5 pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11 or more basic pH. In one aspect, the polypeptide can retain a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity after exposure to conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4 or more acidic pH. In another aspect, the polypeptide can retain a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity after exposure to conditions comprising about pH 7, pH 7.5 pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11 or more basic pH.

In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention has activity at under alkaline conditions, e.g., the alkaline conditions of the gut, e.g., the small intestine. In one aspect, the polypeptide can retains activity after exposure to the acidic pH of the stomach.

The invention provides protein preparations comprising a polypeptide (including peptides) of the invention, wherein the protein preparation comprises a liquid, a solid or a gel. The invention provides heterodimers comprising a polypeptide of the invention and a second protein or domain. The second member of the heterodimer can be a different cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, a different enzyme or another protein. In one aspect, the second domain can be a polypeptide and the heterodimer can be a fusion protein. In one aspect, the second domain can be an epitope or a tag. In one aspect, the invention provides homodimers comprising a polypeptide of the invention.

The invention provides immobilized polypeptides (including peptides) having cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, wherein the immobilized polypeptide comprises a polypeptide of the invention, a polypeptide encoded by a nucleic acid of the invention, or a polypeptide comprising a polypeptide of the invention and a second domain. In one aspect, the

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polypeptide can be immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

The invention also provides arrays comprising an immobilized nucleic acid of the invention, including, e.g., probes of the invention. The invention also provides arrays
5 comprising an antibody of the invention.

The invention provides isolated or recombinant antibodies that specifically bind to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. These antibodies of the invention can be a monoclonal or a polyclonal antibody. The invention provides hybridomas comprising an antibody of the invention,
10 e.g., an antibody that specifically binds to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. The invention provides nucleic acids encoding these antibodies.

The invention provides method of isolating or identifying a polypeptide having cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase
15 enzyme activity comprising the steps of: (a) providing an antibody of the invention; (b) providing a sample comprising polypeptides; and (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity.

The invention provides methods of making an anti-cellulase, e.g., anti-endoglucanase, anti-cellobiohydrolase and/or anti-beta-glucosidase enzyme antibody comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-cellulase, e.g., anti-endoglucanase,
20 anti-cellobiohydrolase and/or anti-beta-glucosidase enzyme antibody. The invention provides methods of making an anti-cellulase, e.g., anti-endoglucanase, anti-cellobiohydrolase and/or anti-beta-glucosidase immune response (cellular or humoral) comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate
25 an immune response (cellular or humoral).

The invention provides methods of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid of the invention operably linked to a promoter; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide. In one

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aspect, the method can further comprise transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

The invention provides methods for identifying a polypeptide having cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme substrate; and (c) contacting the polypeptide or a fragment or variant thereof of step (a) with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity. In one aspect, the substrate is a cellulose-comprising compound.

The invention provides methods for identifying cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme substrate comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test substrate; and (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme substrate.

The invention provides methods of determining whether a test compound specifically binds to a polypeptide comprising the following steps: (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid comprises a nucleic acid of the invention, or, providing a polypeptide of the invention; (b) providing a test compound; (c) contacting the polypeptide with the test compound; and (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

The invention provides methods for identifying a modulator of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprising the following steps: (a) providing a polypeptide of the invention or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test compound;

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(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, wherein a change in the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity. In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity can be measured by providing a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product. A decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity. An increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity.

The invention provides computer systems comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence of the invention (e.g., a polypeptide or peptide encoded by a nucleic acid of the invention). In one aspect, the computer system can further comprise a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon. In another aspect, the sequence comparison algorithm comprises a computer program that indicates polymorphisms. In one aspect, the computer system can further comprise an identifier that identifies one or more features in said sequence. The invention provides computer readable media having stored thereon a polypeptide sequence or a nucleic acid sequence of the invention. The invention provides methods for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence of the

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invention; and (b) identifying one or more features in the sequence with the computer program. The invention provides methods for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first
5 sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) determining differences between the first sequence and the second sequence with the computer program. The step of determining differences between the first sequence and the second sequence can further comprise the step of identifying polymorphisms. In one aspect, the method can further comprise an identifier that identifies one or more
10 features in a sequence. In another aspect, the method can comprise reading the first sequence using a computer program and identifying one or more features in the sequence.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity from an environmental sample
15 comprising the steps of: (a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, wherein the primer pair is capable of amplifying a nucleic acid of the invention; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that
20 nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and, (c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity from an
25 environmental sample. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising an amplification primer sequence pair of the invention, e.g., having at least about 10 to 50 consecutive bases of a sequence of the invention.

The invention provides methods for isolating or recovering a nucleic acid
30 encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity from an environmental sample comprising the steps of: (a) providing a polynucleotide probe comprising a nucleic acid of the invention or a subsequence thereof; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the

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sample is accessible for hybridization to a polynucleotide probe of step (a); (c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and (d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity from an environmental sample. The environmental sample can comprise a water sample, a liquid sample, a soil sample, an air sample or a biological sample. In one aspect, the biological sample can be derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

The invention provides methods of generating a variant of a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity comprising the steps of: (a) providing a template nucleic acid comprising a nucleic acid of the invention; and (b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid. In one aspect, the method can further comprise expressing the variant nucleic acid to generate a variant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme polypeptide. The modifications, additions or deletions can be introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), Chromosomal Saturation Mutagenesis (CSM) or a combination thereof. In another aspect, the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

In one aspect, the method can be iteratively repeated until a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme having an altered or different activity or an altered or different stability from that of a polypeptide

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encoded by the template nucleic acid is produced. In one aspect, the variant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature. In another aspect, the variant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme polypeptide has increased glycosylation as compared to the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme encoded by a template nucleic acid. Alternatively, the variant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptide has a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity under a high temperature, wherein the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme encoded by the template nucleic acid is not active under the high temperature. In one aspect, the method can be iteratively repeated until a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme coding sequence having an altered codon usage from that of the template nucleic acid is produced. In another aspect, the method can be iteratively repeated until a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

20 The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity; the method comprising the following steps: (a)

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providing a nucleic acid of the invention; and, (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme.

5 The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-
10 glucosidase enzyme polypeptide; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in
15 genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

 The invention provides methods for modifying a codon in a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity to decrease its expression in a host cell, the
20 method comprising the following steps: (a) providing a nucleic acid of the invention; and (b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon
25 under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell. In one aspect, the host cell can be a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

 The invention provides methods for producing a library of nucleic acids encoding a plurality of modified cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase
30 and/or beta-glucosidase enzyme active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps: (a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises

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a sequence that hybridizes under stringent conditions to a nucleic acid of the invention, and the nucleic acid encodes a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme active site or a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme substrate binding site; (b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and, (c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme active sites or substrate binding sites. In one aspect, the method comprises mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, and a combination thereof. In another aspect, the method comprises mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

The invention provides methods for making a small molecule comprising the following steps: (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme encoded by a nucleic acid of the invention; (b) providing a substrate for at least one of the enzymes of step (a); and (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions. The invention provides methods for modifying a small molecule comprising the following steps: (a) providing a cellulase, e.g.,

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endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, wherein the enzyme comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention, or a subsequence thereof; (b) providing a small molecule; and (c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, thereby modifying a small molecule by a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymatic reaction. In one aspect, the method can comprise a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. In one aspect, the method can comprise a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions. In another aspect, the method can further comprise the step of testing the library to determine if a particular modified small molecule that exhibits a desired activity is present within the library. The step of testing the library can further comprise the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

The invention provides methods for determining a functional fragment of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme comprising the steps of: (a) providing a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, wherein the enzyme comprises a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, or a subsequence thereof; and (b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, thereby determining a functional fragment of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-

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glucosidase enzyme activity is measured by providing a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

The invention provides methods for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps: (a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid of the invention; (b) culturing the modified cell to generate a plurality of modified cells; (c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and, (d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis. In one aspect, the genetic composition of the cell can be modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene. In one aspect, the method can further comprise selecting a cell comprising a newly engineered phenotype. In another aspect, the method can comprise culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

The invention provides methods of increasing thermotolerance or thermostability of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme polypeptide, the method comprising glycosylating a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme polypeptide, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide of the invention; or a polypeptide encoded by a nucleic acid sequence of the invention, thereby increasing the thermotolerance or thermostability of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptide. In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme specific activity can be thermostable or thermotolerant at a temperature in the range from greater than about 37°C to about 95°C.

The invention provides methods for overexpressing a recombinant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptide in a cell comprising expressing a vector comprising a nucleic acid comprising a nucleic acid of the invention or a nucleic acid sequence of the invention, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual

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inspection, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The invention provides methods of making a transgenic plant comprising the following steps: (a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a nucleic acid sequence of the invention, thereby producing a transformed plant cell; and (b) producing a transgenic plant from the transformed cell. In one aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts. In another aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment. Alternatively, the step (a) can further comprise introducing the heterologous nucleic acid sequence into the plant cell DNA using an *Agrobacterium tumefaciens* host. In one aspect, the plant cell can be a cane sugar, beet, soybean, tomato, potato, corn, rice, wheat, tobacco or barley cell.

The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a nucleic acid of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell. The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

The invention provides feeds or foods comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the invention provides a food, feed, a liquid, e.g., a beverage (such as a fruit juice or a beer), a bread or a dough or a bread product, or a beverage precursor (e.g., a wort), comprising a polypeptide of the invention. The invention provides food or nutritional supplements for an animal comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention.

In one aspect, the polypeptide in the food or nutritional supplement can be glycosylated. The invention provides edible enzyme delivery matrices comprising a

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polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention. In one aspect, the delivery matrix comprises a pellet. In one aspect, the polypeptide can be glycosylated. In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity is thermotolerant. In another aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity is thermostable.

The invention provides a food, a feed or a nutritional supplement comprising a polypeptide of the invention. The invention provides methods for utilizing a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme as a nutritional supplement in an animal diet, the method comprising: preparing a nutritional supplement containing a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme comprising at least thirty contiguous amino acids of a polypeptide of the invention; and administering the nutritional supplement to an animal. The animal can be a human, a ruminant or a monogastric animal. The cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme can be prepared by expression of a polynucleotide encoding the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal. The organism can be selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

The invention provides edible enzyme delivery matrix comprising a thermostable recombinant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, e.g., a polypeptide of the invention. The invention provides methods for delivering a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme supplement to an animal, the method comprising: preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, wherein the pellets readily disperse the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal. The recombinant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme can comprise a polypeptide of the invention. The cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme can be glycosylated to

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provide thermostability at pelletizing conditions. The delivery matrix can be formed by pelletizing a mixture comprising a grain germ and a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. The pelletizing conditions can include application of steam. The pelletizing conditions can comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

In one aspect, invention provides a pharmaceutical composition comprising a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the pharmaceutical composition acts as a digestive aid.

In certain aspects, a cellulose-containing compound is contacted a polypeptide of the invention having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity at a pH in the range of between about pH 3.0 to 9.0, 10.0, 11.0 or more. In other aspects, a cellulose-containing compound is contacted with the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme at a temperature of about 55°C, 60°C, 65°C, 70°C, 75°C, 80°C, 85°C, 90°C, or more.

The details of one or more aspects of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

All publications, patents, patent applications, GenBank sequences and ATCC deposits, cited herein are hereby expressly incorporated by reference for all purposes.

BRIEF DESCRIPTION OF DRAWINGS

The following drawings are illustrative of aspects of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 is a block diagram of a computer system.

Figure 2 is a flow diagram illustrating one aspect of a process for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

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Figure 3 is a flow diagram illustrating one aspect of a process in a computer for determining whether two sequences are homologous.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence.

5 Figure 5 is an illustration of the structure of cellobiose.

Figures 6 and 7 illustrate the results of a TLC analysis of reaction products from cellohexaose, as discussed in detail in Example 1, below.

10 Figure 8 illustrates in graph form data showing the release of cellobiose from PASC by the exemplary enzyme 22/22a (a CBH) of the invention, as discussed in detail in Example 2, below.

Figure 9 illustrates in graph form data showing the release of cellobiose from AVICEL[®] MCC by the exemplary enzyme 22/22a (a CBH) of the invention, as discussed in detail in Example 2, below.

15 Figure 10 illustrates in graphic form data showing a typical GIGAMATRIX[™] breakout, where active clones expressing enzyme able to hydrolyze methylumbelliferyl cellobioside are identified, as discussed in detail in Example 4, below.

Figure 11 illustrates in graph form data showing the activity of selected enzymes against phosphoric acid-swollen cellulose (PASC) by capillary electrophoresis (CE) analysis, as discussed in detail in Example 4, below.

20 Figure 12 illustrates in graph form data from assays of an exemplary enzyme of the invention and subclone variants in AVICEL[®] Microcrystalline Cellulose (MCC), where the reaction products were analyzed by the BCA reducing sugar assay, as discussed in detail in Example 4, below.

25 Figure 13 illustrates in graph form data from primary GSSM screening assays, as discussed in detail in Example 4, below.

Figure 14 illustrates in graph form data from secondary GSSM screening assays, as discussed in detail in Example 4, below.

Figure 15 illustrates in graph form data from mixed, or “blended”, GSSM screening assays, as discussed in detail in Example 4, below.

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Like reference symbols in the various drawings indicate like elements.

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DETAILED DESCRIPTION

The invention provides polypeptides with cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. The invention also provides cellulase enzymes, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, polynucleotides encoding these enzymes, the use of such polynucleotides and polypeptides.

In one aspect, the invention provides a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase, with an increased catalytic rate, improving the process of substrate hydrolysis. This increased efficiency in catalytic rate leads to an increased efficiency in producing sugars that will subsequently be used by microorganisms for ethanol production. In one aspect, microorganisms generating enzyme of the invention are used with ethanol-producing microorganisms. Thus, the invention provides methods for ethanol production and making "clean fuels" based on ethanol, e.g., for transportation using bioethanol.

In one aspect the invention provides compositions (e.g., enzyme preparations, feeds, drugs, dietary supplements) comprising the enzymes, polypeptides or polynucleotides of the invention. These compositions can be formulated in a variety of forms, e.g., as liquids, gels, pills, tablets, sprays, powders, food, feed pellets or encapsulated forms, including nanoencapsulated forms.

Assays for measuring cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, e.g., for determining if a polypeptide has cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, are well known in the art and are within the scope of the invention; see, e.g., Baker WL, Panow A, Estimation of cellulase activity using a glucose-oxidase-Cu(II) reducing assay for glucose, J Biochem Biophys Methods. 1991 Dec, 23(4):265-73; Sharrock KR, Cellulase assay methods: a review, J Biochem Biophys Methods. 1988 Oct, 17(2):81-105; Carder JH, Detection and quantitation of cellulase by Congo red staining of substrates in a cup-plate diffusion assay, Anal Biochem. 1986 Feb 15, 153(1):75-9; Canevascini G., A cellulase assay coupled to cellobiose dehydrogenase, Anal Biochem. 1985 Jun, 147(2):419-27; Huang JS, Tang J, Sensitive assay for cellulase and dextranase. Anal Biochem. 1976 Jun, 73(2):369-77.

The pH of reaction conditions utilized by the invention is another variable parameter for which the invention provides. In certain aspects, the pH of the reaction is

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conducted in the range of about 3.0 to about 9.0. In other aspects, the pH is about 4.5 or the pH is about 7.5 or the pH is about 9. Reaction conditions conducted under alkaline conditions also can be advantageous, e.g., in some industrial or pharmaceutical applications of enzymes of the invention.

5 The invention provides cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptides of the invention in a variety of forms and formulations. In the methods of the invention, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptides of the invention are used in a variety of forms and formulations. For example, purified cellulase, e.g.,
10 endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptides can be used in enzyme preparations deployed in bioethanol production or in pharmaceutical or dietary aid applications. Alternatively, the enzymes of the invention can be used directly in processes to produce bioethanol, make clean fuels, process biowastes, process foods, liquids or feeds, and the like.

15 Alternatively, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptides of the invention can be expressed in a microorganism using procedures known in the art. In other aspects, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptides of the invention can be immobilized on a solid support prior to use in the methods of the
20 invention. Methods for immobilizing enzymes on solid supports are commonly known in the art, for example J. Mol. Cat. B: Enzymatic 6 (1999) 29-39; Chivata et al. Biocatalysis: Immobilized cells and enzymes, J Mol. Cat. 37 (1986) 1-24; Sharma et al., Immobilized Biomaterials Techniques and Applications, Angew. Chem. Int. Ed. Engl. 21 (1982) 837-54; Laskin (Ed.), Enzymes and Immobilized Cells in Biotechnology.

25 Nucleic Acids, Probes and Inhibitory Molecules

 The invention provides isolated and recombinant nucleic acids, e.g., see Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing; nucleic acids encoding polypeptides, including the exemplary polynucleotide sequences of the invention, e.g., see Table 1 and Sequence Listing; including expression cassettes such as expression
30 vectors and various cloning vehicles comprising nucleic acids of the invention. The invention also includes methods for discovering, identifying or isolated new cellulases, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptide sequences using the nucleic acids of the invention. The invention also includes methods for inhibiting the expression of cellulase, e.g., endoglucanase, cellobiohydrolase,

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mannanase and/or beta-glucosidase encoding genes and transcripts using the nucleic acids of the invention.

Also provided are methods for modifying the nucleic acids of the invention, including making variants of nucleic acids of the invention, by, e.g., synthetic ligation
5 reassembly, optimized directed evolution system and/or saturation mutagenesis such as gene site saturation mutagenesis (GSSM). The term “saturation mutagenesis”, Gene Site Saturation Mutagenesis, or “GSSM” includes a method that uses degenerate oligonucleotide primers to introduce point mutations into a polynucleotide, as described in detail, below. The term “optimized directed evolution system” or “optimized directed
10 evolution” includes a method for reassembling fragments of related nucleic acid sequences, e.g., related genes, and explained in detail, below. The term “synthetic ligation reassembly” or “SLR” includes a method of ligating oligonucleotide fragments in a non-stochastic fashion, and explained in detail, below. The term “variant” refers to polynucleotides or polypeptides of the invention modified at one or more base pairs,
15 codons, introns, exons, or amino acid residues (respectively) yet still retain the biological activity of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase of the invention. Variants can be produced by any number of means included methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette
20 mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, GSSM and any combination thereof.

The nucleic acids of the invention can be made, isolated and/or manipulated by, e.g., cloning and expression of cDNA libraries, amplification of message or genomic DNA by PCR, and the like. For example, exemplary sequences of the invention were
25 initially derived from environmental sources. Thus, in one aspect, the invention provides cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme-encoding nucleic acids, and the polypeptides encoded by them, having a common novelty in that they are derived from a common source, e.g., an environmental, mixed culture, or a bacterial source.

30 In practicing the methods of the invention, homologous genes can be modified by manipulating a template nucleic acid, as described herein. The invention can be practiced in conjunction with any method or protocol or device known in the art, which are well described in the scientific and patent literature.

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The phrases “nucleic acid” or “nucleic acid sequence” as used herein refer to an oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense (complementary) strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin. The phrases “nucleic acid” or “nucleic acid sequence” includes oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or RNA (e.g., mRNA, rRNA, tRNA, iRNA) of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin, including, e.g., iRNA, ribonucleoproteins (e.g., e.g., double stranded iRNAs, e.g., iRNPs). The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogues of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones, see e.g., Mata (1997) Toxicol. Appl. Pharmacol. 144:189-197; Strauss-Soukup (1997) Biochemistry 36:8692-8698; Samstag (1996) Antisense Nucleic Acid Drug Dev 6:153-156. “Oligonucleotide” includes either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide can ligate to a fragment that has not been dephosphorylated.

A “coding sequence of” or a “nucleotide sequence encoding” a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences. The term “gene” means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as, where applicable, intervening sequences (introns) between individual coding segments (exons). A promoter sequence is “operably linked to” a coding sequence when RNA polymerase which initiates transcription at the promoter will transcribe the coding sequence into mRNA. “Operably linked” as used herein refers to a functional relationship between two or more nucleic acid (e.g., DNA) segments. It can refer to the functional relationship of transcriptional regulatory sequence to a transcribed sequence. For example, a promoter is operably linked to a coding sequence, such as a nucleic acid of the invention, if it stimulates or modulates the transcription of the coding

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sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, i.e., they are cis-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be physically
5 contiguous or located in close proximity to the coding sequences whose transcription they enhance.

The term "expression cassette" as used herein refers to a nucleotide sequence which is capable of affecting expression of a structural gene (i.e., a protein coding sequence, such as a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or
10 beta-glucosidase enzyme of the invention) in a host compatible with such sequences. Expression cassettes include at least a promoter operably linked with the polypeptide coding sequence; and, optionally, with other sequences, e.g., transcription termination signals. Additional factors necessary or helpful in effecting expression may also be used, e.g., enhancers, alpha-factors. Thus, expression cassettes also include plasmids,
15 expression vectors, recombinant viruses, any form of recombinant "naked DNA" vector, and the like. A "vector" comprises a nucleic acid which can infect, transfect, transiently or permanently transduce a cell. It will be recognized that a vector can be a naked nucleic acid, or a nucleic acid complexed with protein or lipid. The vector optionally comprises viral or bacterial nucleic acids and/or proteins, and/or membranes (e.g., a cell membrane,
20 a viral lipid envelope, etc.). Vectors include, but are not limited to replicons (e.g., RNA replicons, bacteriophages) to which fragments of DNA may be attached and become replicated. Vectors thus include, but are not limited to RNA, autonomous self-replicating circular or linear DNA or RNA (e.g., plasmids, viruses, and the like, see, e.g., U.S. Patent No. 5,217,879), and include both the expression and non-expression plasmids. Where a
25 recombinant microorganism or cell culture is described as hosting an "expression vector" this includes both extra-chromosomal circular and linear DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome.

30 As used herein, the term "recombinant" encompasses nucleic acids adjacent to a "backbone" nucleic acid to which it is not adjacent in its natural environment. In one aspect, to be "enriched" the nucleic acids will represent about 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the invention include nucleic acids such as expression vectors,

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self-replicating nucleic acids, viruses, integrating nucleic acids and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. In one aspect, the enriched nucleic acids represent about 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In one aspect, the enriched nucleic acids represent about 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a one aspect, the enriched nucleic acids represent about 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

One aspect of the invention is an isolated or recombinant nucleic acid comprising one of the sequences of the invention, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive bases of a nucleic acid of the invention. The isolated or recombinant nucleic acids may comprise DNA, including cDNA, genomic DNA and synthetic DNA. The DNA may be double-stranded or single-stranded and if single stranded may be the coding strand or non-coding (anti-sense) strand. Alternatively, the isolated or recombinant nucleic acids comprise RNA.

The isolated or recombinant nucleic acids of the invention may be used to prepare one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention. Accordingly, another aspect of the invention is an isolated or recombinant nucleic acid which encodes one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention. The coding sequences of these nucleic acids may be identical to one of the coding sequences of one of the nucleic acids of the invention or may be different coding sequences which encode one of the of the invention having at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention, as a result of the redundancy or degeneracy of the genetic code. The genetic code is well known to those of skill in the art and can be obtained, e.g., on page 214 of B. Lewin, Genes VI, Oxford University Press, 1997.

The nucleic acids encoding polypeptides of the invention include but are not limited to: the coding sequence of a nucleic acid of the invention and additional coding sequences, such as leader sequences or proprotein sequences and non-coding sequences, such as introns or non-coding sequences 5' and/or 3' of the coding sequence. Thus, as used herein, the term "polynucleotide encoding a polypeptide" encompasses a

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polynucleotide which includes the coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

In one aspect, the nucleic acid sequences of the invention are mutagenized using conventional techniques, such as site directed mutagenesis, or other techniques familiar to those skilled in the art, to introduce silent changes into the polynucleotides of the invention. As used herein, "silent changes" include, for example, changes which do not alter the amino acid sequence encoded by the polynucleotide. Such changes may be desirable in order to increase the level of the polypeptide produced by host cells containing a vector encoding the polypeptide by introducing codons or codon pairs which occur frequently in the host organism.

The invention also relates to polynucleotides which have nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptides of the invention. Such nucleotide changes may be introduced using techniques such as site directed mutagenesis, random chemical mutagenesis, exonuclease III deletion and other recombinant DNA techniques. Alternatively, such nucleotide changes may be naturally occurring allelic variants which are isolated by identifying nucleic acids which specifically hybridize to probes comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention (or the sequences complementary thereto) under conditions of high, moderate, or low stringency as provided herein.

General Techniques

The nucleic acids used to practice this invention, whether RNA, siRNA, miRNA, antisense nucleic acid, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed/generated recombinantly. Recombinant polypeptides (e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes) generated from these nucleic acids can be individually isolated or cloned and tested for a desired activity. Any recombinant expression system can be used, including bacterial, mammalian, yeast, insect or plant cell expression systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Adams (1983) J. Am. Chem. Soc. 105:661; Belousov (1997) Nucleic Acids Res. 25:3440-3444; Frenkel (1995) Free Radic. Biol. Med. 19:373-380; Blommers (1994) Biochemistry 33:7886-7896; Narang (1979)

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Meth. Enzymol. 68:90; Brown (1979) Meth. Enzymol. 68:109; Beaucage (1981) Tetra. Lett. 22:1859; U.S. Patent No. 4,458,066.

Techniques for the manipulation of nucleic acids, such as, e.g., subcloning, labeling probes (e.g., random-primer labeling using Klenow polymerase, nick translation, amplification), sequencing, hybridization and the like are well described in the scientific and patent literature, see, e.g., Sambrook, ed., MOLECULAR CLONING: A LABORATORY MANUAL (2ND ED.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY: HYBRIDIZATION WITH NUCLEIC ACID PROBES, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Another useful means of obtaining and manipulating nucleic acids used to practice the methods of the invention is to clone from genomic samples, and, if desired, screen and re-clone inserts isolated or amplified from, e.g., genomic clones or cDNA clones. Sources of nucleic acid used in the methods of the invention include genomic or cDNA libraries contained in, e.g., mammalian artificial chromosomes (MACs), see, e.g., U.S. Patent Nos. 5,721,118; 6,025,155; human artificial chromosomes, see, e.g., Rosenfeld (1997) Nat. Genet. 15:333-335; yeast artificial chromosomes (YAC); bacterial artificial chromosomes (BAC); P1 artificial chromosomes, see, e.g., Woon (1998) Genomics 50:306-316; P1-derived vectors (PACs), see, e.g., Kern (1997) Biotechniques 23:120-124; cosmids, recombinant viruses, phages or plasmids.

In one aspect, a nucleic acid encoding a polypeptide of the invention is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof.

The invention provides fusion proteins and nucleic acids encoding them. A polypeptide of the invention can be fused to a heterologous peptide or polypeptide, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification. Peptides and polypeptides of the invention can also be synthesized and expressed as fusion proteins with one or more additional domains linked thereto for, e.g., producing a more immunogenic peptide, to more readily isolate a recombinantly synthesized peptide, to identify and isolate antibodies and antibody-expressing B cells, and the like. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts and histidine-

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tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequences such as Factor Xa or enterokinase (Invitrogen, San Diego CA) between a purification domain and the motif-comprising peptide or polypeptide to facilitate purification. For example, an expression vector can include an epitope-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin and an enterokinase cleavage site (see e.g., Williams (1995) Biochemistry 34:1787-1797; Dobeli (1998) Protein Expr. Purif. 12:404-414). The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the epitope from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, see e.g., Kroll (1993) DNA Cell. Biol., 12:441-53.

Transcriptional and translational control sequences

The invention provides nucleic acid (e.g., DNA) sequences of the invention operatively linked to expression (e.g., transcriptional or translational) control sequence(s), e.g., promoters or enhancers, to direct or modulate RNA synthesis/ expression. The expression control sequence can be in an expression vector. Exemplary bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, PL and trp. Exemplary eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein I.

As used herein, the term “promoter” includes all sequences capable of driving transcription of a coding sequence in a cell, e.g., a plant or animal cell. Thus, promoters used in the constructs of the invention include *cis*-acting transcriptional control elements and regulatory sequences that are involved in regulating or modulating the timing and/or rate of transcription of a gene. For example, a promoter can be a *cis*-acting transcriptional control element, including an enhancer, a promoter, a transcription terminator, an origin of replication, a chromosomal integration sequence, 5' and 3' untranslated regions, or an intronic sequence, which are involved in transcriptional regulation. These *cis*-acting sequences can interact with proteins or other biomolecules to carry out (turn on/off, regulate, modulate, etc.) transcription. “Constitutive” promoters are those that drive expression continuously under most environmental conditions and states of development or cell differentiation. “Inducible” or “regulatable” promoters direct expression of the nucleic acid of the invention under the influence of environmental

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conditions or developmental conditions. Examples of environmental conditions that may affect transcription by inducible promoters include anaerobic conditions, elevated temperature, drought, or the presence of light.

“Tissue-specific” promoters are transcriptional control elements that are only active in particular cells or tissues or organs, e.g., in plants or animals. Tissue-specific regulation may be achieved by certain intrinsic factors which ensure that genes encoding proteins specific to a given tissue are expressed. Such factors are known to exist in mammals and plants so as to allow for specific tissues to develop.

Promoters suitable for expressing a polypeptide in bacteria include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the T3 promoter, the T7 promoter, the *gpt* promoter, the lambda PR promoter, the lambda PL promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), and the acid phosphatase promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses, and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used. Promoters suitable for expressing the polypeptide or fragment thereof in bacteria include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the T3 promoter, the T7 promoter, the *gpt* promoter, the lambda P_R promoter, the lambda P_L promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK) and the acid phosphatase promoter. Fungal promoters include the α -factor promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used.

Tissue-Specific Plant Promoters

The invention provides expression cassettes that can be expressed in a tissue-specific manner, e.g., that can express a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention in a tissue-specific manner. The invention also provides plants or seeds that express a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention in a tissue-specific manner. The tissue-specificity can be seed specific, stem specific, leaf specific, root specific, fruit specific and the like.

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The term "plant" includes whole plants, plant parts (e.g., leaves, stems, flowers, roots, etc.), plant protoplasts, seeds and plant cells and progeny of same. The class of plants which can be used in the method of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), as well as gymnosperms. It includes plants of a variety of ploidy levels, including polyploid, diploid, haploid and hemizygous states. As used herein, the term "transgenic plant" includes plants or plant cells into which a heterologous nucleic acid sequence has been inserted, e.g., the nucleic acids and various recombinant constructs (e.g., expression cassettes) of the invention.

In one aspect, a constitutive promoter such as the CaMV 35S promoter can be used for expression in specific parts of the plant or seed or throughout the plant. For example, for overexpression, a plant promoter fragment can be employed which will direct expression of a nucleic acid in some or all tissues of a plant, e.g., a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes known to those of skill. Such genes include, e.g., *ACT11* from *Arabidopsis* (Huang (1996) *Plant Mol. Biol.* 33:125-139); *Cat3* from *Arabidopsis* (GenBank No. U43147, Zhong (1996) *Mol. Gen. Genet.* 251:196-203); the gene encoding stearyl-acyl carrier protein desaturase from *Brassica napus* (Genbank No. X74782, Solocombe (1994) *Plant Physiol.* 104:1167-1176); *GPc1* from maize (GenBank No. X15596; Martinez (1989) *J. Mol. Biol.* 208:551-565); the *Gpc2* from maize (GenBank No. U45855, Manjunath (1997) *Plant Mol. Biol.* 33:97-112); plant promoters described in U.S. Patent Nos. 4,962,028; 5,633,440.

The invention uses tissue-specific or constitutive promoters derived from viruses which can include, e.g., the tobamovirus subgenomic promoter (Kumagai (1995) *Proc. Natl. Acad. Sci. USA* 92:1679-1683; the rice tungro bacilliform virus (RTBV), which replicates only in phloem cells in infected rice plants, with its promoter which drives strong phloem-specific reporter gene expression; the cassava vein mosaic virus (CVMV) promoter, with highest activity in vascular elements, in leaf mesophyll cells, and in root tips (Verdaguer (1996) *Plant Mol. Biol.* 31:1129-1139).

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In one aspect, the plant promoter directs expression of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme-expressing nucleic acid in a specific tissue, organ or cell type (*i.e.* tissue-specific promoters) or may be otherwise under more precise environmental or developmental control or under the control of an inducible promoter. Examples of environmental conditions that may affect transcription include anaerobic conditions, elevated temperature, the presence of light, or sprayed with chemicals/hormones. For example, the invention incorporates the drought-inducible promoter of maize (Busk (1997) *supra*); the cold, drought, and high salt inducible promoter from potato (Kirch (1997) *Plant Mol. Biol.* 33:897 909).

In one aspect, tissue-specific promoters promote transcription only within a certain time frame of developmental stage within that tissue. See, e.g., Blazquez (1998) *Plant Cell* 10:791-800, characterizing the *Arabidopsis* LEAFY gene promoter. See also Cardon (1997) *Plant J* 12:367-77, describing the transcription factor SPL3, which recognizes a conserved sequence motif in the promoter region of the *A. thaliana* floral meristem identity gene AP1; and Mandel (1995) *Plant Molecular Biology*, Vol. 29, pp 995-1004, describing the meristem promoter eIF4. Tissue specific promoters which are active throughout the life cycle of a particular tissue can be used. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily only in cotton fiber cells. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily during the stages of cotton fiber cell elongation, e.g., as described by Rinehart (1996) *supra*. The nucleic acids can be operably linked to the Fbl2A gene promoter to be preferentially expressed in cotton fiber cells (*Ibid*). See also, John (1997) *Proc. Natl. Acad. Sci. USA* 89:5769-5773; John, et al., U.S. Patent Nos. 5,608,148 and 5,602,321, describing cotton fiber-specific promoters and methods for the construction of transgenic cotton plants. Root-specific promoters may also be used to express the nucleic acids of the invention. Examples of root-specific promoters include the promoter from the alcohol dehydrogenase gene (DeLisle (1990) *Int. Rev. Cytol.* 123:39-60). Other promoters that can be used to express the nucleic acids of the invention include, e.g., ovule-specific, embryo-specific, endosperm-specific, integument-specific, seed coat-specific promoters, or some combination thereof; a leaf-specific promoter (see, e.g., Busk (1997) *Plant J.* 11:1285 1295, describing a leaf-specific promoter in maize); the ORF13 promoter from *Agrobacterium rhizogenes* (which exhibits high activity in roots, see, e.g., Hansen (1997) *supra*); a maize pollen specific promoter

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(see, e.g., Guerrero (1990) Mol. Gen. Genet. 224:161-168); a tomato promoter active during fruit ripening, senescence and abscission of leaves and, to a lesser extent, of flowers can be used (see, e.g., Blume (1997) Plant J. 12:731-746); a pistil-specific promoter from the potato SK2 gene (see, e.g., Ficker (1997) Plant Mol. Biol. 35:425-431); the Blec4 gene from pea, which is active in epidermal tissue of vegetative and floral shoot apices of transgenic alfalfa making it a useful tool to target the expression of foreign genes to the epidermal layer of actively growing shoots or fibers; the ovule-specific BEL1 gene (see, e.g., Reiser (1995) Cell 83:735-742, GenBank No. U39944); and/or, the promoter in Klee, U.S. Patent No. 5,589,583, describing a plant promoter region is capable of conferring high levels of transcription in meristematic tissue and/or rapidly dividing cells.

In one aspect, plant promoters which are inducible upon exposure to plant hormones, such as auxins, are used to express the nucleic acids of the invention. For example, the invention can use the auxin-response elements E1 promoter fragment (AuxREs) in the soybean (*Glycine max* L.) (Liu (1997) Plant Physiol. 115:397-407); the auxin-responsive *Arabidopsis* GST6 promoter (also responsive to salicylic acid and hydrogen peroxide) (Chen (1996) Plant J. 10: 955-966); the auxin-inducible parC promoter from tobacco (Sakai (1996) 37:906-913); a plant biotin response element (Streit (1997) Mol. Plant Microbe Interact. 10:933-937); and, the promoter responsive to the stress hormone abscisic acid (Sheen (1996) Science 274:1900-1902).

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents which can be applied to the plant, such as herbicides or antibiotics. For example, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, can be used (De Veylder (1997) Plant Cell Physiol. 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequence can be under the control of, e.g., a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) Plant J. 11:465-473); or, a salicylic acid-responsive element (Stange (1997) Plant J. 11:1315-1324). Using chemically- (e.g., hormone- or pesticide-) induced promoters, i.e., promoter responsive to a chemical which can be applied to the transgenic plant in the field, expression of a polypeptide of the invention can be induced at a particular stage of development of the plant. Thus, the invention also provides for transgenic plants containing an inducible gene encoding for

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polypeptides of the invention whose host range is limited to target plant species, such as corn, rice, barley, soybean, tomato, wheat, potato or other crops, inducible at any stage of development of the crop.

One of skill will recognize that a tissue-specific plant promoter may drive
5 expression of operably linked sequences in tissues other than the target tissue. Thus, in one aspect, a tissue-specific promoter is one that drives expression preferentially in the target tissue or cell type, but may also lead to some expression in other tissues as well.

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents. These reagents include, e.g.,
10 herbicides, synthetic auxins, or antibiotics which can be applied, e.g., sprayed, onto transgenic plants. Inducible expression of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme-producing nucleic acids of the invention will allow the grower to select plants with the optimal cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme expression
15 and/or activity. The development of plant parts can thus controlled. In this way the invention provides the means to facilitate the harvesting of plants and plant parts. For example, in various embodiments, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, is used (De Veylder (1997) Plant Cell Physiol. 38:568-577); application of different herbicide safeners induces distinct gene expression
20 patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequences of the invention are also under the control of a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) Plant J. 11:465-473); or, a salicylic acid-responsive element (Stange (1997) Plant J. 11:1315-1324).

25 In some aspects, proper polypeptide expression may require polyadenylation region at the 3'-end of the coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant (or animal or other) genes, or from genes in the *Agrobacterium* T-DNA.

Expression vectors and cloning vehicles

30 The invention provides expression vectors and cloning vehicles comprising nucleic acids of the invention, e.g., sequences encoding the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention. Expression vectors and cloning vehicles of the invention can comprise viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial

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chromosomes, viral DNA (e.g., vaccinia, adenovirus, fowl pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, *Aspergillus* and yeast). Vectors of the invention can include chromosomal, non-
5 chromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Exemplary vectors are include: bacterial: pQETM vectors (Qiagen), pBLUESCRIPTTM plasmids, pNH vectors, (lambda-ZAP vectors (Stratagene); ptrc99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene), pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia).
10 However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention. "Plasmids" can be commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. Equivalent plasmids to those described herein are known in the art
15 and will be apparent to the ordinarily skilled artisan.

The expression vector can comprise a promoter, a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Mammalian expression vectors can comprise an origin of replication, any necessary ribosome binding sites, a
20 polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

In one aspect, the expression vectors contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include
25 genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli*, and the *S. cerevisiae* TRP1 gene. Promoter regions can be selected from any desired gene using chloramphenicol transferase (CAT) vectors or other vectors with selectable
30 markers.

In one aspect, vectors for expressing the polypeptide or fragment thereof in eukaryotic cells contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA that can be from about 10 to about 300 bp in length. They can act on a promoter to increase its transcription. Exemplary enhancers include the SV40 enhancer

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on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and the adenovirus enhancers.

A nucleic acid sequence can be inserted into a vector by a variety of procedures. In general, the sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. A variety of cloning techniques are known in the art, e.g., as described in Ausubel and Sambrook. Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector can be in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, non-chromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by, e.g., Sambrook.

Particular bacterial vectors which can be used include the commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017), pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden), GEM1 (Promega Biotec, Madison, WI, USA) pQE70, pQE60, pQE-9 (Qiagen), pD10, psiX174 pBLUESCRIPT II KS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK233-3, DR540, pRIT5 (Pharmacia), pKK232-8 and pCM7. Particular eukaryotic vectors include pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other vector may be used as long as it is replicable and viable in the host cell.

The nucleic acids of the invention can be expressed in expression cassettes, vectors or viruses and transiently or stably expressed in plant cells and seeds. One exemplary transient expression system uses episomal expression systems, e.g., cauliflower mosaic virus (CaMV) viral RNA generated in the nucleus by transcription of an episomal mini-chromosome containing supercoiled DNA, see, e.g., Covey (1990) Proc. Natl. Acad. Sci. USA 87:1633-1637. Alternatively, coding sequences, i.e., all or sub-fragments of sequences of the invention can be inserted into a plant host cell genome becoming an integral part of the host chromosomal DNA. Sense or antisense transcripts can be expressed in this manner. A vector comprising the sequences (e.g., promoters or coding regions) from nucleic acids of the invention can comprise a marker gene that

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confers a selectable phenotype on a plant cell or a seed. For example, the marker may encode biocide resistance, e.g., antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

5 Expression vectors capable of expressing nucleic acids and proteins in plants are well known in the art, and can include, e.g., vectors from *Agrobacterium* spp., potato virus X (see, e.g., Angell (1997) EMBO J. 16:3675-3684), tobacco mosaic virus (see, e.g., Casper (1996) Gene 173:69-73), tomato bushy stunt virus (see, e.g., Hillman (1989) Virology 169:42-50), tobacco etch virus (see, e.g., Dolja (1997) Virology 234:243-252),
10 bean golden mosaic virus (see, e.g., Morinaga (1993) Microbiol Immunol. 37:471-476), cauliflower mosaic virus (see, e.g., Cecchini (1997) Mol. Plant Microbe Interact. 10:1094-1101), maize Ac/Ds transposable element (see, e.g., Rubin (1997) Mol. Cell. Biol. 17:6294-6302; Kunze (1996) Curr. Top. Microbiol. Immunol. 204:161-194), and the maize suppressor-mutator (Spm) transposable element (see, e.g., Schlappi (1996) Plant
15 Mol. Biol. 32:717-725); and derivatives thereof.

 In one aspect, the expression vector can have two replication systems to allow it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector can contain at least one sequence homologous
20 to the host cell genome. It can contain two homologous sequences which flank the expression construct. The integrating vector can be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

 Expression vectors of the invention may also include a selectable marker gene to
25 allow for the selection of bacterial strains that have been transformed, e.g., genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers can also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways.

 The DNA sequence in the expression vector is operatively linked to an appropriate
30 expression control sequence(s) (promoter) to direct RNA synthesis. Particular named bacterial promoters include *lacI*, *lacZ*, *T3*, *T7*, *gpt*, *lambda P_R*, *P_L* and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector

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also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using chloramphenicol transferase (CAT) vectors or other vectors with selectable markers. In addition, the expression vectors in one aspect contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Mammalian expression vectors may also comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells may also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA, usually from about 10 to about 300 bp in length that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin and the adenovirus enhancers.

In addition, the expression vectors can contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli* and the *S. cerevisiae TRP1* gene.

In some aspects, the nucleic acid encoding one of the polypeptides of the invention, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. In one aspect, the nucleic acid can encode a fusion polypeptide in which one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof is fused to heterologous peptides or polypeptides, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification.

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The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. A variety of cloning techniques are disclosed in Ausubel *et al.* Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. 1997 and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press (1989). Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector may be, for example, in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, nonchromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, N.Y., (1989).

Host cells and transformed cells

The invention also provides a transformed cell comprising a nucleic acid sequence of the invention, e.g., a sequence encoding a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention, or a vector of the invention. The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, such as bacterial cells, fungal cells, yeast cells, mammalian cells, insect cells, or plant cells. Exemplary bacterial cells include any species of *Streptomyces*, *Staphylococcus* or *Bacillus*, or the exemplary species *E. coli*, *Bacillus subtilis*, *Bacillus cereus*, *Salmonella typhimurium*. Exemplary insect cells include any species of *Spodoptera* or *Drosophila*, including *Drosophila S2* and *Spodoptera Sf9*. Exemplary animal cells include CHO, COS or Bowes melanoma or any mouse or human cell line. The selection of an appropriate host is within the abilities of those skilled in the art. Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature. See, e.g., Weising (1988) Ann. Rev. Genet. 22:421-477; U.S. Patent No. 5,750,870.

The vector can be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate

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transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

5 In one aspect, the nucleic acids or vectors of the invention are introduced into the cells for screening, thus, the nucleic acids enter the cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated by the targeted cell type. Exemplary methods include CaPO_4 precipitation, liposome fusion, lipofection (e.g., LIPOFECTIN™), electroporation, viral infection, etc. The candidate nucleic acids may stably integrate into the genome of the host cell (for example, with retroviral introduction) or may exist either transiently or stably in the
10 cytoplasm (i.e. through the use of traditional plasmids, utilizing standard regulatory sequences, selection markers, etc.). As many pharmaceutically important screens require human or model mammalian cell targets, retroviral vectors capable of transfecting such targets can be used.

Where appropriate, the engineered host cells can be cultured in conventional
15 nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired
20 polypeptide or fragment thereof.

Cells can be harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing
25 agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite
30 chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed

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in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Cell-free translation systems can also be employed to produce a polypeptide of the invention. Cell-free translation systems can use mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

The expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Host cells containing the polynucleotides of interest, e.g., nucleic acids of the invention, can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression and will be apparent to the ordinarily skilled artisan. The clones which are identified as having the specified enzyme activity may then be sequenced to identify the polynucleotide sequence encoding an enzyme having the enhanced activity.

The invention provides a method for overexpressing a recombinant cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme in a cell comprising expressing a vector comprising a nucleic acid of the invention, e.g., a nucleic acid comprising a nucleic acid sequence with at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to an exemplary sequence of the invention over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, or, a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence of the invention. The

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overexpression can be effected by any means, e.g., use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

5 The nucleic acids of the invention can be expressed, or overexpressed, in any in vitro or in vivo expression system. Any cell culture systems can be employed to express, or over-express, recombinant protein, including bacterial, insect, yeast, fungal or mammalian cultures. Over-expression can be effected by appropriate choice of promoters, enhancers, vectors (e.g., use of replicon vectors, dicistronic vectors (see, e.g., Gurtu (1996) Biochem. Biophys. Res. Commun. 229:295-8), media, culture systems and the like. In one aspect, gene amplification using selection markers, e.g., glutamine
10 synthetase (see, e.g., Sanders (1987) Dev. Biol. Stand. 66:55-63), in cell systems are used to overexpress the polypeptides of the invention. The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, mammalian cells, insect cells, or plant cells. The selection of an appropriate host is within the abilities of those skilled in the art.

15 The vector may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

20 Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and
25 the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells can be harvested by centrifugation, disrupted by physical or chemical means and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method,
30 including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography,

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hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

5 Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts (described by Gluzman, *Cell*, 23:175, 1981) and other cell lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

10 The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

15 Alternatively, the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof can be synthetically produced by conventional peptide synthesizers, e.g., as discussed below. In other aspects, fragments or portions of the polypeptides may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length polypeptides.

20 Cell-free translation systems can also be employed to produce one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof using mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

Amplification of Nucleic Acids

30 In practicing the invention, nucleic acids of the invention and nucleic acids encoding the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention, or modified nucleic acids of the invention, can be reproduced by amplification, e.g., PCR. Amplification can also be used to clone or modify the nucleic acids of the invention. Thus, the invention provides amplification

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primer sequence pairs for amplifying nucleic acids of the invention. One of skill in the art can design amplification primer sequence pairs for any part of or the full length of these sequences.

In one aspect, the invention provides a nucleic acid amplified by an amplification primer pair of the invention, e.g., a primer pair as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of a nucleic acid of the invention, and about the first (the 5') 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of the complementary strand. The invention provides amplification primer sequence pairs for amplifying a nucleic acid encoding a polypeptide having a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50 or more consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more consecutive bases of the sequence. The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of the complementary strand of the first member.

The invention provides cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme by amplification, e.g., PCR, using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

Amplification reactions can also be used to quantify the amount of nucleic acid in a sample (such as the amount of message in a cell sample), label the nucleic acid (e.g., to apply it to an array or a blot), detect the nucleic acid, or quantify the amount of a specific nucleic acid in a sample. In one aspect of the invention, message isolated from a cell or a cDNA library are amplified.

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The skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (see, e.g., PCR PROTOCOLS, A GUIDE TO METHODS AND APPLICATIONS, ed. Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES (1995), ed. Innis, Academic Press, Inc., N.Y., ligase chain reaction (LCR) (see, e.g., Wu (1989) Genomics 4:560; Landegren (1988) Science 241:1077; Barringer (1990) Gene 89:117); transcription amplification (see, e.g., Kwoh (1989) Proc. Natl. Acad. Sci. USA 86:1173); and, self-sustained sequence replication (see, e.g., Guatelli (1990) Proc. Natl. Acad. Sci. USA 87:1874); Q Beta replicase amplification (see, e.g., Smith (1997) J. Clin. Microbiol. 35:1477-1491), automated Q-beta replicase amplification assay (see, e.g., Burg (1996) Mol. Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan (1995) Biotechnology 13:563-564.

15 Determining sequence identity in nucleic acids and polypeptides

The invention provides nucleic acids comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity (homology) to an exemplary nucleic acid of the invention (see also Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing) over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550 or more, residues. The invention provides polypeptides comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary polypeptide of the invention (see Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing). The extent of sequence identity (homology) may be determined using any computer program and associated parameters, including those described herein, such as BLAST 2.2.2. or FASTA version 3.0t78, with the default parameters.

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Nucleic acid sequences of the invention can comprise at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive nucleotides of an exemplary sequence of the invention and sequences substantially identical thereto. Homologous sequences and fragments of nucleic acid sequences of the invention can refer to a sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to these sequences. Homology (sequence identity) may be determined using any of the computer programs and parameters described herein, including FASTA version 3.0t78 with the default parameters. Homologous sequences also include RNA sequences in which uridines replace the thymines in the nucleic acid sequences of the invention. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error. It will be appreciated that the nucleic acid sequences of the invention can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. Biochemistry, 3rd Ed., W. H Freeman & Co., New York.) or in any other format which records the identity of the nucleotides in a sequence.

In various aspects, sequence comparison programs identified herein are used in this aspect of the invention, i.e., to determine if a nucleic acid or polypeptide sequence is within the scope of the invention. However, protein and/or nucleic acid sequence identities (homologies) may be evaluated using any sequence comparison algorithm or program known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA and CLUSTALW (see, e.g., Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85(8):2444-2448, 1988; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Thompson Nucleic Acids Res. 22(2):4673-4680, 1994; Higgins *et al.*, Methods Enzymol. 266:383-402, 1996; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Altschul *et al.*, Nature Genetics 3:266-272, 1993).

In one aspect, homology or identity is measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Such software matches similar sequences by assigning degrees of homology to various deletions, substitutions and other modifications. In one aspect, the terms "homology" and "identity" in the context of two or more nucleic acids or polypeptide sequences, refer to

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two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection. In one aspect, for sequence comparison, one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of person & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BBlocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis

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Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC
(Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local
Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench),
MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-
5 sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-
IF. Such alignment programs can also be used to screen genome databases to identify
polynucleotide sequences having substantially identical sequences. A number of genome
databases are available, for example, a substantial portion of the human genome is
available as part of the Human Genome Sequencing Project (Gibbs, 1995). At least
10 twenty-one other genomes have already been sequenced, including, for example, *M.*
genitalium (Fraser *et al.*, 1995), *M. jannaschii* (Bult *et al.*, 1996), *H. influenzae*
(Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997) and yeast (*S. cerevisiae*) (Mewes
et al., 1997) and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also
been made in sequencing the genomes of model organism, such as mouse, *C. elegans* and
15 *Arabidopsis sp.* Several databases containing genomic information annotated with some
functional information are maintained by different organizations and may be accessible
via the internet.

In one aspect, BLAST and BLAST 2.0 algorithms are used, which are described
in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1977 and Altschul *et al.*, J. Mol. Biol.
20 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly
available through the National Center for Biotechnology Information. This algorithm
involves first identifying high scoring sequence pairs (HSPs) by identifying short words
of length W in the query sequence, which either match or satisfy some positive-valued
threshold score T when aligned with a word of the same length in a database sequence. T
25 is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These
initial neighborhood word hits act as seeds for initiating searches to find longer HSPs
containing them. The word hits are extended in both directions along each sequence for
as far as the cumulative alignment score can be increased. Cumulative scores are
calculated using, for nucleotide sequences, the parameters M (reward score for a pair of
30 matching residues; always >0). For amino acid sequences, a scoring matrix is used to
calculate the cumulative score. Extension of the word hits in each direction are halted
when: the cumulative alignment score falls off by the quantity X from its maximum
achieved value; the cumulative score goes to zero or below, due to the accumulation of
one or more negative-scoring residue alignments; or the end of either sequence is reached.

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The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3 and expectations (E) of 10 and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4 and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, Proc. Natl. Acad. Sci. USA 90:5873, 1993). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more in one aspect less than about 0.01 and most in one aspect less than about 0.001.

In one aspect, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- (5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is in one aspect obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are in one aspect identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. In one aspect, the scoring matrix used is the BLOSUM62 matrix (Gonnet (1992))

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Science 256:1443-1445; Henikoff and Henikoff (1993) Proteins 17:49-61). Less in one aspect, the PAM or PAM250 matrices may also be used (see, e.g., Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine.

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some aspects, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

Computer systems and computer program products

The invention provides computers, computer systems, computer readable mediums, computer programs products and the like recorded or stored thereon the nucleic acid and polypeptide sequences of the invention. Additionally, in practicing the methods of the invention, e.g., to determine and identify sequence identities (to determine whether a nucleic acid is within the scope of the invention), structural homologies, motifs and the like *in silico*, a nucleic acid or polypeptide sequence of the invention can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer.

As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid and/or polypeptide sequences of the invention. As used herein, the terms "computer," "computer program" and "processor" are used in their broadest general contexts and incorporate all such devices, as described in detail, below. A "coding sequence of" or a "sequence encodes" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences.

The polypeptides of the invention include exemplary sequences of the invention and sequences substantially identical thereto, and subsequences (fragments) of any of the preceding sequences. In one aspect, substantially identical, or homologous, polypeptide sequences refer to a polypeptide sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or

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more, or complete (100%) sequence identity (homology) to an exemplary sequence of the invention.

Homology (sequence identity) may be determined using any of the computer programs and parameters described herein. A nucleic acid or polypeptide sequence of the invention can be stored, recorded and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid sequences of the invention, one or more of the polypeptide sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more nucleic acid or polypeptide sequences of the invention.

Another aspect of the invention is a computer readable medium having recorded thereon one or more of the nucleic acid sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon one or more of the polypeptide sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more of the nucleic acid or polypeptide sequences as set forth above.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Aspects of the invention include systems (*e.g.*, internet based systems), *e.g.*, computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 1. As used herein, "a computer system" refers to the hardware components, software components and data storage components used to analyze a nucleotide sequence of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. In one aspect, the computer system 100 includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as, for example, the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq, AMD or International Business Machines.

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In one aspect, the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently
5 available computer systems are suitable.

In one particular aspect, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (in one aspect implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some aspects, the
10 computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data storage devices 110.

The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, or a modem capable of connection to a remote data storage system (*e.g.*, via the internet) etc. In some aspects, the internal data storage
15 device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

20 The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100.

Software for accessing and processing the nucleotide sequences of a nucleic acid
25 sequence of the invention, or a polypeptide sequence of the invention, (such as search tools, compare tools and modeling tools etc.) may reside in main memory 115 during execution.

In some aspects, the computer system 100 may further comprise a sequence comparison algorithm for comparing a nucleic acid sequence of the invention, or a
30 polypeptide sequence of the invention, stored on a computer readable medium to a reference nucleotide or polypeptide sequence(s) stored on a computer readable medium. A "sequence comparison algorithm" refers to one or more programs which are implemented (locally or remotely) on the computer system 100 to compare a nucleotide sequence with other nucleotide sequences and/or compounds stored within a data storage

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means. For example, the sequence comparison algorithm may compare the nucleotide sequences of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies or structural motifs.

5 Figure 2 is a flow diagram illustrating one aspect of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK that is available through the Internet.

10 The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed above, the memory could be any type of memory, including RAM or an internal storage device.

15 The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database.

20 Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system.

25 Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences that are within the homology parameters entered by the user will be marked as "same" in the process 200.

30 If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200 moves to a decision state 218 wherein a

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determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database.

It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison.

Accordingly, one aspect of the invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence of the invention, or a polypeptide sequence of the invention and a sequence comparer for conducting the comparison. The sequence comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some aspects, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the nucleic acid sequences of the invention, or the polypeptide sequences of the invention.

Another aspect of the invention is a method for determining the level of homology between a nucleic acid sequence of the invention, or a polypeptide sequence of the invention and a reference nucleotide sequence. The method including reading the nucleic acid code or the polypeptide code and the reference nucleotide or polypeptide sequence through the use of a computer program which determines homology levels and determining homology between the nucleic acid code or polypeptide code and the reference nucleotide or polypeptide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, (*e.g.*, BLAST2N with the default parameters or with any modified parameters). The method may be implemented using the computer systems described above. The method may also be performed by reading at

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least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the above described nucleic acid sequences of the invention, or the polypeptide sequences of the invention through use of the computer program and determining homology between the nucleic acid codes or polypeptide codes and reference nucleotide sequences or polypeptide sequences.

5 Figure 3 is a flow diagram illustrating one aspect of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first
10 sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it is in one aspect in the single letter amino acid code so that the first and sequence sequences can be easily compared.

15 A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two
20 characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read.

 If there are not any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters
25 between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%.

 Alternatively, the computer program may be a computer program which compares the nucleotide sequences of a nucleic acid sequence as set forth in the invention, to one or
30 more reference nucleotide sequences in order to determine whether the nucleic acid code of the invention, differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or a nucleic acid sequence of the invention. In one aspect, the computer program may be

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a program which determines whether a nucleic acid sequence of the invention, contains a single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence.

Accordingly, another aspect of the invention is a method for determining whether a nucleic acid sequence of the invention, differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some aspects, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 3. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30, or 40 or more of the nucleic acid sequences of the invention and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program.

In other aspects the computer based system may further comprise an identifier for identifying features within a nucleic acid sequence of the invention or a polypeptide sequence of the invention. An "identifier" refers to one or more programs which identifies certain features within a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. In one aspect, the identifier may comprise a program which identifies an open reading frame in a nucleic acid sequence of the invention.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG". Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group. Alternatively, the features may be structural polypeptide motifs such as alpha helices, beta sheets, or functional polypeptide motifs such as enzymatic active sites, helix-turn-helix motifs or other motifs known to those skilled in the art.

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Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user.

The process 300 then moves to a decision state 320 wherein a determination is made whether more features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence. It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database.

Accordingly, another aspect of the invention is a method of identifying a feature within a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, comprising reading the nucleic acid code(s) or polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) with the computer program. In one aspect, computer program comprises a computer program which identifies open reading frames. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 40 or more of the nucleic acid sequences of the invention, or the polypeptide sequences of the invention, through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program.

A nucleic acid sequence of the invention, or a polypeptide sequence of the invention, may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, may be stored as text in a word processing file, such as Microsoft WORD™ or WORDPERFECT™ or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2™, SYBASE™, or ORACLE™. In addition, many computer programs and databases may be used as sequence comparison algorithms, identifiers, or sources of reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. The following list is intended not to limit the

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invention but to provide guidance to programs and databases which are useful with the nucleic acid sequences of the invention, or the polypeptide sequences of the invention.

The programs and databases which may be used include, but are not limited to: MACPATTERN™ (EMBL), DISCOVERYBASE™ (Molecular Applications Group), GENEMINE™ (Molecular Applications Group), LOOK™ (Molecular Applications Group), MACLOOK™ (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, J. Mol. Biol. 215: 403, 1990), FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA, 85: 2444, 1988), FASTDB (Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990), CATALYST™ (Molecular Simulations Inc.), Catalyst/SHAPE™ (Molecular Simulations Inc.), Cerius².DBAccess™ (Molecular Simulations Inc.), HYPOGEN™ (Molecular Simulations Inc.), INSIGHT II™, (Molecular Simulations Inc.), DISCOVER™ (Molecular Simulations Inc.), CHARMm™ (Molecular Simulations Inc.), FELIX™ (Molecular Simulations Inc.), DELPHI™, (Molecular Simulations Inc.), QuanteMM™, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), MODELER™ (Molecular Simulations Inc.), ISIS™ (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwent's World Drug Index database, the BioByteMasterFile database, the Genbank database and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites and enzymatic cleavage sites.

30 Hybridization of nucleic acids

The invention provides isolated or recombinant nucleic acids that hybridize under stringent conditions to an exemplary sequence of the invention (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ

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ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165 (see also Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing)). The stringent conditions can be highly stringent conditions, medium stringent conditions and/or low stringent conditions, including the high and reduced stringency conditions described herein. In one aspect, it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention, as discussed below.

“Hybridization” refers to the process by which a nucleic acid strand joins with a complementary strand through base pairing. Hybridization reactions can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Suitably stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature and are well known in the art. In alternative aspects, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. In alternative aspects, nucleic acids of the invention are defined by their ability to hybridize under various stringency conditions (e.g., high, medium, and low), as set forth herein.

In one aspect, hybridization under high stringency conditions comprise about 50% formamide at about 37°C to 42°C. In one aspect, hybridization conditions comprise reduced stringency conditions in about 35% to 25% formamide at about 30°C to 35°C. In one aspect, hybridization conditions comprise high stringency conditions, e.g., at 42°C in

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50% formamide, 5X SSPE, 0.3% SDS and 200 n/ml sheared and denatured salmon sperm DNA. In one aspect, hybridization conditions comprise these reduced stringency conditions, but in 35% formamide at a reduced temperature of 35°C. The temperature range corresponding to a particular level of stringency can be further narrowed by
5 calculating the purine to pyrimidine ratio of the nucleic acid of interest and adjusting the temperature accordingly. Variations on the above ranges and conditions are well known in the art.

In alternative aspects, nucleic acids of the invention as defined by their ability to hybridize under stringent conditions can be between about five residues and the full
10 length of nucleic acid of the invention; e.g., they can be at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 55, 60, 65, 70, 75, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, or more, residues in length. Nucleic acids shorter than full length are also included. These nucleic acids can be useful as, e.g., hybridization probes, labeling probes, PCR oligonucleotide probes, siRNA or miRNA
15 (single or double stranded), antisense or sequences encoding antibody binding peptides (epitopes), motifs, active sites and the like.

In one aspect, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions of about 50% formamide at about 37°C to 42°C. In one aspect, nucleic acids of the invention are defined by their ability to
20 hybridize under reduced stringency comprising conditions in about 35% to 25% formamide at about 30°C to 35°C.

Alternatively, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and a repetitive sequence blocking nucleic acid, such as cot-1 or
25 salmon sperm DNA (e.g., 200 n/ml sheared and denatured salmon sperm DNA). In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency conditions comprising 35% or 40% formamide at a reduced temperature of 35°C or 42°C.

In nucleic acid hybridization reactions, the conditions used to achieve a particular
30 level of stringency will vary, depending on the nature of the nucleic acids being hybridized. For example, the length, degree of complementarity, nucleotide sequence composition (e.g., GC v. AT content) and nucleic acid type (e.g., RNA v. DNA) of the hybridizing regions of the nucleic acids can be considered in selecting hybridization

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conditions. An additional consideration is whether one of the nucleic acids is immobilized, for example, on a filter.

Hybridization may be carried out under conditions of low stringency, moderate stringency or high stringency. As an example of nucleic acid hybridization, a polymer membrane containing immobilized denatured nucleic acids is first prehybridized for 30 minutes at 45°C in a solution consisting of 0.9 M NaCl, 50 mM NaH₂PO₄, pH 7.0, 5.0 mM Na₂EDTA, 0.5% SDS, 10X Denhardt's and 0.5 mg/ml polyriboadenylic acid. Approximately 2×10^7 cpm (specific activity $4-9 \times 10^8$ cpm/ug) of ³²P end-labeled oligonucleotide probe are then added to the solution. After 12-16 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at T_m-10°C for the oligonucleotide probe. The membrane is then exposed to auto-radiographic film for detection of hybridization signals. All of the foregoing hybridizations would be considered to be under conditions of high stringency.

Following hybridization, a filter can be washed to remove any non-specifically bound detectable probe. The stringency used to wash the filters can also be varied depending on the nature of the nucleic acids being hybridized, the length of the nucleic acids being hybridized, the degree of complementarity, the nucleotide sequence composition (*e.g.*, GC v. AT content) and the nucleic acid type (*e.g.*, RNA v. DNA). Examples of progressively higher stringency condition washes are as follows: 2X SSC, 0.1% SDS at room temperature for 15 minutes (low stringency); 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour (moderate stringency); 0.1X SSC, 0.5% SDS for 15 to 30 minutes at between the hybridization temperature and 68°C (high stringency); and 0.15M NaCl for 15 minutes at 72°C (very high stringency). A final low stringency wash can be conducted in 0.1X SSC at room temperature. The examples above are merely illustrative of one set of conditions that can be used to wash filters. One of skill in the art would know that there are numerous recipes for different stringency washes. Some other examples are given below.

In one aspect, hybridization conditions comprise a wash step comprising a wash for 30 minutes at room temperature in a solution comprising 1X 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution.

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Nucleic acids which have hybridized to the probe are identified by autoradiography or other conventional techniques.

The above procedures may be modified to identify nucleic acids having decreasing levels of sequence identity (homology) to the probe sequence. For example, to obtain nucleic acids of decreasing sequence identity (homology) to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a Na⁺ concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be “moderate” conditions above 50°C and “low” conditions below 50°C. A specific example of “moderate” hybridization conditions is when the above hybridization is conducted at 55°C. A specific example of “low stringency” hybridization conditions is when the above hybridization is conducted at 45°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be “moderate” conditions above 25% formamide and “low” conditions below 25% formamide. A specific example of “moderate” hybridization conditions is when the above hybridization is conducted at 30% formamide. A specific example of “low stringency” hybridization conditions is when the above hybridization is conducted at 10% formamide.

However, the selection of a hybridization format may not be critical - it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention. Wash conditions used to identify nucleic acids within the scope of the invention include, e.g.: a salt concentration of about 0.02 molar at pH 7 and a temperature of at least about 50°C or about 55°C to about 60°C; or, a salt concentration of about 0.15 M NaCl at 72°C for about 15 minutes; or, a salt concentration of about 0.2X SSC at a temperature of at least about 50°C or about 55°C to about 60°C for about 15 to about 20 minutes; or, the hybridization complex is washed twice with a solution with a salt concentration of about 2X SSC containing 0.1% SDS at room temperature for 15 minutes and then washed twice by 0.1X SSC containing 0.1%

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SDS at 68°C for 15 minutes; or, equivalent conditions. See Sambrook, Tijssen and Ausubel for a description of SSC buffer and equivalent conditions.

These methods may be used to isolate or identify nucleic acids of the invention. For example, the preceding methods may be used to isolate or identify nucleic acids having a sequence with at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to a nucleic acid sequence selected from the group consisting of one of the sequences of the invention, or fragments comprising at least about 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases thereof and the sequences complementary thereto. Sequence identity (homology) may be measured using the alignment algorithm. For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of the invention. Additionally, the above procedures may be used to isolate nucleic acids which encode polypeptides having at least about 99%, 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% sequence identity (homology) to a polypeptide of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using a sequence alignment algorithm (*e.g.*, such as the FASTA version 3.0t78 algorithm with the default parameters).

Oligonucleotides probes and methods for using them

The invention also provides nucleic acid probes that can be used, *e.g.*, for identifying, amplifying, or isolating nucleic acids encoding a polypeptide having a cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity or fragments thereof or for identifying cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme genes. In one aspect, the probe comprises at least about 10 consecutive bases of a nucleic acid of the invention. Alternatively, a probe of the invention can be at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 150 or about 10 to 50, about 20 to 60 about 30 to 70, consecutive bases of a sequence as set forth in a nucleic acid of the invention. The probes identify a nucleic acid

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by binding and/or hybridization. The probes can be used in arrays of the invention, see discussion below, including, e.g., capillary arrays. The probes of the invention can also be used to isolate other nucleic acids or polypeptides.

The isolated or recombinant nucleic acids of the invention, the sequences
5 complementary thereto, or a fragment comprising at least about 10, 15, 20, 25, 30, 35, 40,
50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the
invention, or the sequences complementary thereto may also be used as probes to
determine whether a biological sample, such as a soil sample, contains an organism
having a nucleic acid sequence of the invention or an organism from which the nucleic
10 acid was obtained. In such procedures, a biological sample potentially harboring the
organism from which the nucleic acid was isolated is obtained and nucleic acids are
obtained from the sample. The nucleic acids are contacted with the probe under
conditions which permit the probe to specifically hybridize to any complementary
sequences from which are present therein.

15 Where necessary, conditions which permit the probe to specifically hybridize to
complementary sequences may be determined by placing the probe in contact with
complementary sequences from samples known to contain the complementary sequence
as well as control sequences which do not contain the complementary sequence.
Hybridization conditions, such as the salt concentration of the hybridization buffer, the
20 formamide concentration of the hybridization buffer, or the hybridization temperature,
may be varied to identify conditions which allow the probe to hybridize specifically to
complementary nucleic acids.

If the sample contains the organism from which the nucleic acid was isolated,
specific hybridization of the probe is then detected. Hybridization may be detected by
25 labeling the probe with a detectable agent such as a radioactive isotope, a fluorescent dye
or an enzyme capable of catalyzing the formation of a detectable product.

Many methods for using the labeled probes to detect the presence of
complementary nucleic acids in a sample are familiar to those skilled in the art. These
include Southern Blots, Northern Blots, colony hybridization procedures and dot blots.
30 Protocols for each of these procedures are provided in Ausubel *et al.* Current Protocols in
Molecular Biology, John Wiley 503 Sons, Inc. (1997) and Sambrook *et al.*, Molecular
Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press (1989).

Alternatively, more than one probe (at least one of which is capable of specifically
hybridizing to any complementary sequences which are present in the nucleic acid

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sample), may be used in an amplification reaction to determine whether the sample contains an organism containing a nucleic acid sequence of the invention (*e.g.*, an organism from which the nucleic acid was isolated). In one aspect, the probes comprise oligonucleotides. In one aspect, the amplification reaction may comprise a PCR reaction. 5 PCR protocols are described in Ausubel and Sambrook, *supra*. Alternatively, the amplification may comprise a ligase chain reaction, 3SR, or strand displacement reaction. (See Barany, F., "The Ligase Chain Reaction in a PCR World", *PCR Methods and Applications* 1:5-16, 1991; E. Fahy *et al.*, "Self-sustained Sequence Replication (3SR): An Isothermal Transcription-based Amplification System Alternative to PCR", *PCR Methods and Applications* 1:25-33, 1991; and Walker G.T. *et al.*, "Strand Displacement 10 Amplification-an Isothermal *in vitro* DNA Amplification Technique", *Nucleic Acid Research* 20:1691-1696, 1992). In such procedures, the nucleic acids in the sample are contacted with the probes, the amplification reaction is performed and any resulting amplification product is detected. The amplification product may be detected by performing 15 gel electrophoresis on the reaction products and staining the gel with an intercalator such as ethidium bromide. Alternatively, one or more of the probes may be labeled with a radioactive isotope and the presence of a radioactive amplification product may be detected by autoradiography after gel electrophoresis.

Probes derived from sequences near the ends of the sequences of the invention, 20 may also be used in chromosome walking procedures to identify clones containing genomic sequences located adjacent to the sequences of the invention. Such methods allow the isolation of genes which encode additional proteins from the host organism.

In one aspect, the isolated or recombinant nucleic acids of the invention, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 25 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive bases of one of the sequences of the invention, or the sequences complementary thereto are used as probes to identify and isolate related nucleic acids. In some aspects, the related nucleic acids may be cDNAs or genomic DNAs from organisms other than the one from which the nucleic acid was isolated. For example, the other organisms may be related organisms. In such 30 procedures, a nucleic acid sample is contacted with the probe under conditions which permit the probe to specifically hybridize to related sequences. Hybridization of the probe to nucleic acids from the related organism is then detected using any of the methods described above.

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By varying the stringency of the hybridization conditions used to identify nucleic acids, such as cDNAs or genomic DNAs, which hybridize to the detectable probe, nucleic acids having different levels of homology to the probe can be identified and isolated. Stringency may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature, T_m , is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly complementary probe. Very stringent conditions are selected to be equal to or about 5°C lower than the T_m for a particular probe. The melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100µg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100µg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

In one aspect, hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. In one aspect, the filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 5-10°C below the T_m . In one aspect, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Usually, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

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Inhibiting Expression of Cellulase Enzymes

The invention provides nucleic acids complementary to (e.g., antisense sequences to) the nucleic acids of the invention, e.g., cellulase enzyme-encoding nucleic acids, e.g., nucleic acids comprising antisense, siRNA, miRNA, ribozymes. Nucleic acids of the invention comprising antisense sequences can be capable of inhibiting the transport, splicing or transcription of cellulase enzyme-encoding genes. The inhibition can be effected through the targeting of genomic DNA or messenger RNA. The transcription or function of targeted nucleic acid can be inhibited, for example, by hybridization and/or cleavage. One exemplary set of inhibitors provided by the present invention includes oligonucleotides which are able to either bind cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme gene or message, in either case preventing or inhibiting the production or function of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. The association can be through sequence specific hybridization. Another useful class of inhibitors includes oligonucleotides which cause inactivation or cleavage of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme message. The oligonucleotide can have enzyme activity which causes such cleavage, such as ribozymes. The oligonucleotide can be chemically modified or conjugated to an enzyme or composition capable of cleaving the complementary nucleic acid. A pool of many different such oligonucleotides can be screened for those with the desired activity. Thus, the invention provides various compositions for the inhibition of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme expression on a nucleic acid and/or protein level, e.g., antisense, siRNA, miRNA and ribozymes comprising cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme sequences of the invention and the anti-cellulase, e.g., anti-endoglucanase, anti-cellobiohydrolase and/or anti-beta-glucosidase antibodies of the invention.

Inhibition of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme expression can have a variety of industrial applications. For example, inhibition of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme expression can slow or prevent spoilage. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, e.g., antibodies, antisense oligonucleotides, ribozymes, siRNA and miRNA are

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used to slow or prevent spoilage. Thus, in one aspect, the invention provides methods and compositions comprising application onto a plant or plant product (e.g., a cereal, a grain, a fruit, seed, root, leaf, etc.) antibodies, antisense oligonucleotides, ribozymes, siRNA and miRNA of the invention to slow or prevent spoilage. These compositions also
5 can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme gene of the invention).

The compositions of the invention for the inhibition of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme expression
10 (e.g., antisense, iRNA, ribozymes, antibodies) can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., as anti-microbials for, e.g., *Salmonella*.

Antisense Oligonucleotides

The invention provides antisense oligonucleotides capable of binding cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme
15 message which, in one aspect, can inhibit cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity by targeting mRNA. Strategies for designing antisense oligonucleotides are well described in the scientific and patent literature, and the skilled artisan can design such cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme
20 oligonucleotides using the novel reagents of the invention. For example, gene walking/ RNA mapping protocols to screen for effective antisense oligonucleotides are well known in the art, see, e.g., Ho (2000) Methods Enzymol. 314:168-183, describing an RNA mapping assay, which is based on standard molecular techniques to provide an easy and
25 reliable method for potent antisense sequence selection. See also Smith (2000) Eur. J. Pharm. Sci. 11:191-198.

Naturally occurring nucleic acids are used as antisense oligonucleotides. The antisense oligonucleotides can be of any length; for example, in alternative aspects, the antisense oligonucleotides are between about 5 to 100, about 10 to 80, about 15 to 60,
30 about 18 to 40. The optimal length can be determined by routine screening. The antisense oligonucleotides can be present at any concentration. The optimal concentration can be determined by routine screening. A wide variety of synthetic, non-naturally occurring nucleotide and nucleic acid analogues are known which can address this potential problem. For example, peptide nucleic acids (PNAs) containing non-ionic

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backbones, such as N-(2-aminoethyl) glycine units can be used. Antisense oligonucleotides having phosphorothioate linkages can also be used, as described in WO 97/03211; WO 96/39154; Mata (1997) Toxicol Appl Pharmacol 144:189-197; Antisense Therapeutics, ed. Agrawal (Humana Press, Totowa, N.J., 1996). Antisense oligonucleotides having synthetic DNA backbone analogues provided by the invention can also include phosphoro-dithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, and morpholino carbamate nucleic acids, as described above.

Combinatorial chemistry methodology can be used to create vast numbers of oligonucleotides that can be rapidly screened for specific oligonucleotides that have appropriate binding affinities and specificities toward any target, such as the sense and antisense cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme sequences of the invention (see, e.g., Gold (1995) J. of Biol. Chem. 270:13581-13584).

Inhibitory Ribozymes

The invention provides ribozymes capable of binding cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme message. These ribozymes can inhibit cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity by, e.g., targeting mRNA. Strategies for designing ribozymes and selecting the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme-specific antisense sequence for targeting are well described in the scientific and patent literature, and the skilled artisan can design such ribozymes using the novel reagents of the invention. Ribozymes act by binding to a target RNA through the target RNA binding portion of a ribozyme which is held in close proximity to an enzymatic portion of the RNA that cleaves the target RNA. Thus, the ribozyme recognizes and binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cleave and inactivate the target RNA. Cleavage of a target RNA in such a manner will destroy its ability to direct synthesis of an encoded protein if the cleavage occurs in the coding sequence. After a ribozyme has bound and cleaved its RNA target, it can be released from that RNA to bind and cleave new targets repeatedly.

In some circumstances, the enzymatic nature of a ribozyme can be advantageous over other technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its transcription, translation or association

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with another molecule) as the effective concentration of ribozyme necessary to effect a therapeutic treatment can be lower than that of an antisense oligonucleotide. This potential advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In one aspect, a ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding, but also on the mechanism by which the molecule inhibits the expression of the RNA to which it binds. That is, the inhibition is caused by cleavage of the RNA target and so specificity is defined as the ratio of the rate of cleavage of the targeted RNA over the rate of cleavage of non-targeted RNA. This cleavage mechanism is dependent upon factors additional to those involved in base pairing. Thus, the specificity of action of a ribozyme can be greater than that of antisense oligonucleotide binding the same RNA site.

The ribozyme of the invention, e.g., an enzymatic ribozyme RNA molecule, can be formed in a hammerhead motif, a hairpin motif, as a hepatitis delta virus motif, a group I intron motif and/or an RNaseP-like RNA in association with an RNA guide sequence. Examples of hammerhead motifs are described by, e.g., Rossi (1992) *Aids Research and Human Retroviruses* 8:183; hairpin motifs by Hampel (1989) *Biochemistry* 28:4929, and Hampel (1990) *Nuc. Acids Res.* 18:299; the hepatitis delta virus motif by Perrotta (1992) *Biochemistry* 31:16; the RNaseP motif by Guerrier-Takada (1983) *Cell* 35:849; and the group I intron by Cech U.S. Pat. No. 4,987,071. The recitation of these specific motifs is not intended to be limiting. Those skilled in the art will recognize that a ribozyme of the invention, e.g., an enzymatic RNA molecule of this invention, can have a specific substrate binding site complementary to one or more of the target gene RNA regions. A ribozyme of the invention can have a nucleotide sequence within or surrounding that substrate binding site which imparts an RNA cleaving activity to the molecule.

RNA interference (RNAi)

In one aspect, the invention provides an RNA inhibitory molecule, a so-called "RNAi" molecule, comprising a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme sequence of the invention. The RNAi molecule can comprise a double-stranded RNA (dsRNA) molecule, e.g., siRNA and/or miRNA. The RNAi molecule, e.g., siRNA and/or miRNA, can inhibit expression of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme gene. In one aspect, the RNAi molecule, e.g., siRNA and/or miRNA, is about 15,

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16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length. While the invention is not limited by any particular mechanism of action, the RNAi can enter a cell and cause the degradation of a single-stranded RNA (ssRNA) of similar or identical sequences, including endogenous mRNAs. When a cell is exposed to double-stranded RNA (dsRNA), mRNA from the homologous gene is selectively degraded by a process called RNA interference (RNAi). A possible basic mechanism behind RNAi is the breaking of a double-stranded RNA (dsRNA) matching a specific gene sequence into short pieces called short interfering RNA, which trigger the degradation of mRNA that matches its sequence. In one aspect, the RNAi's of the invention are used in gene-silencing therapeutics, see, e.g., Shuey (2002) Drug Discov. Today 7:1040-1046. In one aspect, the invention provides methods to selectively degrade RNA using the RNAi's molecules, e.g., siRNA and/or miRNA, of the invention. The process may be practiced *in vitro*, *ex vivo* or *in vivo*. In one aspect, the RNAi molecules of the invention can be used to generate a loss-of-function mutation in a cell, an organ or an animal. Methods for making and using RNAi molecules, e.g., siRNA and/or miRNA, for selectively degrade RNA are well known in the art, see, e.g., U.S. Patent No. 6,506,559; 6,511,824; 6,515,109; 6,489,127.

Modification of Nucleic Acids – Making Variant Enzymes of the Invention

The invention provides methods of generating variants of the nucleic acids of the invention, e.g., those encoding a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. These methods can be repeated or used in various combinations to generate cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes having an altered or different activity or an altered or different stability from that of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme encoded by the template nucleic acid. These methods also can be repeated or used in various combinations, e.g., to generate variations in gene/ message expression, message translation or message stability. In another aspect, the genetic composition of a cell is altered by, e.g., modification of a homologous gene *ex vivo*, followed by its reinsertion into the cell.

For example, in one aspect, the invention provides isolated or recombinant nucleic acids having a sequence comprising at least one nucleotide base residue modification of SEQ ID NO:163, wherein the modification comprises one or more of the following changes: a nucleotide at any one of positions 265 to 267 is modified to CGT, CGC, CGA, CGG, AGA or AGG; a nucleotide at any one of positions 307 to 309 is modified to GGT,

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GGC, GGA or GGG; a nucleotide at any one of positions 328 to 330 is modified to GGT, GGC, GGA or GGG; a nucleotide at any one of positions 340 to 342 is modified to TTA, TTG, CTT, CTC, CTA or CTG; a nucleotide at any one of positions 469 to 471 is modified to TCT, TCC, TCA, TCG, AGT or AGC; a nucleotide at any one of positions 1441 to 1443 is modified to TTT or TTC; a nucleotide at any one of positions 1648 to 1650 is modified to AAT or AAC; or, a nucleotide at any one of positions 1768 to 1770 is modified to CGT, CGC, CGA, CGG, AGA or AGG. In another aspect, the invention provides isolated or recombinant polypeptides having a sequence comprising at least one amino acid residue modification of SEQ ID NO:164, wherein the modification comprises one or more of the following changes: a methionine at amino acid position 89 is modified to arginine; a phenylalanine at amino acid position 103 is modified to glycine; a proline at amino acid position 110 is modified to glycine; a tyrosine at amino acid position 114 is modified to leucine; an alanine at amino acid position 157 is modified to serine; a tryptophan at amino acid position 481 is modified to phenylalanine; a proline at amino acid position 550 is modified to asparagine; or a glycine at amino acid position 590 is modified to arginine.

In another aspect, the invention provides isolated or recombinant nucleic acids having a sequence comprising a nucleotide residue sequence modification of an exemplary sequence of the invention (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc.) wherein the modification comprises one or more of the following changes: a nucleotide at the equivalent of any one of positions 265 to 267 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG; a nucleotide at the equivalent of any one of positions 307 to 309 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG; a nucleotide at the equivalent of any one of positions 328 to 330 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG; a nucleotide at the equivalent of any one of positions 340 to 342 of SEQ ID NO:163 are changed to TTA, TTG, CTT, CTC, CTA or CTG; a nucleotide at the equivalent of any one of positions 469 to 471 of SEQ ID NO:163 are changed to TCT, TCC, TCA, TCG, AGT or AGC; a nucleotide at the equivalent of positions 1441 to 1443 of SEQ ID NO:163 are changed to TTT or TTC; a nucleotide at the equivalent of any one of positions 1648 to 1650 of SEQ ID NO:163 are changed to AAT or AAC; or a nucleotide at the equivalent of any one of positions 1768 to 1770 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG. In another aspect, the invention provides isolated or recombinant nucleic acids having a sequence comprising a nucleotide

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residue sequence modification of any nucleic acid of the invention, wherein the modification comprises one or more of the following changes: a nucleotide at the equivalent of any one of positions 265 to 267 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG; a nucleotide at the equivalent of any one of positions 307 to 309 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG; a nucleotide at the equivalent of any one of positions 328 to 330 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG; a nucleotide at the equivalent of any one of positions 340 to 342 of SEQ ID NO:163 are changed to TTA, TTG, CTT, CTC, CTA or CTG; a nucleotide at the equivalent of any one of positions 469 to 471 of SEQ ID NO:163 are changed to TCT, TCC, TCA, TCG, AGT or AGC; a nucleotide at the equivalent of positions 1441 to 1443 of SEQ ID NO:163 are changed to TTT or TTC; a nucleotide at the equivalent of any one of positions 1648 to 1650 of SEQ ID NO:163 are changed to AAT or AAC; or, a nucleotide at the equivalent of any one of positions 1768 to 1770 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG.

In another aspect, the invention provides isolated or recombinant polypeptides having a sequence comprising an amino acid residue modification of an exemplary sequence of the invention (e.g., SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc.) wherein the modification comprises one or more of the following changes: an amino acid at the equivalent of the methionine at amino acid position 89 of SEQ ID NO:164 is changed to an arginine; an amino acid at the equivalent of the phenylalanine at amino acid position 103 of SEQ ID NO:164 is changed to a glycine; an amino acid at the equivalent of the proline at amino acid position 110 of SEQ ID NO:164 is changed to a glycine; an amino acid at the equivalent of the tyrosine at amino acid position 114 of SEQ ID NO:164 is changed to a leucine; an amino acid at the equivalent of the alanine at amino acid position 157 of SEQ ID NO:164 is changed to a serine; an amino acid at the equivalent of the tryptophan at amino acid position 481 of SEQ ID NO:164 is changed to a phenylalanine; an amino acid at the equivalent of the proline at amino acid position 550 of SEQ ID NO:164 is changed to an asparagine; or an amino acid at the equivalent of the glycine at amino acid position 590 of SEQ ID NO:164 is changed to an arginine.

In another aspect, the invention provides isolated or recombinant polypeptides having a sequence comprising an amino acid residue modification of any polypeptide of the invention, wherein the modification comprises one or more of the following changes: an amino acid at the equivalent of the methionine at amino acid position 89 of SEQ ID

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NO:164 is changed to an arginine; an amino acid at the equivalent of the phenylalanine at amino acid position 103 of SEQ ID NO:164 is changed to a glycine; an amino acid at the equivalent of the proline at amino acid position 110 of SEQ ID NO:164 is changed to a glycine; an amino acid at the equivalent of the tyrosine at amino acid position 114 of SEQ ID NO:164 is changed to a leucine; an amino acid at the equivalent of the alanine at amino acid position 157 of SEQ ID NO:164 is changed to a serine; an amino acid at the equivalent of the tryptophan at amino acid position 481 of SEQ ID NO:164 is changed to a phenylalanine; an amino acid at the equivalent of the proline at amino acid position 550 of SEQ ID NO:164 is changed to an asparagine; or an amino acid at the equivalent of the glycine at amino acid position 590 of SEQ ID NO:164 is changed to an arginine.

A nucleic acid of the invention can be altered by any means. For example, random or stochastic methods, or, non-stochastic, or "directed evolution," methods, see, e.g., U.S. Patent No. 6,361,974. Methods for random mutation of genes are well known in the art, see, e.g., U.S. Patent No. 5,830,696. For example, mutagens can be used to randomly mutate a gene. Mutagens include, e.g., ultraviolet light or gamma irradiation, or a chemical mutagen, e.g., mitomycin, nitrous acid, photoactivated psoralens, alone or in combination, to induce DNA breaks amenable to repair by recombination. Other chemical mutagens include, for example, sodium bisulfite, nitrous acid, hydroxylamine, hydrazine or formic acid. Other mutagens are analogues of nucleotide precursors, e.g., nitrosoguanidine, 5-bromouracil, 2-aminopurine, or acridine. These agents can be added to a PCR reaction in place of the nucleotide precursor thereby mutating the sequence. Intercalating agents such as proflavine, acriflavine, quinacrine and the like can also be used.

Any technique in molecular biology can be used, e.g., random PCR mutagenesis, see, e.g., Rice (1992) Proc. Natl. Acad. Sci. USA 89:5467-5471; or, combinatorial multiple cassette mutagenesis, see, e.g., Crameri (1995) Biotechniques 18:194-196. Alternatively, nucleic acids, e.g., genes, can be reassembled after random, or "stochastic," fragmentation, see, e.g., U.S. Patent Nos. 6,291,242; 6,287,862; 6,287,861; 5,955,358; 5,830,721; 5,824,514; 5,811,238; 5,605,793. In alternative aspects, modifications, additions or deletions are introduced by error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive

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sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, Chromosomal Saturation Mutagenesis (CSM) and/or a combination of these and other methods.

The following publications describe a variety of recursive recombination procedures and/or methods which can be incorporated into the methods of the invention:

10 Stemmer (1999) "Molecular breeding of viruses for targeting and other clinical properties" Tumor Targeting 4:1-4; Ness (1999) Nature Biotechnology 17:893-896; Chang (1999) "Evolution of a cytokine using DNA family shuffling" Nature Biotechnology 17:793-797; Minshull (1999) "Protein evolution by molecular breeding" Current Opinion in Chemical Biology 3:284-290; Christians (1999) "Directed evolution of thymidine kinase for AZT phosphorylation using DNA family shuffling" Nature 15 Biotechnology 17:259-264; Cramer (1998) "DNA shuffling of a family of genes from diverse species accelerates directed evolution" Nature 391:288-291; Cramer (1997) "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," Nature Biotechnology 15:436-438; Zhang (1997) "Directed evolution of an effective fucosidase 20 from a galactosidase by DNA shuffling and screening" Proc. Natl. Acad. Sci. USA 94:4504-4509; Patten et al. (1997) "Applications of DNA Shuffling to Pharmaceuticals and Vaccines" Current Opinion in Biotechnology 8:724-733; Cramer et al. (1996) "Construction and evolution of antibody-phage libraries by DNA shuffling" Nature Medicine 2:100-103; Gates et al. (1996) "Affinity selective isolation of ligands from 25 peptide libraries through display on a lac repressor 'headpiece dimer'" Journal of Molecular Biology 255:373-386; Stemmer (1996) "Sexual PCR and Assembly PCR" In: The Encyclopedia of Molecular Biology. VCH Publishers, New York. pp.447-457; Cramer and Stemmer (1995) "Combinatorial multiple cassette mutagenesis creates all the permutations of mutant and wildtype cassettes" BioTechniques 18:194-195; Stemmer et al. (1995) "Single-step assembly of a gene and entire plasmid from large numbers of 30 oligodeoxyribonucleotides" Gene, 164:49-53; Stemmer (1995) "The Evolution of Molecular Computation" Science 270: 1510; Stemmer (1995) "Searching Sequence Space" Bio/Technology 13:549-553; Stemmer (1994) "Rapid evolution of a protein in vitro by DNA shuffling" Nature 370:389-391; and Stemmer (1994) "DNA shuffling by

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random fragmentation and reassembly: In vitro recombination for molecular evolution." Proc. Natl. Acad. Sci. USA 91:10747-10751.

Mutational methods of generating diversity include, for example, site-directed mutagenesis (Ling et al. (1997) "Approaches to DNA mutagenesis: an overview" Anal Biochem. 254(2): 157-178; Dale et al. (1996) "Oligonucleotide-directed random mutagenesis using the phosphorothioate method" Methods Mol. Biol. 57:369-374; Smith (1985) "In vitro mutagenesis" Ann. Rev. Genet. 19:423-462; Botstein & Shortle (1985) "Strategies and applications of in vitro mutagenesis" Science 229:1193-1201; Carter (1986) "Site-directed mutagenesis" Biochem. J. 237:1-7; and Kunkel (1987) "The efficiency of oligonucleotide directed mutagenesis" in Nucleic Acids & Molecular Biology (Eckstein, F. and Lilley, D. M. J. eds., Springer Verlag, Berlin)); mutagenesis using uracil containing templates (Kunkel (1985) "Rapid and efficient site-specific mutagenesis without phenotypic selection" Proc. Natl. Acad. Sci. USA 82:488-492; Kunkel et al. (1987) "Rapid and efficient site-specific mutagenesis without phenotypic selection" Methods in Enzymol. 154, 367-382; and Bass et al. (1988) "Mutant Trp repressors with new DNA-binding specificities" Science 242:240-245); oligonucleotide-directed mutagenesis (Methods in Enzymol. 100: 468-500 (1983); Methods in Enzymol. 154: 329-350 (1987); Zoller (1982) "Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment" Nucleic Acids Res. 10:6487-6500; Zoller & Smith (1983) "Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors" Methods in Enzymol. 100:468-500; and Zoller (1987) Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template" Methods in Enzymol. 154:329-350); phosphorothioate-modified DNA mutagenesis (Taylor (1985) "The use of phosphorothioate-modified DNA in restriction enzyme reactions to prepare nicked DNA" Nucl. Acids Res. 13: 8749-8764; Taylor (1985) "The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA" Nucl. Acids Res. 13: 8765-8787 (1985); Nakamaye (1986) "Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis" Nucl. Acids Res. 14: 9679-9698; Sayers (1988) "Y-T Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis" Nucl. Acids Res. 16:791-802; and Sayers et al. (1988) "Strand specific cleavage of phosphorothioate-containing DNA by reaction with restriction endonucleases in the presence of ethidium bromide" Nucl. Acids Res. 16:

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803-814); mutagenesis using gapped duplex DNA (Kramer et al. (1984) "The gapped duplex DNA approach to oligonucleotide-directed mutation construction" Nucl. Acids Res. 12: 9441-9456; Kramer & Fritz (1987) Methods in Enzymol. "Oligonucleotide-directed construction of mutations via gapped duplex DNA" 154:350-367; Kramer (1988) "Improved enzymatic in vitro reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations" Nucl. Acids Res. 16: 7207; and Fritz (1988) "Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions *in vitro*" Nucl. Acids Res. 16: 6987-6999).

Additional protocols that can be used to practice the invention include point mismatch repair (Kramer (1984) "Point Mismatch Repair" Cell 38:879-887), mutagenesis using repair-deficient host strains (Carter et al. (1985) "Improved oligonucleotide site-directed mutagenesis using M13 vectors" Nucl. Acids Res. 13: 4431-4443; and Carter (1987) "Improved oligonucleotide-directed mutagenesis using M13 vectors" Methods in Enzymol. 154: 382-403), deletion mutagenesis (Eghtedarzadeh (1986) "Use of oligonucleotides to generate large deletions" Nucl. Acids Res. 14: 5115), restriction-selection and restriction-selection and restriction-purification (Wells et al. (1986) "Importance of hydrogen-bond formation in stabilizing the transition state of subtilisin" Phil. Trans. R. Soc. Lond. A 317: 415-423), mutagenesis by total gene synthesis (Nambiar et al. (1984) "Total synthesis and cloning of a gene coding for the ribonuclease S protein" Science 223: 1299-1301; Sakamar and Khorana (1988) "Total synthesis and expression of a gene for the α -subunit of bovine rod outer segment guanine nucleotide-binding protein (transducin)" Nucl. Acids Res. 14: 6361-6372; Wells et al. (1985) "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites" Gene 34:315-323; and Grundstrom et al. (1985) "Oligonucleotide-directed mutagenesis by microscale 'shot-gun' gene synthesis" Nucl. Acids Res. 13: 3305-3316), double-strand break repair (Mandecki (1986); Arnold (1993) "Protein engineering for unusual environments" Current Opinion in Biotechnology 4:450-455. "Oligonucleotide-directed double-strand break repair in plasmids of *Escherichia coli*: a method for site-specific mutagenesis" Proc. Natl. Acad. Sci. USA, 83:7177-7181). Additional details on many of the above methods can be found in Methods in Enzymology Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis methods.

Protocols that can be used to practice the invention are described, e.g., in U.S. Patent Nos. 5,605,793 to Stemmer (Feb. 25, 1997), "Methods for In Vitro

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Recombination;" U.S. Pat. No. 5,811,238 to Stemmer et al. (Sep. 22, 1998) "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" U.S. Pat. No. 5,830,721 to Stemmer et al. (Nov. 3, 1998), "DNA Mutagenesis by Random Fragmentation and Reassembly;" U.S. Pat. No. 5,834,252 to Stemmer, et al. (Nov. 10, 1998) "End-Complementary Polymerase Reaction;" U.S. Pat. No. 5,837,458 to Minshull, et al. (Nov. 17, 1998), "Methods and Compositions for Cellular and Metabolic Engineering;" WO 95/22625, Stemmer and Crameri, "Mutagenesis by Random Fragmentation and Reassembly;" WO 96/33207 by Stemmer and Lipschutz "End Complementary Polymerase Chain Reaction;" WO 97/20078 by Stemmer and Crameri "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" WO 97/35966 by Minshull and Stemmer, "Methods and Compositions for Cellular and Metabolic Engineering;" WO 99/41402 by Punnonen et al. "Targeting of Genetic Vaccine Vectors;" WO 99/41383 by Punnonen et al. "Antigen Library Immunization;" WO 99/41369 by Punnonen et al. "Genetic Vaccine Vector Engineering;" WO 99/41368 by Punnonen et al. "Optimization of Immunomodulatory Properties of Genetic Vaccines;" EP 752008 by Stemmer and Crameri, "DNA Mutagenesis by Random Fragmentation and Reassembly;" EP 0932670 by Stemmer "Evolving Cellular DNA Uptake by Recursive Sequence Recombination;" WO 99/23107 by Stemmer et al., "Modification of Virus Tropism and Host Range by Viral Genome Shuffling;" WO 99/21979 by Apt et al., "Human Papillomavirus Vectors;" WO 98/31837 by del Cardayre et al. "Evolution of Whole Cells and Organisms by Recursive Sequence Recombination;" WO 98/27230 by Patten and Stemmer, "Methods and Compositions for Polypeptide Engineering;" WO 98/27230 by Stemmer et al., "Methods for Optimization of Gene Therapy by Recursive Sequence Shuffling and Selection," WO 00/00632, "Methods for Generating Highly Diverse Libraries," WO 00/09679, "Methods for Obtaining in Vitro Recombined Polynucleotide Sequence Banks and Resulting Sequences," WO 98/42832 by Arnold et al., "Recombination of Polynucleotide Sequences Using Random or Defined Primers," WO 99/29902 by Arnold et al., "Method for Creating Polynucleotide and Polypeptide Sequences," WO 98/41653 by Vind, "An in Vitro Method for Construction of a DNA Library," WO 98/41622 by Borchert et al., "Method for Constructing a Library Using DNA Shuffling," and WO 98/42727 by Pati and Zarling, "Sequence Alterations using Homologous Recombination."

Protocols that can be used to practice the invention (providing details regarding various diversity generating methods) are described, e.g., in U.S. Patent application serial

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no. (USSN) 09/407,800, "SHUFFLING OF CODON ALTERED GENES" by Patten et al. filed Sep. 28, 1999; "EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE SEQUENCE RECOMBINATION" by del Cardayre et al., United States Patent No. 6,379,964; "OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION" by Crameri et al., United States Patent Nos. 6,319,714; 6,368,861; 6,376,246; 6,423,542; 6,426,224 and PCT/US00/01203; "USE OF CODON-VARIED OLIGONUCLEOTIDE SYNTHESIS FOR SYNTHETIC SHUFFLING" by Welch et al., United States Patent No. 6,436,675; "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jan. 18, 2000, (PCT/US00/01202) and, e.g. "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jul. 18, 2000 (U.S. Ser. No. 09/618,579); "METHODS OF POPULATING DATA STRUCTURES FOR USE IN EVOLUTIONARY SIMULATIONS" by Selifonov and Stemmer, filed Jan. 18, 2000 (PCT/US00/01138); and "SINGLE-STRANDED NUCLEIC ACID TEMPLATE-MEDIATED RECOMBINATION AND NUCLEIC ACID FRAGMENT ISOLATION" by Affholter, filed Sep. 6, 2000 (U.S. Ser. No. 09/656,549); and United States Patent Nos. 6,177,263; 6,153,410.

Non-stochastic, or "directed evolution," methods include, e.g., saturation mutagenesis, such as Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), or a combination thereof are used to modify the nucleic acids of the invention to generate cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes with new or altered properties (e.g., activity under highly acidic or alkaline conditions, high or low temperatures, and the like). Polypeptides encoded by the modified nucleic acids can be screened for an activity before testing for glucan hydrolysis or other activity. Any testing modality or protocol can be used, e.g., using a capillary array platform. See, e.g., U.S. Patent Nos. 6,361,974; 6,280,926; 5,939,250.

Gene Site Saturation mutagenesis, or, GSSM

The invention also provides methods for making enzyme using Gene Site Saturation mutagenesis, or, GSSM, as described herein, and also in U.S. Patent Nos. 6,171,820 and 6,579,258. In one aspect, codon primers containing a degenerate N,N,G/T sequence are used to introduce point mutations into a polynucleotide, e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or an

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antibody of the invention, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position, e.g., an amino acid residue in an enzyme active site or ligand binding site targeted to be modified. These oligonucleotides can comprise a contiguous first homologous sequence, a degenerate N,N,G/T sequence, and, optionally, a second homologous sequence. The downstream progeny translational products from the use of such oligonucleotides include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,G/T sequence includes codons for all 20 amino acids. In one aspect, one such degenerate oligonucleotide (comprised of, e.g., one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate cassettes are used – either in the same oligonucleotide or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. For example, more than one N,N,G/T sequence can be contained in one oligonucleotide to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligonucleotides serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

In one aspect, simultaneous mutagenesis of two or more contiguous amino acid positions is done using an oligonucleotide that contains contiguous N,N,G/T triplets, i.e. a degenerate (N,N,G/T)_n sequence. In another aspect, degenerate cassettes having less degeneracy than the N,N,G/T sequence are used. For example, it may be desirable in some instances to use (e.g. in an oligonucleotide) a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (e.g. in an oligo) a degenerate N,N,N triplet sequence.

In one aspect, use of degenerate triplets (e.g., N,N,G/T triplets) allows for systematic and easy generation of a full range of possible natural amino acids (for a total of 20 amino acids) into each and every amino acid position in a polypeptide (in alternative aspects, the methods also include generation of less than all possible substitutions per amino acid residue, or codon, position). For example, for a 100 amino

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acid polypeptide, 2000 distinct species (i.e. 20 possible amino acids per position X 100 amino acid positions) can be generated. Through the use of an oligonucleotide or set of oligonucleotides containing a degenerate N,N,G/T triplet, 32 individual sequences can code for all 20 possible natural amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using at least one such oligonucleotide, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligonucleotide in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel. Nondegenerate oligonucleotides can optionally be used in combination with degenerate primers disclosed; for example, nondegenerate oligonucleotides can be used to generate specific point mutations in a working polynucleotide. This provides one means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

In one aspect, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide (e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes) molecules such that all 20 natural amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide (other aspects use less than all 20 natural combinations). The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (e.g. cloned into a suitable host, e.g., *E. coli* host, using, e.g., an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide, such as increased glucan hydrolysis activity under alkaline or acidic conditions), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

In one aspect, upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino

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acid, and each of two favorable changes) and 3 positions. Thus, there are 3 x 3 x 3 or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (i.e. 2 at each of three positions) and no change at any position.

5 In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

10 The invention also provides for the use of proprietary codon primers (containing a degenerate N,N,N sequence) to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position (Gene Site Saturation Mutagenesis (GSSM)). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,N sequence and in one aspect but not
15 necessarily a second homologous sequence. The downstream progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,N sequence includes codons for all 20 amino acids.

In one aspect, one such degenerate oligo (comprised of one degenerate N,N,N
20 cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,N cassettes are used — either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,N sequence can be contained in one oligo to introduce amino acid
25 mutations at more than one site. This plurality of N,N,N sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,N sequence, to introduce any combination or permutation of amino acid additions, deletions and/or substitutions.

30 In one aspect, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,N triplets, *i.e.* a degenerate (N,N,N)_n sequence. In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,N sequence. For example, it may be desirable in some instances to use (*e.g.* in an oligo) a degenerate

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triplet sequence comprised of only one N, where the N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (*e.g.*, in an oligo) a degenerate N,N,N triplet sequence, N,N,G/T, or an N,N, G/C triplet sequence.

In one aspect, use of a degenerate triplet (such as N,N,G/T or an N,N, G/C triplet sequence) is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of possible amino acids (for a total of 20 amino acids) into each and every amino acid position in a polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

This invention also provides for the use of nondegenerate oligos, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

Thus, in one aspect of this invention, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when

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compared to the parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

In one aspect, upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, a favorable amino acid changes is identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

The invention provides for the use of saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

In addition to performing mutagenesis along the entire sequence of a gene, the instant invention provides that mutagenesis can be use to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized is in one aspect every integer from 15 to 100,000. Thus, instead of mutagenizing every position along a molecule, one can subject every or a discrete number of bases (in one aspect a subset totaling from 15 to 100,000) to mutagenesis. In one aspect, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized may be a codon. The mutations can be introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. Exemplary cassettes can have from 1 to 500 bases. Each nucleotide position in such heterologous cassettes be N, A, C, G, T, A/C, A/G, A/T, C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T (E can be referred to as a designer oligo).

In one aspect, saturation mutagenesis is comprised of mutagenizing a complete set of mutagenic cassettes (wherein each cassette is in one aspect about 1-500 bases in length) in defined polynucleotide sequence to be mutagenized (wherein the sequence to be mutagenized is in one aspect from about 15 to 100,000 bases in length). Thus, a group of mutations (ranging from 1 to 100 mutations) is introduced into each cassette to be

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mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons and groupings of particular nucleotide cassettes.

In one aspect, defined sequences to be mutagenized include a whole gene, pathway, cDNA, an entire open reading frame (ORF) and entire promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a “defined sequences” for this purpose may be any polynucleotide that a 15 base-polynucleotide sequence and polynucleotide sequences of lengths between 15 bases and 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

In one aspect, a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 and 20 amino acids at each position and a library of polypeptides encoded thereby.

Synthetic Ligation Reassembly (SLR)

The invention provides a non-stochastic gene modification system termed “synthetic ligation reassembly,” or simply “SLR,” a “directed evolution process,” to generate polypeptides, e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes or antibodies of the invention, with new or altered properties.

SLR is a method of ligating oligonucleotide fragments together non-stochastically. This method differs from stochastic oligonucleotide shuffling in that the nucleic acid building blocks are not shuffled, concatenated or chimerized randomly, but rather are assembled non-stochastically. See, e.g., U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776. In one aspect, SLR comprises the following steps: (a) providing a template polynucleotide, wherein the template polynucleotide comprises sequence encoding a homologous gene; (b) providing a plurality of building block polynucleotides, wherein the building block polynucleotides are designed to cross-over reassemble with the template polynucleotide at a predetermined sequence, and a building block polynucleotide comprises a sequence that is a variant of the homologous gene and a sequence homologous to the template polynucleotide flanking the variant

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sequence; (c) combining a building block polynucleotide with a template polynucleotide such that the building block polynucleotide cross-over reassembles with the template polynucleotide to generate polynucleotides comprising homologous gene sequence variations.

5 SLR does not depend on the presence of high levels of homology between polynucleotides to be rearranged. Thus, this method can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. SLR can be used to generate libraries comprised of over 10^{1000} different progeny chimeras. Thus, aspects of the present invention include non-stochastic methods
10 of producing a set of finalized chimeric nucleic acid molecule having an overall assembly order that is chosen by design. This method includes the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

15 The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends. If more than one assembly step is to be used, then the
20 overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In one aspect, the annealed building pieces are treated with an enzyme, such as a ligase (e.g. T4 DNA ligase), to achieve covalent bonding of the building pieces.

In one aspect, the design of the oligonucleotide building blocks is obtained by
25 analyzing a set of progenitor nucleic acid sequence templates that serve as a basis for producing a progeny set of finalized chimeric polynucleotides. These parental oligonucleotide templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, e.g., chimerized or shuffled. In one aspect of this method, the sequences of a plurality of parental nucleic
30 acid templates are aligned in order to select one or more demarcation points. The demarcation points can be located at an area of homology, and are comprised of one or more nucleotides. These demarcation points are in one aspect shared by at least two of the progenitor templates. The demarcation points can thereby be used to delineate the boundaries of oligonucleotide building blocks to be generated in order to rearrange the

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parental polynucleotides. The demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the final chimeric progeny molecules. A demarcation point can be an area of homology (comprised of at least one homologous nucleotide base) shared by at least two parental polynucleotide sequences. Alternatively, a demarcation point can be an area of homology that is shared by at least half of the parental polynucleotide sequences, or, it can be an area of homology that is shared by at least two thirds of the parental polynucleotide sequences. Even more in one aspect a serviceable demarcation points is an area of homology that is shared by at least three fourths of the parental polynucleotide sequences, or, it can be shared by at almost all of the parental polynucleotide sequences. In one aspect, a demarcation point is an area of homology that is shared by all of the parental polynucleotide sequences.

In one aspect, a ligation reassembly process is performed exhaustively in order to generate an exhaustive library of progeny chimeric polynucleotides. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, in another aspect, the assembly order (i.e. the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic) as described above. Because of the non-stochastic nature of this invention, the possibility of unwanted side products is greatly reduced.

In another aspect, the ligation reassembly method is performed systematically. For example, the method is performed in order to generate a systematically compartmentalized library of progeny molecules, with compartments that can be screened systematically, e.g. one by one. In other words this invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, a design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, these methods allow a potentially very large number of progeny molecules to be examined systematically in smaller groups. Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, these methods provide for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant ligation

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reassembly invention, the progeny molecules generated in one aspect comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. The saturation mutagenesis and optimized directed evolution methods also can be used to generate different progeny molecular species. It is appreciated that the invention provides freedom of choice and control regarding the selection of demarcation points, the size and number of the nucleic acid building blocks, and the size and design of the couplings. It is appreciated, furthermore, that the requirement for intermolecular homology is highly relaxed for the operability of this invention. In fact, demarcation points can even be chosen in areas of little or no intermolecular homology. For example, because of codon wobble, i.e. the degeneracy of codons, nucleotide substitutions can be introduced into nucleic acid building blocks without altering the amino acid originally encoded in the corresponding progenitor template. Alternatively, a codon can be altered such that the coding for an originally amino acid is altered. This invention provides that such substitutions can be introduced into the nucleic acid building block in order to increase the incidence of intermolecular homologous demarcation points and thus to allow an increased number of couplings to be achieved among the building blocks, which in turn allows a greater number of progeny chimeric molecules to be generated.

Synthetic gene reassembly

In one aspect, the present invention provides a non-stochastic method termed synthetic gene reassembly, that is somewhat related to stochastic shuffling, save that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-stochastically. See, e.g., U.S. Patent No. 6,537,776.

The synthetic gene reassembly method does not depend on the presence of a high level of homology between polynucleotides to be shuffled. The invention can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. Conceivably, synthetic gene reassembly can even be used to generate libraries comprised of over 10^{1000} different progeny chimeras.

Thus, in one aspect, the invention provides a non-stochastic method of producing a set of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

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The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be “serviceable” for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In a one aspect of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (*e.g.*, T4 DNA ligase) to achieve covalent bonding of the building pieces.

In a another aspect, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules. These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized or shuffled.

In one exemplification, the invention provides for the chimerization of a family of related genes and their encoded family of related products. In a particular exemplification, the encoded products are enzymes. The cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the present invention can be mutagenized in accordance with the methods described herein.

Thus according to one aspect of the invention, the sequences of a plurality of progenitor nucleic acid templates (*e.g.*, polynucleotides of the invention) are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the progeny molecules.

In one aspect, a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates and in one aspect at almost all of the progenitor templates. Even more in one aspect still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

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In a one aspect, the gene reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.* the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

In another aspect, the method provides that the gene reassembly process is performed systematically, for example to generate a systematically compartmentalized library, with compartments that can be screened systematically, *e.g.*, one by one. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, the instant invention provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant gene reassembly invention, the progeny molecules generated in one aspect comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. In a particularly aspect, such a generated library is comprised of greater than 10^3 to greater than 10^{1000} different progeny molecular species.

In one aspect, a set of finalized chimeric nucleic acid molecules, produced as described is comprised of a polynucleotide encoding a polypeptide. According to one aspect, this polynucleotide is a gene, which may be a man-made gene. According to another aspect, this polynucleotide is a gene pathway, which may be a man-made gene pathway. The invention provides that one or more man-made genes generated by the invention may be incorporated into a man-made gene pathway, such as pathway operable in a eukaryotic organism (including a plant).

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In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

Thus, according to another aspect, the invention provides that a nucleic acid building block can be used to introduce an intron. Thus, the invention provides that functional introns may be introduced into a man-made gene of the invention. The invention also provides that functional introns may be introduced into a man-made gene pathway of the invention. Accordingly, the invention provides for the generation of a chimeric polynucleotide that is a man-made gene containing one (or more) artificially introduced intron(s).

The invention also provides for the generation of a chimeric polynucleotide that is a man-made gene pathway containing one (or more) artificially introduced intron(s). In one aspect, the artificially introduced intron(s) are functional in one or more host cells for gene splicing much in the way that naturally-occurring introns serve functionally in gene splicing. The invention provides a process of producing man-made intron-containing polynucleotides to be introduced into host organisms for recombination and/or splicing.

A man-made gene produced using the invention can also serve as a substrate for recombination with another nucleic acid. Likewise, a man-made gene pathway produced using the invention can also serve as a substrate for recombination with another nucleic acid. In one aspect, the recombination is facilitated by, or occurs at, areas of homology between the man-made, intron-containing gene and a nucleic acid, which serves as a recombination partner. In one aspect, the recombination partner may also be a nucleic acid generated by the invention, including a man-made gene or a man-made gene pathway. Recombination may be facilitated by or may occur at areas of homology that exist at the one (or more) artificially introduced intron(s) in the man-made gene.

In one aspect, the synthetic gene reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which in one aspect has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (*i.e.* each having an overhang of zero nucleotides), or in one aspect one blunt end and one

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overhang, or more in one aspect still two overhangs. In one aspect, a useful overhang for this purpose may be a 3' overhang or a 5' overhang. Thus, a nucleic acid building block may have a 3' overhang or alternatively a 5' overhang or alternatively two 3' overhangs or alternatively two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design and is not random.

In one aspect, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos) and contacting them so as to allow them to anneal to form a double-stranded nucleic acid building block. A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Exemplary sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other exemplary size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between) and upper limits of from 2 bp to 100, 000 bp (including every integer value in between).

Many methods exist by which a double-stranded nucleic acid building block can be generated that is serviceable for the invention; and these are known in the art and can be readily performed by the skilled artisan. According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another aspect, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this aspect, a double-stranded nucleic acid building block can be used to introduce codon degeneracy. In one aspect the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,G/T cassettes or alternatively using one or more N,N,N cassettes.

The *in vivo* recombination method of the invention can be performed blindly on a pool of unknown hybrids or alleles of a specific polynucleotide or sequence. However, it is not necessary to know the actual DNA or RNA sequence of the specific polynucleotide. The approach of using recombination within a mixed population of genes can be useful for the generation of any useful proteins, for example, a cellulase of the

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invention or a variant thereof. This approach may be used to generate proteins having altered specificity or activity. The approach may also be useful for the generation of hybrid nucleic acid sequences, for example, promoter regions, introns, exons, enhancer sequences, 3' untranslated regions or 5' untranslated regions of genes. Thus this approach may be used to generate genes having increased rates of expression. This approach may also be useful in the study of repetitive DNA sequences. Finally, this approach may be useful to make ribozymes or aptamers of the invention.

In one aspect the invention described herein is directed to the use of repeated cycles of reductive reassortment, recombination and selection which allow for the directed molecular evolution of highly complex linear sequences, such as DNA, RNA or proteins through recombination.

Optimized Directed Evolution System

The invention provides a non-stochastic gene modification system termed "optimized directed evolution system" to generate polypeptides, e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes or antibodies of the invention, with new or altered properties. In one aspect, optimized directed evolution is directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of nucleic acids through recombination.

Optimized directed evolution allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events. A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. This method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, this method provides a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. Previously, if one generated, for example, 10^{13} chimeric molecules during a reaction, it would be extremely difficult to test such a high number of chimeric variants for a particular activity. Moreover, a significant portion of the progeny population would have a very

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high number of crossover events which resulted in proteins that were less likely to have increased levels of a particular activity. By using these methods, the population of chimeric molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

One method for creating a chimeric progeny polynucleotide sequence is to create oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide in one aspect includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. Alternatively protocols for practicing these methods of the invention can be found in U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776; 6,361,974.

The number of oligonucleotides generated for each parental variant bears a relationship to the total number of resulting crossovers in the chimeric molecule that is ultimately created. For example, three parental nucleotide sequence variants might be provided to undergo a ligation reaction in order to find a chimeric variant having, for example, greater activity at high temperature. As one example, a set of 50 oligonucleotide sequences can be generated corresponding to each portions of each parental variant. Accordingly, during the ligation reassembly process there could be up to 50 crossover events within each of the chimeric sequences. The probability that each of the generated chimeric polynucleotides will contain oligonucleotides from each parental variant in alternating order is very low. If each oligonucleotide fragment is present in the ligation reaction in the same molar quantity it is likely that in some positions oligonucleotides from the same parental polynucleotide will ligate next to one another and thus not result in a crossover event. If the concentration of each oligonucleotide from each parent is kept constant during any ligation step in this example, there is a 1/3 chance (assuming 3 parents) that an oligonucleotide from the same parental variant will ligate within the chimeric sequence and produce no crossover.

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Accordingly, a probability density function (PDF) can be determined to predict the population of crossover events that are likely to occur during each step in a ligation reaction given a set number of parental variants, a number of oligonucleotides corresponding to each variant, and the concentrations of each variant during each step in the ligation reaction. The statistics and mathematics behind determining the PDF is described below. By utilizing these methods, one can calculate such a probability density function, and thus enrich the chimeric progeny population for a predetermined number of crossover events resulting from a particular ligation reaction. Moreover, a target number of crossover events can be predetermined, and the system then programmed to calculate the starting quantities of each parental oligonucleotide during each step in the ligation reaction to result in a probability density function that centers on the predetermined number of crossover events. These methods are directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of a nucleic acid encoding a polypeptide through recombination. This system allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events. A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. The method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, these methods provide a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. By using the methods described herein, the population of chimeric molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which

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oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

In one aspect, the method creates a chimeric progeny polynucleotide sequence by creating oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide in one aspect includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. See also U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776; 6,361,974.

Determining Crossover Events

Aspects of the invention include a system and software that receive a desired crossover probability density function (PDF), the number of parent genes to be reassembled, and the number of fragments in the reassembly as inputs. The output of this program is a "fragment PDF" that can be used to determine a recipe for producing reassembled genes, and the estimated crossover PDF of those genes. The processing described herein is in one aspect performed in MATLAB™ (The Mathworks, Natick, Massachusetts) a programming language and development environment for technical computing.

Iterative Processes

Any process of the invention can be iteratively repeated, e.g., a nucleic acid encoding an altered or new cellulase phenotype, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention, can be identified, re-isolated, again modified, re-tested for activity. This process can be iteratively repeated until a desired phenotype is engineered. For example, an entire biochemical anabolic or catabolic pathway can be engineered into a cell, including, e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity.

Similarly, if it is determined that a particular oligonucleotide has no affect at all on the desired trait (e.g., a new cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme phenotype), it can be removed as a variable by synthesizing larger parental oligonucleotides that include the sequence to be removed. Since incorporating the sequence within a larger sequence prevents any crossover events, there will no longer be any variation of this sequence in the progeny polynucleotides. This iterative practice of determining which oligonucleotides are most related to the

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desired trait, and which are unrelated, allows more efficient exploration all of the possible protein variants that might be provide a particular trait or activity.

In vivo shuffling

In various aspects, *in vivo* shuffling of molecules is used in methods of the invention to provide variants of polypeptides of the invention, e.g., antibodies of the invention or cellulases of the invention, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, and the like. *In vivo* shuffling can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves 1) the recognition of homologies; 2) strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally 3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

In another aspect, the invention includes a method for producing a hybrid polynucleotide from at least a first polynucleotide and a second polynucleotide. The invention can be used to produce a hybrid polynucleotide by introducing at least a first polynucleotide and a second polynucleotide (e.g., one, or both, being an exemplary cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme-encoding sequence of the invention) which share at least one region of partial sequence homology into a suitable host cell. The regions of partial sequence homology promote processes which result in sequence reorganization producing a hybrid polynucleotide. The term "hybrid polynucleotide", as used herein, is any nucleotide sequence which results from the method of the present invention and contains sequence from at least two original polynucleotide sequences. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

In one aspect, *vivo* reassortment focuses on "inter-molecular" processes collectively referred to as "recombination"; which in bacteria, is generally viewed as a "RecA-dependent" phenomenon. The invention can rely on recombination processes of a host cell to recombine and re-assort sequences, or the cells' ability to mediate reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion.

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This process of “reductive reassortment” occurs by an “intra-molecular”, RecA-independent process.

In another aspect of the invention, novel polynucleotides can be generated by the process of reductive reassortment. The method involves the generation of constructs containing consecutive sequences (original encoding sequences), their insertion into an appropriate vector and their subsequent introduction into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences and results in the production of novel molecular species. Various treatments may be applied to enhance the rate of reassortment. These could include treatment with ultra-violet light, or DNA damaging chemicals and/or the use of host cell lines displaying enhanced levels of “genetic instability”. Thus the reassortment process may involve homologous recombination or the natural property of quasi-repeated sequences to direct their own evolution.

Repeated or “quasi-repeated” sequences play a role in genetic instability. In one aspect, “quasi-repeats” are repeats that are not restricted to their original unit structure. Quasi-repeated units can be presented as an array of sequences in a construct; consecutive units of similar sequences. Once ligated, the junctions between the consecutive sequences become essentially invisible and the quasi-repetitive nature of the resulting construct is now continuous at the molecular level. The deletion process the cell performs to reduce the complexity of the resulting construct operates between the quasi-repeated sequences. The quasi-repeated units provide a practically limitless repertoire of templates upon which slippage events can occur. In one aspect, the constructs containing the quasi-repeats thus effectively provide sufficient molecular elasticity that deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units.

When the quasi-repeated sequences are all ligated in the same orientation, for instance head to tail or vice versa, the cell cannot distinguish individual units. Consequently, the reductive process can occur throughout the sequences. In contrast, when for example, the units are presented head to head, rather than head to tail, the inversion delineates the endpoints of the adjacent unit so that deletion formation will favor the loss of discrete units. Thus, it is preferable with the present method that the sequences are in the same orientation. Random orientation of quasi-repeated sequences

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will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. However, while having fewer of the contiguous sequences in the same orientation decreases the efficiency, it may still provide sufficient elasticity for the effective recovery of novel molecules. Constructs can be made with the quasi-repeated sequences in the same orientation to allow higher efficiency.

Sequences can be assembled in a head to tail orientation using any of a variety of methods, including the following:

- a) Primers that include a poly-A head and poly-T tail which when made single-stranded would provide orientation can be utilized. This is accomplished by having the first few bases of the primers made from RNA and hence easily removed RNaseH.
- b) Primers that include unique restriction cleavage sites can be utilized. Multiple sites, a battery of unique sequences and repeated synthesis and ligation steps would be required.
- c) The inner few bases of the primer could be thiolated and an exonuclease used to produce properly tailed molecules.

In one aspect, the recovery of the re-assorted sequences relies on the identification of cloning vectors with a reduced repetitive index (RI). The re-assorted encoding sequences can then be recovered by amplification. The products are re-cloned and expressed. The recovery of cloning vectors with reduced RI can be affected by:

- 1) The use of vectors only stably maintained when the construct is reduced in complexity.
- 2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and size fractionated on either an agarose gel, or column with a low molecular weight cut off utilizing standard procedures.
- 3) The recovery of vectors containing interrupted genes which can be selected when insert size decreases.
- 4) The use of direct selection techniques with an expression vector and the appropriate selection.

Encoding sequences (for example, genes) from related organisms may demonstrate a high degree of homology and encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats.

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However, while the examples illustrated below demonstrate the reassortment of nearly identical original encoding sequences (quasi-repeats), this process is not limited to such nearly identical repeats.

The following example demonstrates an exemplary method of the invention.

5 Encoding nucleic acid sequences (quasi-repeats) derived from three (3) unique species are described. Each sequence encodes a protein with a distinct set of properties. Each of the sequences differs by a single or a few base pairs at a unique position in the sequence. The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the
10 population of ligated molecules. The number of quasi-repeat units can be controlled by the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

Once formed, the constructs may, or may not be size fractionated on an agarose gel according to published protocols, inserted into a cloning vector and transfected into an
15 appropriate host cell. The cells are then propagated and “reductive reassortment” is effected. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an “intra-molecular” mechanism, or mediated by recombination-like events through “inter-molecular” mechanisms is
20 immaterial. The end result is a reassortment of the molecules into all possible combinations.

Optionally, the method comprises the additional step of screening the library members of the shuffled pool to identify individual shuffled library members having the ability to bind or otherwise interact, or catalyze a particular reaction (*e.g.*, such as
25 catalytic domain of an enzyme) with a predetermined macromolecule, such as for example a proteinaceous receptor, an oligosaccharide, virion, or other predetermined compound or structure.

The polypeptides that are identified from such libraries can be used for therapeutic, diagnostic, research and related purposes (*e.g.*, catalysts, solutes for
30 increasing osmolarity of an aqueous solution and the like) and/or can be subjected to one or more additional cycles of shuffling and/or selection.

In another aspect, it is envisioned that prior to or during recombination or reassortment, polynucleotides generated by the method of the invention can be subjected to agents or processes which promote the introduction of mutations into the original

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polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded therefrom. The agents or processes which promote mutagenesis can include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-Adenine (*See* Sun and Hurley, (1992); an
5 N-acetylated or deacetylated 4'-fluoro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See* , for example, van de Poll *et al.* (1992)); or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See* also, van de Poll *et al.* (1992), pp. 751-758); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon (PAH) DNA adduct capable of inhibiting DNA replication, such as
10 7-bromomethyl-benz[*a*]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-BP"), 1,2-dibromo-3-chloropropane ("DBCP"), 2-bromoacrolein (2BA), benzo[*a*]pyrene-7,8-dihydrodiol-9-10-epoxide ("BPDE"), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-*f*]-quinoline ("N-hydroxy-IQ") and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-*f*]-pyridine ("N-hydroxy-PhIP"). Exemplary means for
15 slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-1065-(N3-Adenine). Particularly encompassed means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

20 In another aspect the invention is directed to a method of producing recombinant proteins having biological activity by treating a sample comprising double-stranded template polynucleotides encoding a wild-type protein under conditions according to the invention which provide for the production of hybrid or re-assorted polynucleotides.

Producing sequence variants

25 The invention also provides additional methods for making sequence variants of the nucleic acid (e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme) sequences of the invention. The invention also provides additional methods for isolating cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes using the nucleic acids and polypeptides of
30 the invention. In one aspect, the invention provides for variants of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme coding sequence (e.g., a gene, cDNA or message) of the invention, which can be altered by any means, including, e.g., random or stochastic methods, or, non-stochastic, or "directed evolution," methods, as described above.

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The isolated variants may be naturally occurring. Variant can also be created *in vitro*. Variants may be created using genetic engineering techniques such as site directed mutagenesis, random chemical mutagenesis, Exonuclease III deletion procedures, and standard cloning techniques. Alternatively, such variants, fragments, analogs, or derivatives may be created using chemical synthesis or modification procedures. Other methods of making variants are also familiar to those skilled in the art. These include procedures in which nucleic acid sequences obtained from natural isolates are modified to generate nucleic acids which encode polypeptides having characteristics which enhance their value in industrial or laboratory applications. In such procedures, a large number of variant sequences having one or more nucleotide differences with respect to the sequence obtained from the natural isolate are generated and characterized. These nucleotide differences can result in amino acid changes with respect to the polypeptides encoded by the nucleic acids from the natural isolates.

For example, variants may be created using error prone PCR. In one aspect of error prone PCR, the PCR is performed under conditions where the copying fidelity of the DNA polymerase is low, such that a high rate of point mutations is obtained along the entire length of the PCR product. Error prone PCR is described, e.g., in Leung (1989) Technique 1:11-15) and Caldwell (1992) PCR Methods Applic. 2:28-33. Briefly, in such procedures, nucleic acids to be mutagenized are mixed with PCR primers, reaction buffer, MgCl₂, MnCl₂, Taq polymerase and an appropriate concentration of dNTPs for achieving a high rate of point mutation along the entire length of the PCR product. For example, the reaction may be performed using 20 fmoles of nucleic acid to be mutagenized, 30 pmole of each PCR primer, a reaction buffer comprising 50mM KCl, 10mM Tris HCl (pH 8.3) and 0.01% gelatin, 7mM MgCl₂, 0.5mM MnCl₂, 5 units of Taq polymerase, 0.2mM dGTP, 0.2mM dATP, 1mM dCTP, and 1mM dTTP. PCR may be performed for 30 cycles of 94°C for 1 min, 45°C for 1 min, and 72°C for 1 min. However, it will be appreciated that these parameters may be varied as appropriate. The mutagenized nucleic acids are cloned into an appropriate vector and the activities of the polypeptides encoded by the mutagenized nucleic acids are evaluated.

In one aspect, variants are created using oligonucleotide directed mutagenesis to generate site-specific mutations in any cloned DNA of interest. Oligonucleotide mutagenesis is described, e.g., in Reidhaar-Olson (1988) Science 241:53-57. Briefly, in such procedures a plurality of double stranded oligonucleotides bearing one or more mutations to be introduced into the cloned DNA are synthesized and inserted into the

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cloned DNA to be mutagenized. In one aspect, clones containing the mutagenized DNA are recovered, expressed, and the activities of the polypeptide encoded therein assessed.

Another method for generating variants is assembly PCR. Assembly PCR involves the assembly of a PCR product from a mixture of small DNA fragments. A large number of different PCR reactions occur in parallel in the same vial, with the products of one reaction priming the products of another reaction. Assembly PCR is described in, e.g., U.S. Patent No. 5,965,408.

In one aspect, sexual PCR mutagenesis is an exemplary method of generating variants of the invention. In one aspect of sexual PCR mutagenesis forced homologous recombination occurs between DNA molecules of different but highly related DNA sequence *in vitro*, as a result of random fragmentation of the DNA molecule based on sequence homology, followed by fixation of the crossover by primer extension in a PCR reaction. Sexual PCR mutagenesis is described, e.g., in Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751. Briefly, in such procedures a plurality of nucleic acids to be recombined are digested with DNase to generate fragments having an average size of 50-200 nucleotides. Fragments of the desired average size are purified and resuspended in a PCR mixture. PCR is conducted under conditions which facilitate recombination between the nucleic acid fragments. For example, PCR may be performed by resuspending the purified fragments at a concentration of 10-30ng/ μ l in a solution of 0.2mM of each dNTP, 2.2mM MgCl₂, 50mM KCL, 10mM Tris HCl, pH 9.0, and 0.1% Triton X-100. 2.5 units of Taq polymerase per 100:1 of reaction mixture is added and PCR is performed using the following regime: 94°C for 60 seconds, 94°C for 30 seconds, 50-55°C for 30 seconds, 72°C for 30 seconds (30-45 times) and 72°C for 5 minutes. However, it will be appreciated that these parameters may be varied as appropriate. In some aspects, oligonucleotides may be included in the PCR reactions. In other aspects, the Klenow fragment of DNA polymerase I may be used in a first set of PCR reactions and Taq polymerase may be used in a subsequent set of PCR reactions. Recombinant sequences are isolated and the activities of the polypeptides they encode are assessed.

In one aspect, variants are created by *in vivo* mutagenesis. In some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an *E. coli* strain, which carries mutations in one or more of the DNA repair pathways. Such "mutator" strains have a higher random mutation rate than that of a wild-type parent. Propagating the DNA in one of these strains will eventually generate random mutations within the DNA. Mutator strains suitable for

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use for *in vivo* mutagenesis are described in PCT Publication No. WO 91/16427, published October 31, 1991, entitled "Methods for Phenotype Creation from Multiple Gene Populations".

5 Variants may also be generated using cassette mutagenesis. In cassette mutagenesis a small region of a double stranded DNA molecule is replaced with a synthetic oligonucleotide "cassette" that differs from the native sequence. The oligonucleotide often contains completely and/or partially randomized native sequence.

10 Recursive ensemble mutagenesis may also be used to generate variants. Recursive ensemble mutagenesis is an algorithm for protein engineering (protein mutagenesis) developed to produce diverse populations of phenotypically related mutants whose members differ in amino acid sequence. This method uses a feedback mechanism to control successive rounds of combinatorial cassette mutagenesis. Recursive ensemble mutagenesis is described, e.g., in Arkin (1992) Proc. Natl. Acad. Sci. USA 89:7811-7815.

15 In some aspects, variants are created using exponential ensemble mutagenesis. Exponential ensemble mutagenesis is a process for generating combinatorial libraries with a high percentage of unique and functional mutants, wherein small groups of residues are randomized in parallel to identify, at each altered position, amino acids which lead to functional proteins. Exponential ensemble mutagenesis is described, e.g., in Delegrave (1993) Biotechnology Res. 11:1548-1552. Random and site-directed
20 mutagenesis are described, e.g., in Arnold (1993) Current Opinion in Biotechnology 4:450-455.

In some aspects, the variants are created using shuffling procedures wherein portions of a plurality of nucleic acids which encode distinct polypeptides are fused together to create chimeric nucleic acid sequences which encode chimeric polypeptides as
25 described in U.S. Patent No. 5,965,408, filed July 9, 1996, entitled, "Method of DNA Reassembly by Interrupting Synthesis" and U.S. Patent No. 5,939,250, filed May 22, 1996, entitled, "Production of Enzymes Having Desired Activities by Mutagenesis.

The variants of the polypeptides of the invention may be variants in which one or more of the amino acid residues of the polypeptides of the sequences of the invention are
30 substituted with a conserved or non-conserved amino acid residue (in one aspect a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code.

In one aspect, conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. In one aspect,

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conservative substitutions of the invention comprise the following replacements:

replacements of an aliphatic amino acid such as Alanine, Valine, Leucine and Isoleucine with another aliphatic amino acid; replacement of a Serine with a Threonine or vice versa; replacement of an acidic residue such as Aspartic acid and Glutamic acid with another
5 acidic residue; replacement of a residue bearing an amide group, such as Asparagine and Glutamine, with another residue bearing an amide group; exchange of a basic residue such as Lysine and Arginine with another basic residue; and replacement of an aromatic residue such as Phenylalanine, Tyrosine with another aromatic residue.

Other variants are those in which one or more of the amino acid residues of a
10 polypeptide of the invention includes a substituent group. In one aspect, other variants are those in which the polypeptide is associated with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol). Additional variants are those in which additional amino acids are fused to the polypeptide, such as a leader sequence, a secretory sequence, a proprotein sequence or a sequence
15 which facilitates purification, enrichment, or stabilization of the polypeptide.

In some aspects, the fragments, derivatives and analogs retain the same biological function or activity as the polypeptides of the invention. In other aspects, the fragment, derivative, or analog includes a proprotein, such that the fragment, derivative, or analog can be activated by cleavage of the proprotein portion to produce an active polypeptide.

20 *Optimizing codons to achieve high levels of protein expression in host cells*

The invention provides methods for modifying cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase, enzyme-encoding nucleic acids to modify (e.g., optimize) codon usage. In one aspect, the invention provides methods for modifying codons in a nucleic acid encoding a cellulase, e.g., endoglucanase,
25 cellobiohydrolase, mannanase and/or beta-glucosidase enzyme to increase or decrease its expression in a host cell. The invention also provides nucleic acids encoding a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme modified to increase its expression in a host cell, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme so modified, and methods
30 of making the modified cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes. The method comprises identifying a “non-preferred” or a “less preferred” codon in cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase, enzyme-encoding nucleic acid and replacing one or more of these non- preferred or less preferred codons with a “preferred codon” encoding

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the same amino acid as the replaced codon and at least one non- preferred or less preferred codon in the nucleic acid has been replaced by a preferred codon encoding the same amino acid. A preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non- preferred or less preferred codon is a codon under-

5 represented in coding sequences in genes in the host cell.

Host cells for expressing the nucleic acids, expression cassettes and vectors of the invention include bacteria, yeast, fungi, plant cells, insect cells and mammalian cells (see discussion, above). Thus, the invention provides methods for optimizing codon usage in all of these cells, codon-altered nucleic acids and polypeptides made by the codon-altered

10 nucleic acids. Exemplary host cells include gram negative bacteria, such as *Escherichia coli*; gram positive bacteria, such as *Streptomyces* sp., *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, *Bacillus subtilis*, *Bacillus cereus*. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as *Saccharomyces* sp., including *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, and

15 *Kluyveromyces lactis*, *Hansenula polymorpha*, *Aspergillus niger*, and mammalian cells and cell lines and insect cells and cell lines. Thus, the invention also includes nucleic acids and polypeptides optimized for expression in these organisms and species.

For example, the codons of a nucleic acid encoding a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme isolated

20 from a bacterial cell are modified such that the nucleic acid is optimally expressed in a bacterial cell different from the bacteria from which the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme was derived, a yeast, a fungi, a plant cell, an insect cell or a mammalian cell. Methods for optimizing codons are well known in the art, see, e.g., U.S. Patent No. 5,795,737; Baca (2000) Int. J. Parasitol. 30:113-118; Hale (1998) Protein Expr. Purif. 12:185-188; Narum (2001) Infect. Immun. 69:7250-7253. See also Narum (2001) Infect. Immun. 69:7250-7253, describing optimizing codons in mouse systems; Outchkourov (2002) Protein Expr. Purif. 24:18-24, describing optimizing codons in yeast; Feng (2000) Biochemistry 39:15399-15409, describing optimizing codons in *E. coli*; Humphreys (2000) Protein Expr. Purif. 20:252-

25 264, describing optimizing codon usage that affects secretion in *E. coli*.

Transgenic non-human animals

The invention provides transgenic non-human animals comprising a nucleic acid, a polypeptide (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme), an expression cassette or vector or a transfected or transformed

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cell of the invention. The invention also provides methods of making and using these transgenic non-human animals.

The transgenic non-human animals can be, e.g., dogs, goats, rabbits, sheep, pigs (including all swine, hogs and related animals), cows, rats and mice, comprising the nucleic acids of the invention. These animals can be used, e.g., as *in vivo* models to study cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, or, as models to screen for agents that change the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity *in vivo*. The coding sequences for the polypeptides to be expressed in the transgenic non-human animals can be designed to be constitutive, or, under the control of tissue-specific, developmental-specific or inducible transcriptional regulatory factors.

Transgenic non-human animals can be designed and generated using any method known in the art; see, e.g., U.S. Patent Nos. 6,211,428; 6,187,992; 6,156,952; 6,118,044; 6,111,166; 6,107,541; 5,959,171; 5,922,854; 5,892,070; 5,880,327; 5,891,698; 5,639,940; 5,573,933; 5,387,742; 5,087,571, describing making and using transformed cells and eggs and transgenic mice, rats, rabbits, sheep, pigs and cows. See also, e.g., Pollock (1999) J. Immunol. Methods 231:147-157, describing the production of recombinant proteins in the milk of transgenic dairy animals; Baguisi (1999) Nat. Biotechnol. 17:456-461, demonstrating the production of transgenic goats. U.S. Patent No. 6,211,428, describes making and using transgenic non-human mammals which express in their brains a nucleic acid construct comprising a DNA sequence. U.S. Patent No. 5,387,742, describes injecting cloned recombinant or synthetic DNA sequences into fertilized mouse eggs, implanting the injected eggs in pseudo-pregnant females, and growing to term transgenic mice. U.S. Patent No. 6,187,992, describes making and using a transgenic mouse.

“Knockout animals” can also be used to practice the methods of the invention. For example, in one aspect, the transgenic or modified animals of the invention comprise a “knockout animal,” e.g., a “knockout mouse,” engineered not to express an endogenous gene, which is replaced with a gene expressing a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention, or, a fusion protein comprising a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention.

Transgenic Plants and Seeds

The invention provides transgenic plants and seeds comprising a nucleic acid, a polypeptide (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or

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beta-glucosidase enzyme), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides plant products, e.g., oils, seeds, leaves, extracts and the like, comprising a nucleic acid and/or a polypeptide (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme) of the invention. The transgenic plant can be dicotyledonous (a dicot) or monocotyledonous (a monocot). The invention also provides methods of making and using these transgenic plants and seeds. The transgenic plant or plant cell expressing a polypeptide of the present invention may be constructed in accordance with any method known in the art. See, for example, U.S. Patent No. 6,309,872.

Nucleic acids and expression constructs of the invention can be introduced into a plant cell by any means. For example, nucleic acids or expression constructs can be introduced into the genome of a desired plant host, or, the nucleic acids or expression constructs can be episomes. Introduction into the genome of a desired plant can be such that the host's cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme production is regulated by endogenous transcriptional or translational control elements. The invention also provides "knockout plants" where insertion of gene sequence by, e.g., homologous recombination, has disrupted the expression of the endogenous gene. Means to generate "knockout" plants are well-known in the art, see, e.g., Strepp (1998) Proc Natl. Acad. Sci. USA 95:4368-4373; Miao (1995) Plant J 7:359-365. See discussion on transgenic plants, below.

The nucleic acids of the invention can be used to confer desired traits on essentially any plant, e.g., on starch-producing plants, such as potato, tomato, soybean, beets, corn, wheat, rice, barley, and the like. Nucleic acids of the invention can be used to manipulate metabolic pathways of a plant in order to optimize or alter host's expression of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. The can change cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity in a plant. Alternatively, a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention can be used in production of a transgenic plant to produce a compound not naturally produced by that plant. This can lower production costs or create a novel product.

In one aspect, the first step in production of a transgenic plant involves making an expression construct for expression in a plant cell. These techniques are well known in the art. They can include selecting and cloning a promoter, a coding sequence for

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facilitating efficient binding of ribosomes to mRNA and selecting the appropriate gene terminator sequences. One exemplary constitutive promoter is CaMV35S, from the cauliflower mosaic virus, which generally results in a high degree of expression in plants. Other promoters are more specific and respond to cues in the plant's internal or external environment. An exemplary light-inducible promoter is the promoter from the *cab* gene,
5 encoding the major chlorophyll a/b binding protein.

In one aspect, the nucleic acid is modified to achieve greater expression in a plant cell. For example, a sequence of the invention is likely to have a higher percentage of A-T nucleotide pairs compared to that seen in a plant, some of which prefer G-C nucleotide
10 pairs. Therefore, A-T nucleotides in the coding sequence can be substituted with G-C nucleotides without significantly changing the amino acid sequence to enhance production of the gene product in plant cells.

Selectable marker gene can be added to the gene construct in order to identify plant cells or tissues that have successfully integrated the transgene. This may be
15 necessary because achieving incorporation and expression of genes in plant cells is a rare event, occurring in just a few percent of the targeted tissues or cells. Selectable marker genes encode proteins that provide resistance to agents that are normally toxic to plants, such as antibiotics or herbicides. Only plant cells that have integrated the selectable marker gene will survive when grown on a medium containing the appropriate antibiotic
20 or herbicide. As for other inserted genes, marker genes also require promoter and termination sequences for proper function.

In one aspect, making transgenic plants or seeds comprises incorporating sequences of the invention and, optionally, marker genes into a target expression construct (e.g., a plasmid), along with positioning of the promoter and the terminator
25 sequences. This can involve transferring the modified gene into the plant through a suitable method. For example, a construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. For example, see, e.g., Christou
30 (1997) *Plant Mol. Biol.* 35:197-203; Pawlowski (1996) *Mol. Biotechnol.* 6:17-30; Klein (1987) *Nature* 327:70-73; Takumi (1997) *Genes Genet. Syst.* 72:63-69, discussing use of particle bombardment to introduce transgenes into wheat; and Adam (1997) *supra*, for use of particle bombardment to introduce YACs into plant cells. For example, Rinehart (1997) *supra*, used particle bombardment to generate transgenic cotton plants. Apparatus

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for accelerating particles is described U.S. Pat. No. 5,015,580; and, the commercially available BioRad (Biolistics) PDS-2000 particle acceleration instrument; see also, John, U.S. Patent No. 5,608,148; and Ellis, U.S. Patent No. 5,681,730, describing particle-mediated transformation of gymnosperms.

5 In one aspect, protoplasts can be immobilized and injected with a nucleic acids, e.g., an expression construct. Although plant regeneration from protoplasts is not easy with cereals, plant regeneration is possible in legumes using somatic embryogenesis from protoplast derived callus. Organized tissues can be transformed with naked DNA using gene gun technique, where DNA is coated on tungsten microprojectiles, shot 1/100th the
10 size of cells, which carry the DNA deep into cells and organelles. Transformed tissue is then induced to regenerate, usually by somatic embryogenesis. This technique has been successful in several cereal species including maize and rice.

 Nucleic acids, e.g., expression constructs, can also be introduced in to plant cells using recombinant viruses. Plant cells can be transformed using viral vectors, such as,
15 e.g., tobacco mosaic virus derived vectors (Rouwendal (1997) Plant Mol. Biol. 33:989-999), see Porta (1996) "Use of viral replicons for the expression of genes in plants," Mol. Biotechnol. 5:209-221.

 Alternatively, nucleic acids, e.g., an expression construct, can be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host
20 will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, e.g., Horsch (1984) *Science* 233:496-498; Fraley (1983) *Proc. Natl. Acad. Sci. USA* 80:4803 (1983); *Gene Transfer to Plants*, Potrykus, ed. (Springer-Verlag, Berlin 1995). The DNA in an *A. tumefaciens* cell is
25 contained in the bacterial chromosome as well as in another structure known as a Ti (tumor-inducing) plasmid. The Ti plasmid contains a stretch of DNA termed T-DNA (~20 kb long) that is transferred to the plant cell in the infection process and a series of vir (virulence) genes that direct the infection process. *A. tumefaciens* can only infect a plant
30 through wounds: when a plant root or stem is wounded it gives off certain chemical signals, in response to which, the vir genes of *A. tumefaciens* become activated and direct a series of events necessary for the transfer of the T-DNA from the Ti plasmid to the plant's chromosome. The T-DNA then enters the plant cell through the wound. One

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speculation is that the T-DNA waits until the plant DNA is being replicated or transcribed, then inserts itself into the exposed plant DNA. In order to use *A. tumefaciens* as a transgene vector, the tumor-inducing section of T-DNA have to be removed, while retaining the T-DNA border regions and the vir genes. The transgene is then inserted
5 between the T-DNA border regions, where it is transferred to the plant cell and becomes integrated into the plant's chromosomes.

The invention provides for the transformation of monocotyledonous plants using the nucleic acids of the invention, including important cereals, see Hiei (1997) Plant Mol. Biol. 35:205-218. See also, e.g., Horsch, Science (1984) 233:496; Fraley (1983) Proc.
10 Natl. Acad. Sci USA 80:4803; Thykjaer (1997) supra; Park (1996) Plant Mol. Biol. 32:1135-1148, discussing T-DNA integration into genomic DNA. See also D'Halluin, U.S. Patent No. 5,712,135, describing a process for the stable integration of a DNA comprising a gene that is functional in a cell of a cereal, or other monocotyledonous plant.

15 In one aspect, the third step involves selection and regeneration of whole plants capable of transmitting the incorporated target gene to the next generation. Such regeneration techniques may use manipulation of certain phytohormones in a tissue culture growth medium. In one aspect, the method uses a biocide and/or herbicide marker that has been introduced together with the desired nucleotide sequences. Plant
20 regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described
25 generally in Klee (1987) Ann. Rev. of Plant Phys. 38:467-486. To obtain whole plants from transgenic tissues such as immature embryos, they can be grown under controlled environmental conditions in a series of media containing nutrients and hormones, a process known as tissue culture. Once whole plants are generated and produce seed, evaluation of the progeny begins.

30 In one aspect, after the expression cassette is stably incorporated in transgenic plants, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. Since transgenic expression of the nucleic acids of the invention leads to phenotypic changes, plants comprising the recombinant nucleic acids of the invention can be sexually

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crossed with a second plant to obtain a final product. Thus, the seed of the invention can be derived from a cross between two transgenic plants of the invention, or a cross between a plant of the invention and another plant. The desired effects (e.g., expression of the polypeptides of the invention to produce a plant in which flowering behavior is altered) can be enhanced when both parental plants express the polypeptides (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme) of the invention. The desired effects can be passed to future plant generations by standard propagation means.

In one aspect, the nucleic acids and polypeptides of the invention are expressed in or inserted in any plant or seed. Transgenic plants of the invention can be dicotyledonous or monocotyledonous. Examples of monocot transgenic plants of the invention are grasses, such as meadow grass (blue grass, *Poa*), forage grass such as festuca, lolium, temperate grass, such as *Agrostis*, and cereals, e.g., wheat, oats, rye, barley, rice, sorghum, and maize (corn). Examples of dicot transgenic plants of the invention are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous plants (family *Brassicaceae*), such as cauliflower, rape seed, and the closely related model organism *Arabidopsis thaliana*. Thus, the transgenic plants and seeds of the invention include a broad range of plants, including, but not limited to, species from the genera *Anacardium*, *Arachis*, *Asparagus*, *Atropa*, *Avena*, *Brassica*, *Citrus*, *Citrullus*, *Capsicum*, *Carthamus*, *Cocos*, *Coffea*, *Cucumis*, *Cucurbita*, *Daucus*, *Elaeis*, *Fragaria*, *Glycine*, *Gossypium*, *Helianthus*, *Heterocallis*, *Hordeum*, *Hyoscyamus*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*, *Malus*, *Manihot*, *Majorana*, *Medicago*, *Nicotiana*, *Olea*, *Oryza*, *Panicum*, *Pennisetum*, *Persea*, *Phaseolus*, *Pistachia*, *Pisum*, *Pyrus*, *Prunus*, *Raphanus*, *Ricinus*, *Secale*, *Senecio*, *Sinapis*, *Solanum*, *Sorghum*, *Theobromus*, *Trigonella*, *Triticum*, *Vicia*, *Vitis*, *Vigna*, and *Zea*.

In alternative embodiments, the nucleic acids of the invention are expressed in plants which contain fiber cells, including, e.g., cotton, silk cotton tree (Kapok, *Ceiba pentandra*), desert willow, creosote bush, winterfat, balsa, ramie, kenaf, hemp, roselle, jute, sisal abaca and flax. In alternative embodiments, the transgenic plants of the invention can be members of the genus *Gossypium*, including members of any *Gossypium* species, such as *G. arboreum*; *G. herbaceum*, *G. barbadense*, and *G. hirsutum*.

The invention also provides for transgenic plants to be used for producing large amounts of the polypeptides (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or antibody) of the invention. For example,

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see Palmgren (1997) Trends Genet. 13:348; Chong (1997) Transgenic Res. 6:289-296 (producing human milk protein beta-casein in transgenic potato plants using an auxin-inducible, bidirectional mannopine synthase (mas1',2') promoter with *Agrobacterium tumefaciens*-mediated leaf disc transformation methods).

5 Using known procedures, one of skill can screen for plants of the invention by detecting the increase or decrease of transgene mRNA or protein in transgenic plants. Means for detecting and quantitation of mRNAs or proteins are well known in the art.

Polypeptides and peptides

10 In one aspect, the invention provides isolated or recombinant polypeptides having a sequence identity (e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity, or homology) to an exemplary sequence of the
15 invention, e.g., proteins having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID
20 NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID
25 NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
30 NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ ID NO:166 (see also Tables 1, 2, and 3, Examples 1 and 4, below, and Sequence Listing)). The percent sequence identity can be over the full length of the polypeptide, or,

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the identity can be over a region of at least about 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues.

Polypeptides of the invention can also be shorter than the full length of exemplary polypeptides. In alternative aspects, the invention provides polypeptides (peptides, fragments) ranging in size between about 5 and the full length of a polypeptide, e.g., an enzyme, such as a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme; exemplary sizes being of about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, or more residues, e.g., contiguous residues of an exemplary cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention. Peptides of the invention (e.g., a subsequence of an exemplary polypeptide of the invention) can be useful as, e.g., labeling probes, antigens (immunogens), toleragens, motifs, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme active sites (e.g., "catalytic domains"), signal sequences and/or prepro domains.

In alternative aspects, polypeptides of the invention having cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity are members of a genus of polypeptides sharing specific structural elements, e.g., amino acid residues, that correlate with cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. These shared structural elements can be used for the routine generation of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase variants. These shared structural elements of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention can be used as guidance for the routine generation of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes variants within the scope of the genus of polypeptides of the invention.

As used herein, the terms "cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase" encompass any polypeptide or enzymes capable of catalyzing the complete or partial breakdown and/or hydrolysis of cellulose (e.g., exemplary polypeptides of the invention, see also Tables 1, 2, and 3, Examples 1 and 4, below), or any modification of a cellulose or lignocellulotic material, e.g., a biomass material comprising lignocellulose.

In some aspects, a polypeptide of the invention can have an alternative enzymatic activity, for example, as set forth in Table 3, below. For example, the polypeptide having

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a sequence as set forth in SEQ ID NO:164, encoded, e.g., by SEQ ID NO:163, can have Alkaline endoglucanase/cellulase activity; the polypeptide having a sequence as set forth in SEQ ID NO:110, encoded, e.g., by SEQ ID NO:109, can have xylanase activity; the polypeptide having a sequence as set forth in SEQ ID NO:12, encoded, e.g., by SEQ ID NO:11, can have NAD binding oxidoreductase activity; the polypeptide having a sequence as set forth in SEQ ID NO:118, encoded, e.g., by SEQ ID NO:117, can have short chain dehydrogenase activity; the polypeptide having a sequence as set forth in SEQ ID NO:14, encoded, e.g., by SEQ ID NO:13, can have NADH dependent dehydrogenase activity; the polypeptide having a sequence as set forth in SEQ ID NO:138, encoded, e.g., by SEQ ID NO:137, can have peptidase activity; the polypeptide having a sequence as set forth in SEQ ID NO:162, encoded, e.g., by SEQ ID NO:161, can have Alkaline endoglucanase activity, in addition to cellulase activity; the polypeptide having a sequence as set forth in SEQ ID NO:42, encoded, e.g., by SEQ ID NO:41, can have cysteinyl tRNA synthetase activity; the polypeptide having a sequence as set forth in SEQ ID NO:32, encoded, e.g., by SEQ ID NO:31, can have cellodextrin phosphorylase activity; the polypeptide having a sequence as set forth in SEQ ID NO:50, encoded, e.g., by SEQ ID NO:49, can have fdhd/narq oxidoreductase activity; the polypeptide having a sequence as set forth in SEQ ID NO:54, encoded, e.g., by SEQ ID NO:53, can have a radical S-adenosylmethionine (SAM) activity; the polypeptide having a sequence as set forth in SEQ ID NO:58, encoded, e.g., by SEQ ID NO:57, can have a subtilisin like protease activity; etc., as set forth below:

Table 3:

SEQ ID NO:	Enzymatic Activity	Signalp Cleavage Site	Signal Sequence	Source	EC Number
163, 164	Alkaline endoglucanase/cellulase	1-30	MSCRTLMSRRVGVGGLLWGGFLFLRTGSGVTG	Unknown	
1, 2	ORF 001 – family 1 (β -glucosidase)			Unknown	3.2.1.21
101, 102	ORF 003 – family 5 (cellulase)	1-29	MRNHLNVPFYFIFFFLIASIFTVCSSSTA	Unknown	3.2.1.4
103, 104	family 5 (cellulase)	1-20	MLIIGLLVLLGFSSCGRQA	Unknown	3.2.1.4
105, 106	family 5 (cellulase)			Unknown	3.2.1.4
107, 108	family 5 (cellulase)	1-32	MEKQICSNVFSTMLIGLLVLLGFSSCGRQA	Unknown	3.2.1.4
109, 110	family 10 (xylanase)	1-28	MKTHSFNLRSRITLLTAALLFIGATAGA	Unknown	3.2.1.8
11, 12	ORF 003 – NAD binding oxidoreductase			Unknown	1.1.1.18
111, 112	family 5 (cellulase)	1-22	MRRLITIILATAVAAILSTTSCS	Unknown	3.2.1.4
113, 114	ORF 003 – family 10	1-27	MKVTRTAVAGIVAAAVLITIGTSTASA	Unknown	3.2.1.8
115, 116	ORF 004 – short chain dehydrogenase			Unknown	1.1.1.100
117, 118	ORF 011 – short chain dehydrogenase	1-19	MPKVMLVTGSGRGIGAAVA	Unknown	1...
119, 120	ORF 002 – oxidoreductase			Unknown	1.4.3.16

121,	ORF 004 – family 5 (cellulase)		Unknown	3.2.1.4
122	ORF 006 – family 1 (β-glucosidase)		Unknown	3.2.1.21
123,	ORF 009 – family 1 (β-glucosidase)		Unknown	3.2.1.21
124	ORF 004 – short chain dehydrogenase		Unknown	1.1.1.100
125,	ORF 010 – short chain dehydrogenase		Unknown	1...
126	ORF 005 – NADH dependent dehydrogenase	MPKVMLVTGGSRGIGAAVA	Unknown	1.1.1.18
127,	ORF 007 – family 5 (cellulase)		Unknown	3.2.1.4
128	ORF 006 – family 1 (β-glucosidase)		Unknown	3.2.1.21
129,	ORF 001 – cellulase (glycosyl hydrolase family 5)		Unknown	3.2.1.4
130	ORF 001 – peptidase_M37		Unknown	3.5.1.
131,	ORF 001 – threonine dehydrogenase		Unknown	1...
132	ORF 005 – family 1 (β-glucosidase)		Unknown	3.2.1.21
133,	ORF 003 – family 1 (β-glucosidase)		Unknown	3.2.1.21
134	ORF 002 – family 1 (β-glucosidase)		Unknown	3.2.1.21
135,	family 10 (xylanase)	MLKVLRKPIISGLALALLPAGAAGA	Unknown	3.2.1.8
136	family 5 (cellulase)		Unknown	3.2.1.4
137,	ORF 007 – family 1 (β-glucosidase)		Unknown	3.2.1.21
138			Unknown	3.2.1.21
139,			Unknown	3.2.1.21
140			Unknown	3.2.1.21
141,			Unknown	3.2.1.21
142			Unknown	3.2.1.21
143,			Unknown	3.2.1.21
144			Unknown	3.2.1.21
145,			Unknown	3.2.1.21
146			Unknown	3.2.1.21
147,			Unknown	3.2.1.21
148			Unknown	3.2.1.21
149,			Unknown	3.2.1.21
150			Unknown	3.2.1.21
151,			Unknown	3.2.1.21
152			Unknown	3.2.1.21

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153, 154 155, 156 157, 158 159, 160	family 5 (cellulase) family 5 (cellulase) family 5 (cellulase) family 10 (xylanase)			Unknown Unknown Unknown Unknown	3.2.1.4 3.2.1.4 3.2.1.4 3.2.1.8
161, 162 165, 166	Alkaline endoglucanase/cellulase xylanase	1-30	MSCRTLMSRRVGWGLLLWGGLFLRTGSVTG	Unknown	
17, 18	ORF 005 – β -lactamase	1-23	MRYVLISCLALASLCAQPLPVST	Unknown	3.5.2.6
19, 20	ORF 008 – family 10 (xylanase)	1-20	MPVLFALFLVASSCAAQSLA	Unknown <i>Clostridium thermocellum</i>	3.2.1.8 3.2.1.4
21, 22	ORF 001 – family 5 (cellulase)			<i>Clostridium thermocellum</i>	3.2.1.
23, 24	ORF 003 – Family 16 + CBM	1-26	MYKRLLSSVLIIMLLSAWSPISVQA	<i>Clostridium thermocellum</i>	3.2.1.21
25, 26	ORF 001 – family 1 (β -glucosidase)			Unknown	3.2.1.21
27, 28	ORF 002 – family 1 (β -glucosidase)			Unknown	3.2.1.21
29, 30	ORF 004 – family 1 (β -glucosidase)			Unknown	3.2.1.21
3, 4	ORF 008 – family 1 (β -glucosidase)			Unknown	3.2.1.21
31, 32	ORF 002 – cellodextrin phosphorylase			Unknown	2.4.1.20
33, 34	ORF 006 – family 1 (β -glucosidase)			Unknown	3.2.1.21
35, 36	ORF 007 – family 5 (cellulase)	1-23	MNKILKLFSSLLLFAGICPALQA	Unknown	3.2.1.4

37, 38	ORF 011 – family 1 (β -glucosidase)	Unknown	3.2.1.21
39, 40	ORF 004 – putative oxidoreductase	Unknown	4.1.1.
41, 42	ORF 004 – cysteinyl tRNA synthetase	Unknown	6.1.1.16
43, 44	ORF 011 –	Unknown	
45, 46	ORF 006 – family 1 (β -glucosidase)	Unknown	3.2.1.21
47, 48	ORF 002 – family 1 (β -glucosidase)	Unknown	3.2.1.21
49, 50	ORF 006 – fdhd/narq oxidoreductase	Unknown	
5, 6	ORF 012 – family 6 (cellulase)	Unknown	3.2.1.91
51, 52	ORF 001 – family 5 (cellulase)	Unknown	3.2.1.4
53, 54	ORF 002 – Radical SAM family	Unknown	1...
55, 56	ORF 004 – family 1 (β -glucosidase)	Unknown	3.2.1.21
57, 58	ORF 001 – subtilisin like protease	Unknown	
59, 60	family 5 (cellulase)	Unknown	3.2.1.4
61, 62	family 5 (cellulase) ORF 1	Unknown	3.2.1.4
63, 64	family 5 (cellulase) ORF 4	Unknown	3.2.1.4
65, 66	family 10 (xylanase)	Unknown	3.2.1.8
67, 68	family 5 (cellulase)- ORF 2	Unknown	3.2.1.4

MVWTPARSTLAGSSEIPLMTMNIFFPNRKDSRMSLWIKL
GILCMMAGTVMVHG

MKRREFMLGGAGVAALASTLGVSA

MNTLLPRRRLWSSTAILRTLAAAGALAAAGMVLAPVSAAN
A

MKYIFSIIIMMILIGFIPVYGFG

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69, 70	family 26 (mannanase) - ORF4	1-20	MSFKNHILLSLLIVLLFFSA	Unknown	3.2.1.78
7, 8	ORF 003 – Isocitrate dehydrogenase			Unknown	1.1.1.42
71, 72	family 5 (cellulase)	1-21	MKLLKLLIFLLITVIFSDVSA	Unknown	3.2.1.4
73, 74	family 10 (xylanase)			Unknown	3.2.1.21
75, 76	family 5 (cellulase)	1-21	MLRKLIVSVFGFVMLTSA AAA	Unknown	3.2.1.4
77, 78	family 5 (cellulase)	1-28	MKRKRVIHSLIVFFFLMIGSFTSCGSVA	Unknown	3.2.1.4
79, 80	family 5 (cellulase)	1-25	MKYKAIFYLIVLILFY SINIYANA	Unknown	3.2.1.4
81, 82	family 5 (cellulase)	1-25	MNLLAQYFSGFLIFLISIFFVSSA	Unknown	3.2.1.4
83, 84	ORF 008 – dehydrogenase			Unknown	3.5.4.25
85, 86	ORF 008 – family 1 (β -glucosidase)			Unknown	3.2.1.21
87, 88	family 5 (cellulase)	1-23	MRKSVFTLAVFLSALFAFTSCQN	Unknown	3.2.1.4
89, 90	family 5 (cellulase)	1-29	MKRSVSIFIACLLMTVLTISGVAAP EASA	Unknown	3.2.1.4
9, 10	ORF 004 – family 10 (xylanase)	1-26	MRSVRIVTFALAAALAVPLVTSTATA	Unknown	3.2.1.8
91, 92	ORF 001 – family 3			Unknown	3.2.1.52
93, 94	ORF 002 – alpha-rhamnosidase			Unknown	
95, 96	ORF 001 – family 3			Unknown	3.2.1.21
97, 98	ORF 003 – beta-glucuronidase			Unknown	3.2.1.31
99, 100	ORF 012 – family 1 (β -glucosidase)			Unknown	3.2.1.21

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“Amino acid” or “amino acid sequence” as used herein refer to an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these and to naturally occurring or synthetic molecules. “Amino acid” or “amino acid sequence” include an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these, and to naturally occurring or synthetic molecules. The term “polypeptide” as used herein, refers to amino acids joined to each other by peptide bonds or modified peptide bonds, *i.e.*, peptide isosteres and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications.

Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, glucan hydrolase processing, phosphorylation, prenylation, racemization, selenoylation, sulfation and transfer-RNA mediated addition of amino acids to protein such as arginylation. (See Creighton, T.E., *Proteins – Structure and Molecular Properties* 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)). The peptides and polypeptides of the invention also include all “mimetic” and “peptidomimetic” forms, as described in further detail, below.

As used herein, the term “isolated” means that the material (e.g., a protein or nucleic acid of the invention) is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such

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polynucleotides or polypeptides could be part of a composition and still be isolated in that such vector or composition is not part of its natural environment. As used herein, the term “purified” does not require absolute purity; rather, it is intended as a relative definition.

Individual nucleic acids obtained from a library have been conventionally purified to
5 electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The purified nucleic acids of the invention have been purified from the remainder of the genomic DNA in the organism by at least 10^4 - 10^6 fold. In one aspect, the term “purified” includes nucleic acids which have been purified from the remainder of the genomic DNA or from other sequences
10 in a library or other environment by at least one order of magnitude, e.g., in one aspect, two or three orders, or, four or five orders of magnitude.

“Recombinant” polypeptides or proteins refer to polypeptides or proteins produced by recombinant DNA techniques; *i.e.*, produced from cells transformed by an exogenous DNA construct encoding the desired polypeptide or protein. “Synthetic”
15 polypeptides or protein are those prepared by chemical synthesis. Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., Solid Phase Peptide Synthesis, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12))
20 and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen *et al*, *Proc. Natl. Acad. Sci., USA*, 81:3998 (1984) and provide for synthesizing peptides upon the tips of a multitude of “rods” or “pins” all of which are connected to a single plate.

25 The phrase “substantially identical” in the context of two nucleic acids or polypeptides, refers to two or more sequences that have, e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,
30 97%, 98%, 99%, or more nucleotide or amino acid residue (sequence) identity, when compared and aligned for maximum correspondence, as measured using one of the known sequence comparison algorithms or by visual inspection. In alternative aspects, the substantial identity exists over a region of at least about 100 or more residues and most commonly the sequences are substantially identical over at least about 150 to 200 or

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more residues. In some aspects, the sequences are substantially identical over the entire length of the coding regions.

Additionally a “substantially identical” amino acid sequence is a sequence that differs from a reference sequence by one or more conservative or non-conservative amino acid substitutions, deletions, or insertions. In one aspect, the substitution occurs at a site that is not the active site of the molecule, or, alternatively the substitution occurs at a site that is the active site of the molecule, provided that the polypeptide essentially retains its functional (enzymatic) properties. A conservative amino acid substitution, for example, substitutes one amino acid for another of the same class (*e.g.*, substitution of one hydrophobic amino acid, such as isoleucine, valine, leucine, or methionine, for another, or substitution of one polar amino acid for another, such as substitution of arginine for lysine, glutamic acid for aspartic acid or glutamine for asparagine). One or more amino acids can be deleted, for example, from a cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptide, resulting in modification of the structure of the polypeptide, without significantly altering its biological activity. For example, amino- or carboxyl-terminal amino acids that are not required for cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme biological activity can be removed. Modified polypeptide sequences of the invention can be assayed for cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme biological activity by any number of methods, including contacting the modified polypeptide sequence with a substrate and determining whether the modified polypeptide decreases the amount of specific substrate in the assay or increases the bioproducts of the enzymatic reaction of a functional cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptide with the substrate.

“Fragments” as used herein are a portion of a naturally occurring protein which can exist in at least two different conformations. Fragments can have the same or substantially the same amino acid sequence as the naturally occurring protein. Fragments which have different three dimensional structures as the naturally occurring protein are also included. An example of this, is a “pro-form” molecule, such as a low activity proprotein that can be modified by cleavage to produce a mature enzyme with significantly higher activity.

In one aspect, the invention provides crystal (three-dimensional) structures of proteins and peptides, *e.g.*, cellulases, of the invention; which can be made and analyzed

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using the routine protocols well known in the art, e.g., as described in MacKenzie (1998) Crystal structure of the family 7 endoglucanase I (Cel7B) from *Humicola insolens* at 2.2 Å resolution and identification of the catalytic nucleophile by trapping of the covalent glycosyl-enzyme intermediate, *Biochem. J.* 335:409-416; Sakon (1997) Structure and mechanism of endo/exocellulase E4 from *Thermomonospora fusca*, *Nat. Struct. Biol.* 4:810-818; Varrot (1999) Crystal structure of the catalytic core domain of the family 6 cellobiohydrolase II, Cel6A, from *Humicola insolens*, at 1.92 Å resolution, *Biochem. J.* 337:297-304; illustrating and identifying specific structural elements as guidance for the routine generation of cellulase variants of the invention, and as guidance for identifying enzyme species within the scope of the invention.

Polypeptides and peptides of the invention can be isolated from natural sources, be synthetic, or be recombinantly generated polypeptides. Peptides and proteins can be recombinantly expressed *in vitro* or *in vivo*. The peptides and polypeptides of the invention can be made and isolated using any method known in the art. Polypeptide and peptides of the invention can also be synthesized, whole or in part, using chemical methods well known in the art. See e.g., Caruthers (1980) *Nucleic Acids Res. Symp. Ser.* 215-223; Horn (1980) *Nucleic Acids Res. Symp. Ser.* 225-232; Banga, A.K., *Therapeutic Peptides and Proteins, Formulation, Processing and Delivery Systems* (1995) Technomic Publishing Co., Lancaster, PA. For example, peptide synthesis can be performed using various solid-phase techniques (see e.g., Roberge (1995) *Science* 269:202; Merrifield (1997) *Methods Enzymol.* 289:3-13) and automated synthesis may be achieved, e.g., using the ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions provided by the manufacturer.

The peptides and polypeptides of the invention can also be glycosylated. The glycosylation can be added post-translationally either chemically or by cellular biosynthetic mechanisms, wherein the later incorporates the use of known glycosylation motifs, which can be native to the sequence or can be added as a peptide or added in the nucleic acid coding sequence. The glycosylation can be O-linked or N-linked.

The peptides and polypeptides of the invention, as defined above, include all “mimetic” and “peptidomimetic” forms. The terms “mimetic” and “peptidomimetic” refer to a synthetic chemical compound which has substantially the same structural and/or functional characteristics of the polypeptides of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogues of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino

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acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants or members of a genus of polypeptides of the invention (e.g., having about 50% or more sequence identity to an exemplary sequence of the invention), routine experimentation will determine whether a mimetic is within the scope of the invention, i.e., that its structure and/or function is not substantially altered. Thus, in one aspect, a mimetic composition is within the scope of the invention if it has a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes activity.

Polypeptide mimetic compositions of the invention can contain any combination of non-natural structural components. In alternative aspect, mimetic compositions of the invention include one or all of the following three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. For example, a polypeptide of the invention can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g., -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄-), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola (1983) in Chemistry and Biochemistry of Amino Acids, Peptides and Proteins, Vol. 7, pp 267-357, "Peptide Backbone Modifications," Marcell Dekker, NY).

A polypeptide of the invention can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues. Non-natural residues are well described in the scientific and patent literature; a few exemplary non-natural compositions useful as mimetics of natural amino acid residues and guidelines are described below. Mimetics of aromatic amino acids can be generated by replacing by, e.g., D- or L- naphylalanine; D- or L- phenylglycine; D- or L- 2 thieneylalanine; D- or L-1, -2, 3-, or 4- pyreneylalanine; D- or L-3 thieneylalanine; D-

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or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-p-fluoro-phenylalanine; D- or L-p-biphenylphenylalanine; D- or L-p-methoxy-biphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylainines, where alkyl can be substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, e.g., thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings.

10 Mimetics of acidic amino acids can be generated by substitution by, e.g., non-carboxylate amino acids while maintaining a negative charge; (phosphono)alanine; sulfated threonine. Carboxyl side groups (e.g., aspartyl or glutamyl) can also be selectively modified by reaction with carbodiimides ($R'-N-C-N-R'$) such as, e.g., 1-cyclohexyl-3(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3(4-azonia- 4,4-

15 dimetholpentyl) carbodiimide. Aspartyl or glutamyl can also be converted to asparaginyll and glutaminyll residues by reaction with ammonium ions. Mimetics of basic amino acids can be generated by substitution with, e.g., (in addition to lysine and arginine) the amino acids ornithine, citrulline, or (guanidino)-acetic acid, or (guanidino)alkyl-acetic acid, where alkyl is defined above. Nitrile derivative (e.g., containing the CN-moiety in place

20 of COOH) can be substituted for asparagine or glutamine. Asparaginyll and glutaminyll residues can be deaminated to the corresponding aspartyl or glutamyl residues. Arginine residue mimetics can be generated by reacting arginyll with, e.g., one or more conventional reagents, including, e.g., phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, or ninhydrin, in one aspect under alkaline conditions. Tyrosine residue

25 mimetics can be generated by reacting tyrosyl with, e.g., aromatic diazonium compounds or tetranitromethane. N-acetylimidizol and tetranitromethane can be used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Cysteine residue mimetics can be generated by reacting cysteinyll residues with, e.g., alpha-haloacetates such as 2-chloroacetic acid or chloroacetamide and corresponding amines; to give carboxymethyl or

30 carboxyamidomethyl derivatives. Cysteine residue mimetics can also be generated by reacting cysteinyll residues with, e.g., bromo-trifluoroacetone, alpha-bromo-beta-(5-imidozoyl) propionic acid; chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide; methyl 2-pyridyl disulfide; p-chloromercuribenzoate; 2-chloromercuri-4-nitrophenol; or, chloro-7-nitrobenzo-oxa-1,3-diazole. Lysine mimetics can be generated

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(and amino terminal residues can be altered) by reacting lysinyl with, e.g., succinic or other carboxylic acid anhydrides. Lysine and other alpha-amino-containing residue mimetics can also be generated by reaction with imidoesters, such as methyl picolinimidate, pyridoxal phosphate, pyridoxal, chloroborohydride, trinitro-
5 benzenesulfonic acid, O-methylisourea, 2,4, pentanedione, and transamidase-catalyzed reactions with glyoxylate. Mimetics of methionine can be generated by reaction with, e.g., methionine sulfoxide. Mimetics of proline include, e.g., pipecolic acid, thiazolidine carboxylic acid, 3- or 4- hydroxy proline, dehydroproline, 3- or 4-methylproline, or 3,3,- dimethylproline. Histidine residue mimetics can be generated by reacting histidyl with,
10 e.g., diethylprocarbonate or para-bromophenacyl bromide. Other mimetics include, e.g., those generated by hydroxylation of proline and lysine; phosphorylation of the hydroxyl groups of seryl or threonyl residues; methylation of the alpha-amino groups of lysine, arginine and histidine; acetylation of the N-terminal amine; methylation of main chain amide residues or substitution with N-methyl amino acids; or amidation of C-terminal
15 carboxyl groups.

In one aspect, a residue, e.g., an amino acid, of a polypeptide of the invention can also be replaced by an amino acid (or peptidomimetic residue) of the opposite chirality. In one aspect, any amino acid naturally occurring in the L-configuration (which can also be referred to as the R or S, depending upon the structure of the chemical entity) can be
20 replaced with the amino acid of the same chemical structural type or a peptidomimetic, but of the opposite chirality, referred to as the D- amino acid, but also can be referred to as the R- or S- form.

The invention also provides methods for modifying the polypeptides of the invention by either natural processes, such as post-translational processing (e.g.,
25 phosphorylation, acylation, etc), or by chemical modification techniques, and the resulting modified polypeptides. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide
30 may have many types of modifications. In one aspect, modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation,

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formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-RNA mediated addition of amino acids to protein such as arginylation. See, e.g., Creighton, T.E., *Proteins – Structure and Molecular Properties* 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983).

Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., *Solid Phase Peptide Synthesis*, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen et al, *Proc. Natl. Acad. Sci., USA*, 81:3998 (1984) and provide for synthesizing peptides upon the tips of a multitude of “rods” or “pins” all of which are connected to a single plate. When such a system is utilized, a plate of rods or pins is inverted and inserted into a second plate of corresponding wells or reservoirs, which contain solutions for attaching or anchoring an appropriate amino acid to the pin's or rod's tips. By repeating such a process step, i.e., inverting and inserting the rod's and pin's tips into appropriate solutions, amino acids are built into desired peptides. In addition, a number of available Fmoc peptide synthesis systems are available. For example, assembly of a polypeptide or fragment can be carried out on a solid support using an Applied Biosystems, Inc. Model 431A™ automated peptide synthesizer. Such equipment provides ready access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

The polypeptides of the invention include cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes in an active or inactive form. For example, the polypeptides of the invention include proproteins before “maturation” or processing of prepro sequences, e.g., by a proprotein-processing enzyme, such as a proprotein convertase to generate an “active” mature protein. The polypeptides of the invention include cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes inactive for other reasons, e.g., before “activation” by a

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post-translational processing event, e.g., an endo- or exo-peptidase or proteinase action, a phosphorylation event, an amidation, a glycosylation or a sulfation, a dimerization event, and the like. The polypeptides of the invention include all active forms, including active subsequences, e.g., catalytic domains or active sites, of the enzyme.

5 The invention includes immobilized cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, anti-cellulase, e.g., anti-endoglucanase, anti-cellobiohydrolase and/or anti-beta-glucosidase antibodies and fragments thereof. The invention provides methods for inhibiting cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity,
10 e.g., using dominant negative mutants or anti-cellulase, e.g., anti-endoglucanase, anti-cellobiohydrolase and/or anti-beta-glucosidase antibodies of the invention. The invention includes heterocomplexes, e.g., fusion proteins, heterodimers, etc., comprising the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention.

15 Polypeptides of the invention can have a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity under various conditions, e.g., extremes in pH and/or temperature, oxidizing agents, and the like. The invention provides methods leading to alternative cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme preparations with different
20 catalytic efficiencies and stabilities, e.g., towards temperature, oxidizing agents and changing wash conditions. In one aspect, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme variants can be produced using techniques of site-directed mutagenesis and/or random mutagenesis. In one aspect, directed evolution can be used to produce a great variety of cellulase, e.g., endoglucanase,
25 cellobiohydrolase, mannanase and/or beta-glucosidase enzyme variants with alternative specificities and stability.

 The proteins of the invention are also useful as research reagents to identify cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme modulators, e.g., activators or inhibitors of cellulase, e.g., endoglucanase,
30 cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity. Briefly, test samples (compounds, broths, extracts, and the like) are added to cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme assays to determine their ability to inhibit substrate cleavage. Inhibitors identified in this way can be used in industry and research to reduce or prevent undesired proteolysis. As with

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cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, inhibitors can be combined to increase the spectrum of activity.

The enzymes of the invention are also useful as research reagents to digest proteins or in protein sequencing. For example, the cellulase, e.g., endoglucanase,
5 cellobiohydrolase, mannanase and/or beta-glucosidase enzymes may be used to break polypeptides into smaller fragments for sequencing using, e.g. an automated sequencer.

The invention also provides methods of discovering new cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes using the nucleic acids, polypeptides and antibodies of the invention. In one aspect, phagemid
10 libraries are screened for expression-based discovery of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes. In another aspect, lambda phage libraries are screened for expression-based discovery of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes. Screening of the phage or phagemid libraries can allow the detection of toxic clones;
15 improved access to substrate; reduced need for engineering a host, by-passing the potential for any bias resulting from mass excision of the library; and, faster growth at low clone densities. Screening of phage or phagemid libraries can be in liquid phase or in solid phase. In one aspect, the invention provides screening in liquid phase. This gives a greater flexibility in assay conditions; additional substrate flexibility; higher sensitivity
20 for weak clones; and ease of automation over solid phase screening.

The invention provides screening methods using the proteins and nucleic acids of the invention and robotic automation to enable the execution of many thousands of biocatalytic reactions and screening assays in a short period of time, e.g., per day, as well as ensuring a high level of accuracy and reproducibility (see discussion of arrays, below).
25 As a result, a library of derivative compounds can be produced in a matter of weeks. For further teachings on modification of molecules, including small molecules, see PCT/US94/09174; U.S. Pat. No. 6,245,547.

In one aspect, polypeptides or fragments of the invention are obtained through biochemical enrichment or purification procedures. The sequence of potentially
30 homologous polypeptides or fragments may be determined by cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme assays (see, e.g., Examples 1, 2 and 3, below), gel electrophoresis and/or microsequencing. The sequence of the prospective polypeptide or fragment of the invention can be compared to an exemplary polypeptide of the invention, or a fragment, e.g., comprising at least about

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5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof using any of the programs described above.

Another aspect of the invention is an assay for identifying fragments or variants of the invention, which retain the enzymatic function of the polypeptides of the invention.

5 For example the fragments or variants of said polypeptides, may be used to catalyze biochemical reactions, which indicate that the fragment or variant retains the enzymatic activity of a polypeptide of the invention. An exemplary assay for determining if fragments of variants retain the enzymatic activity of the polypeptides of the invention includes the steps of: contacting the polypeptide fragment or variant with a substrate
10 molecule under conditions which allow the polypeptide fragment or variant to function and detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate.

The present invention exploits the unique catalytic properties of enzymes. Whereas the use of biocatalysts (i.e., purified or crude enzymes, non-living or living
15 cells) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds, such as small molecules. Each biocatalyst is specific for one functional group, or several related functional groups and can react with
20 many starting compounds containing this functional group.

In one aspect, the biocatalytic reactions produce a population of derivatives from a single starting compound. These derivatives can be subjected to another round of biocatalytic reactions to produce a second population of derivative compounds. Thousands of variations of the original small molecule or compound can be produced
25 with each iteration of biocatalytic derivatization.

Enzymes react at specific sites of a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical methods. This high degree of biocatalytic specificity provides the means to identify a single active compound within the library. The library is characterized by the series of
30 biocatalytic reactions used to produce it, a so-called "biosynthetic history". Screening the library for biological activities and tracing the biosynthetic history identifies the specific reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies

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and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library.

5 In one aspect, procedural steps are performed using robotic automation enabling the execution of many thousands of biocatalytic reactions and/or screening assays per day as well as ensuring a high level of accuracy and reproducibility. Robotic automation can also be used to screen for cellulase activity to determine if a polypeptide is within the scope of the invention. As a result, in one aspect, a library of derivative compounds can
10 be produced in a matter of weeks which would take years to produce using "traditional" chemical or enzymatic screening methods.

In a particular aspect, the invention provides a method for modifying small molecules, comprising contacting a polypeptide encoded by a polynucleotide described herein or enzymatically active fragments thereof with a small molecule to produce a
15 modified small molecule. A library of modified small molecules is tested to determine if a modified small molecule is present within the library, which exhibits a desired activity. A specific biocatalytic reaction which produces the modified small molecule of desired activity is identified by systematically eliminating each of the biocatalytic reactions used to produce a portion of the library and then testing the small molecules produced in the
20 portion of the library for the presence or absence of the modified small molecule with the desired activity. The specific biocatalytic reactions which produce the modified small molecule of desired activity is optionally repeated. The biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the structure of a small molecule, each biocatalyst is specific for one structural
25 moiety or a group of related structural moieties; and each biocatalyst reacts with many different small molecules which contain the distinct structural moiety.

Cellulase, e.g., endoglucanase, cellobiohydrolase and/or beta-glucosidase enzyme signal sequences, prepro and catalytic domains

The invention provides cellulase, e.g., endoglucanase, cellobiohydrolase,
30 mannanase and/or beta-glucosidase enzyme signal sequences (e.g., signal peptides (SPs)), prepro domains and catalytic domains (CDs). The SPs, prepro domains and/or CDs of the invention can be isolated or recombinant peptides or can be part of a fusion protein, e.g., as a heterologous domain in a chimeric protein. The invention provides nucleic acids encoding these catalytic domains (CDs), prepro domains and signal sequences (SPs, e.g.,

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a peptide having a sequence comprising/ consisting of amino terminal residues of a polypeptide of the invention).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of or comprising a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46, or 1 to 47, or more, of a polypeptide of the invention, e.g., exemplary polypeptides of the invention, see also Table 3, Examples 1 and 4, below, and Sequence Listing. For example, Table 3, above, sets forth exemplary signal (leader) sequences of the invention, e.g., as in the polypeptide having a sequence as set forth in SEQ ID NO:164, encoded, e.g., by SEQ ID NO:163, has a signal sequence comprising (or consisting of) the amino terminal 30 residues, or, MSCRTLMSRRVGWGLLLWGGLFLRTGSVTG. Additional signal sequences are similarly set forth in Table 3.

In one aspect, the invention provides signal sequences comprising the first 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or more amino terminal residues of a polypeptide of the invention.

The invention includes polypeptides with or without a signal sequence and/or a prepro sequence. The invention includes polypeptides with heterologous signal sequences and/or prepro sequences. The prepro sequence (including a sequence of the invention used as a heterologous prepro domain) can be located on the amino terminal or the carboxy terminal end of the protein. The invention also includes isolated or recombinant signal sequences, prepro sequences and catalytic domains (e.g., "active sites") comprising sequences of the invention. The polypeptide comprising a signal sequence of the invention can be a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention or another cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or another enzyme or other polypeptide. Methods for identifying "prepro" domain sequences and signal sequences are well known in the art, see, e.g., Van de Ven (1993) Crit. Rev. Oncog. 4(2):115-136. For example, to identify a prepro sequence, the protein is purified from the extracellular space and the N-terminal protein sequence is determined and compared to the unprocessed form.

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The cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme signal sequences (SPs) and/or prepro sequences of the invention can be isolated or recombinant peptides, or, sequences joined to another cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or a non-cellulase, e.g., non-endoglucanase, non-cellobiohydrolase and/or non-beta-glucosidase polypeptide, e.g., as a fusion (chimeric) protein. In one aspect, the invention provides polypeptides comprising cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme signal sequences of the invention. In one aspect, polypeptides comprising cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme signal sequences SPs and/or prepro of the invention comprise sequences heterologous to a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention (e.g., a fusion protein comprising an SP and/or prepro of the invention and sequences from another cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or a non-cellulase, e.g., non-endoglucanase, non-cellobiohydrolase and/or non-beta-glucosidase protein). In one aspect, the invention provides cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention with heterologous SPs and/or prepro sequences, e.g., sequences with a yeast signal sequence. A cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention can comprise a heterologous SP and/or prepro in a vector, e.g., a pPIC series vector (Invitrogen, Carlsbad, CA).

In one aspect, SPs and/or prepro sequences of the invention are identified following identification of novel cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase polypeptides. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. The signal sequences can vary in length from about 10 to 65, or more, amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. For example, in one aspect, novel cellulase, e.g., endoglucanase,

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cellobiohydrolase, mannanase and/or beta-glucosidase enzyme signal peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. (Nielsen (1997)

5 "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." Protein Engineering 10:1-6.

In some aspects cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention do not have SPs and/or prepro sequences or "domains." In one aspect, the invention provides the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the
10 invention lacking all or part of an SP and/or a prepro domain. In one aspect, the invention provides a nucleic acid sequence encoding a signal sequence (SP) and/or prepro from one cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme operably linked to a nucleic acid sequence of a different cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme or,
15 optionally, a signal sequence (SPs) and/or prepro domain from a non-cellulase, e.g., non-endoglucanase, non-cellobiohydrolase and/or non-beta-glucosidase protein may be desired.

The invention also provides isolated or recombinant polypeptides comprising signal sequences (SPs), prepro domain and/or catalytic domains (CDs) of the invention
20 and heterologous sequences. The heterologous sequences are sequences not naturally associated (e.g., to a enzyme) with an SP, prepro domain and/or CD. The sequence to which the SP, prepro domain and/or CD are not naturally associated can be on the SP's, prepro domain and/or CD's amino terminal end, carboxy terminal end, and/or on both ends of the SP and/or CD. In one aspect, the invention provides an isolated or
25 recombinant polypeptide comprising (or consisting of) a polypeptide comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention with the proviso that it is not associated with any sequence to which it is naturally associated (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme sequence). Similarly in one aspect, the invention provides isolated or
30 recombinant nucleic acids encoding these polypeptides. Thus, in one aspect, the isolated or recombinant nucleic acid of the invention comprises coding sequence for a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention and a heterologous sequence (i.e., a sequence not naturally associated with the a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention). The

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heterologous sequence can be on the 3' terminal end, 5' terminal end, and/or on both ends of the SP, prepro domain and/or CD coding sequence.

Hybrid (chimeric) cellulase, e.g., endoglucanase, cellobiohydrolase and/or beta-glucosidase enzymes and peptide libraries

5 In one aspect, the invention provides hybrid cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes and fusion proteins, including peptide libraries, comprising sequences of the invention. The peptide libraries of the invention can be used to isolate peptide modulators (e.g., activators or inhibitors) of targets, such as cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-
10 glucosidase enzyme substrates, receptors, enzymes. The peptide libraries of the invention can be used to identify formal binding partners of targets, such as ligands, e.g., cytokines, hormones and the like. In one aspect, the invention provides chimeric proteins comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention or a combination thereof and a heterologous sequence (see above).

15 In one aspect, the fusion proteins of the invention (e.g., the peptide moiety) are conformationally stabilized (relative to linear peptides) to allow a higher binding affinity for targets. The invention provides fusions of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention and other peptides, including known and random peptides. They can be fused in such a manner that
20 the structure of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes is not significantly perturbed and the peptide is metabolically or structurally conformationally stabilized. This allows the creation of a peptide library that is easily monitored both for its presence within cells and its quantity.

Amino acid sequence variants of the invention can be characterized by a
25 predetermined nature of the variation, a feature that sets them apart from a naturally occurring form, e.g., an allelic or interspecies variation of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme sequence. In one aspect, the variants of the invention exhibit the same qualitative biological activity as the naturally occurring analogue. Alternatively, the variants can be selected for having
30 modified characteristics. In one aspect, while the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme

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variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, as discussed herein for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants can be done using, e.g., assays of glucan hydrolysis. In
5 alternative aspects, amino acid substitutions can be single residues; insertions can be on the order of from about 1 to 20 amino acids, although considerably larger insertions can be done. Deletions can range from about 1 to about 20, 30, 40, 50, 60, 70 residues or more. To obtain a final derivative with the optimal properties, substitutions, deletions, insertions or any combination thereof may be used. Generally, these changes are done on
10 a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances.

The invention provides cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes where the structure of the polypeptide backbone, the secondary or the tertiary structure, e.g., an alpha-helical or beta-sheet
15 structure, has been modified. In one aspect, the charge or hydrophobicity has been modified. In one aspect, the bulk of a side chain has been modified. Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative. For example, substitutions can be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example a
20 alpha-helical or a beta-sheet structure; a charge or a hydrophobic site of the molecule, which can be at an active site; or a side chain. The invention provides substitutions in polypeptide of the invention where (a) a hydrophilic residues, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue
25 having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine. The variants can exhibit the same qualitative biological activity (i.e., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme
30 activity) although variants can be selected to modify the characteristics of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes as needed.

In one aspect, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention comprise epitopes or purification tags, signal

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sequences or other fusion sequences, etc. In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention can be fused to a random peptide to form a fusion polypeptide. By "fused" or "operably linked" herein is meant that the random peptide and the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme are linked together, in such a manner as to minimize the disruption to the stability of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme structure, e.g., it retains cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity. The fusion polypeptide (or fusion polynucleotide encoding the fusion polypeptide) can comprise further components as well, including multiple peptides at multiple loops.

In one aspect, the peptides and nucleic acids encoding them are randomized, either fully randomized or they are biased in their randomization, e.g. in nucleotide/residue frequency generally or per position. "Randomized" means that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. In one aspect, the nucleic acids which give rise to the peptides can be chemically synthesized, and thus may incorporate any nucleotide at any position. Thus, when the nucleic acids are expressed to form peptides, any amino acid residue may be incorporated at any position. The synthetic process can be designed to generate randomized nucleic acids, to allow the formation of all or most of the possible combinations over the length of the nucleic acid, thus forming a library of randomized nucleic acids. The library can provide a sufficiently structurally diverse population of randomized expression products to affect a probabilistically sufficient range of cellular responses to provide one or more cells exhibiting a desired response. Thus, the invention provides an interaction library large enough so that at least one of its members will have a structure that gives it affinity for some molecule, protein, or other factor.

In one aspect, a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention is a multidomain enzyme that comprises a signal peptide, a carbohydrate binding module, a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme catalytic domain, a linker and/or another catalytic domain.

The invention provides a methods and sequences for generating chimeric polypeptides which may encode biologically active hybrid polypeptides (e.g., hybrid cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase

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enzymes). In one aspect, the original polynucleotides (e.g., an exemplary nucleic acid of the invention) encode biologically active polypeptides. In one aspect, a method of the invention produces new hybrid polypeptides by utilizing cellular processes which integrate the sequence of the original polynucleotides such that the resulting hybrid polynucleotide encodes a polypeptide demonstrating activities derived, but different, from the original biologically active polypeptides (e.g., cellulase or antibody of the invention). For example, the original polynucleotides may encode a particular enzyme (e.g., cellulase) from or found in different microorganisms. An enzyme encoded by a first polynucleotide from one organism or variant may, for example, function effectively under a particular environmental condition, *e.g.* high salinity. An enzyme encoded by a second polynucleotide from a different organism or variant may function effectively under a different environmental condition, such as extremely high temperatures. A hybrid polynucleotide containing sequences from the first and second original polynucleotides may encode an enzyme which exhibits characteristics of both enzymes encoded by the original polynucleotides. Thus, the enzyme encoded by the hybrid polynucleotide of the invention may function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

In one aspect, a hybrid polypeptide generated by a method of the invention may exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding cellulase, *e.g.*, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, the resulting hybrid polypeptide encoded by a hybrid polynucleotide can be screened for specialized non-cellulase, *e.g.*, non-endoglucanase, non-cellobiohydrolase and/or non-beta-glucosidase enzyme activities, *e.g.*, hydrolase, peptidase, phosphorylase, etc., activities, obtained from each of the original enzymes. In one aspect, the hybrid polypeptide is screened to ascertain those chemical functionalities which distinguish the hybrid polypeptide from the original parent polypeptides, such as the temperature, pH or salt concentration at which the hybrid polypeptide functions.

In one aspect, the invention relates to a method for producing a biologically active hybrid polypeptide and screening such a polypeptide for enhanced activity by:

- 1) introducing at least a first polynucleotide in operable linkage and a second polynucleotide in operable linkage, the at least first polynucleotide and

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second polynucleotide sharing at least one region of partial sequence
homology, into a suitable host cell;

- 2) growing the host cell under conditions which promote sequence
reorganization resulting in a hybrid polynucleotide in operable linkage;
- 3) expressing a hybrid polypeptide encoded by the hybrid polynucleotide;
- 4) screening the hybrid polypeptide under conditions which promote
identification of enhanced biological activity; and
- 5) isolating the a polynucleotide encoding the hybrid polypeptide.

Isolating and discovering cellulase enzymes

The invention provides methods for isolating and discovering cellulases, e.g.,
endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes and the
nucleic acids that encode them. Polynucleotides or enzymes may be isolated from
individual organisms ("isolates"), collections of organisms that have been grown in
defined media ("enrichment cultures"), or, uncultivated organisms ("environmental
samples"). The organisms can be isolated by, e.g., *in vivo* biopanning (see discussion,
below). The use of a culture-independent approach to derive polynucleotides encoding
novel bioactivities from environmental samples is most preferable since it allows one to
access untapped resources of biodiversity. Polynucleotides or enzymes also can be
isolated from any one of numerous organisms, e.g. bacteria. In addition to whole cells,
polynucleotides or enzymes also can be isolated from crude enzyme preparations derived
from cultures of these organisms, e.g., bacteria.

"Environmental libraries" are generated from environmental samples and
represent the collective genomes of naturally occurring organisms archived in cloning
vectors that can be propagated in suitable prokaryotic hosts. Because the cloned DNA is
initially extracted directly from environmental samples, the libraries are not limited to the
small fraction of prokaryotes that can be grown in pure culture. Additionally, a
normalization of the environmental DNA present in these samples could allow more
equal representation of the DNA from all of the species present in the original sample.
This can dramatically increase the efficiency of finding interesting genes from minor
constituents of the sample which may be under-represented by several orders of
magnitude compared to the dominant species.

In one aspect, gene libraries generated from one or more uncultivated
microorganisms are screened for an activity of interest. Potential pathways encoding
bioactive molecules of interest are first captured in prokaryotic cells in the form of gene

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expression libraries. In one aspect, polynucleotides encoding activities of interest are isolated from such libraries and introduced into a host cell. The host cell is grown under conditions which promote recombination and/or reductive reassortment creating potentially active biomolecules with novel or enhanced activities.

5 *In vivo* biopanning may be performed utilizing a FACS-based and non-optical (e.g., magnetic) based machines. In one aspect, complex gene libraries are constructed with vectors which contain elements which stabilize transcribed RNA. For example, the inclusion of sequences which result in secondary structures such as hairpins which are designed to flank the transcribed regions of the RNA would serve to enhance their
10 stability, thus increasing their half life within the cell. The probe molecules used in the biopanning process consist of oligonucleotides labeled with reporter molecules that only fluoresce upon binding of the probe to a target molecule. These probes are introduced into the recombinant cells from the library using one of several transformation methods. The probe molecules bind to the transcribed target mRNA resulting in DNA/RNA
15 heteroduplex molecules. Binding of the probe to a target will yield a fluorescent signal which is detected and sorted by the FACS machine during the screening process.

 In one aspect, subcloning is performed to further isolate sequences of interest. In subcloning, a portion of DNA is amplified, digested, generally by restriction enzymes, to cut out the desired sequence, the desired sequence is ligated into a recipient vector and is
20 amplified. At each step in subcloning, the portion is examined for the activity of interest, in order to ensure that DNA that encodes the structural protein has not been excluded. The insert may be purified at any step of the subcloning, for example, by gel electrophoresis prior to ligation into a vector or where cells containing the recipient vector and cells not containing the recipient vector are placed on selective media
25 containing, for example, an antibiotic, which will kill the cells not containing the recipient vector. Specific methods of subcloning cDNA inserts into vectors are well-known in the art (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press (1989)). In another aspect, the enzymes of the invention are subclones. Such subclones may differ from the parent clone by, for example, length, a
30 mutation, a tag or a label.

 The microorganisms from which the polynucleotide may be discovered, isolated or prepared include prokaryotic microorganisms, such as *Eubacteria* and *Archaeobacteria* and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be discovered, isolated or prepared from environmental samples in

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which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms can be used. Enzymes of this invention can function at temperatures above 100°C, e.g., as those found in terrestrial hot springs and deep sea thermal vents, or at temperatures below 0°C, e.g., as those found in arctic waters, in a saturated salt environment, e.g., as those found in the Dead Sea, at pH values around 0, e.g., as those found in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11, e.g., as those found in sewage sludge. In one aspect, enzymes of the invention have high activity throughout a wide range of temperatures and pHs.

Polynucleotides selected and isolated as hereinabove described are introduced into a suitable host cell. A suitable host cell is any cell which is capable of promoting recombination and/or reductive reassortment. The selected polynucleotides are in one aspect already in a vector which includes appropriate control sequences. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or in one aspect, the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation.

Exemplary hosts include bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; and plant cells; see discussion, above. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

Various mammalian cell culture systems can be employed to express recombinant protein; examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in "SV40-transformed simian cells support the replication of early SV40 mutants" (Gluzman, 1981) and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors can comprise an origin of replication, a suitable promoter and enhancer and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice and

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polyadenylation sites may be used to provide the required nontranscribed genetic elements.

In another aspect, nucleic acids, polypeptides and methods of the invention are used in biochemical pathways, or to generate novel polynucleotides encoding
5 biochemical pathways from one or more operons or gene clusters or portions thereof. For example, bacteria and many eukaryotes have a coordinated mechanism for regulating genes whose products are involved in related processes. The genes are clustered, in structures referred to as "gene clusters," on a single chromosome and are transcribed together under the control of a single regulatory sequence, including a single promoter
10 which initiates transcription of the entire cluster. Thus, a gene cluster is a group of adjacent genes that are either identical or related, usually as to their function (an example of a biochemical pathway encoded by gene clusters are polyketides).

In one aspect, gene cluster DNA is isolated from different organisms and ligated into vectors, e.g., vectors containing expression regulatory sequences which can control
15 and regulate the production of a detectable protein or protein-related array activity from the ligated gene clusters. Use of vectors which have an exceptionally large capacity for exogenous DNA introduction can be appropriate for use with such gene clusters and are described by way of example herein to include the f-factor (or fertility factor) of *E. coli*. This f-factor of *E. coli* is a plasmid which affects high-frequency transfer of itself during
20 conjugation and is ideal to achieve and stably propagate large DNA fragments, such as gene clusters from mixed microbial samples. One aspect is to use cloning vectors, referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA. When integrated with DNA from a mixed uncultured environmental sample, this
25 makes it possible to achieve large genomic fragments in the form of a stable "environmental DNA library." Another type of vector for use in the present invention is a cosmid vector. Cosmid vectors were originally designed to clone and propagate large segments of genomic DNA. Cloning into cosmid vectors is described in detail in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor
30 Laboratory Press (1989). Once ligated into an appropriate vector, two or more vectors containing different polyketide synthase gene clusters can be introduced into a suitable host cell. Regions of partial sequence homology shared by the gene clusters will promote processes which result in sequence reorganization resulting in a hybrid gene cluster. The

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novel hybrid gene cluster can then be screened for enhanced activities not found in the original gene clusters.

Methods for screening for various enzyme activities are known to those of skill in the art and are discussed throughout the present specification, see, e.g., Examples 1, 2 and 3, below. Such methods may be employed when isolating the polypeptides and polynucleotides of the invention.

In one aspect, the invention provides methods for discovering and isolating cellulases, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase, or compounds to modify the activity of these enzymes, using a whole cell approach (see discussion, below). Putative clones encoding cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase from genomic DNA library can be screened.

Screening Methodologies and "On-line" Monitoring Devices

In practicing the methods of the invention, a variety of apparatus and methodologies can be used to in conjunction with the polypeptides and nucleic acids of the invention, e.g., to screen polypeptides for cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, to screen compounds as potential modulators, e.g., activators or inhibitors, of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, for antibodies that bind to a polypeptide of the invention, for nucleic acids that hybridize to a nucleic acid of the invention, to screen for cells expressing a polypeptide of the invention and the like. In addition to the array formats described in detail below for screening samples, alternative formats can also be used to practice the methods of the invention. Such formats include, for example, mass spectrometers, chromatographs, e.g., high-throughput HPLC and other forms of liquid chromatography, and smaller formats, such as 1536-well plates, 384-well plates and so on. High throughput screening apparatus can be adapted and used to practice the methods of the invention, see, e.g., U.S. Patent Application Nos. 20020001809; 20050272044.

Capillary Arrays

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. Capillary arrays, such as the

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GIGAMATRIX™, Diversa Corporation, San Diego, CA; and arrays described in, e.g., U.S. Patent Application No. 20020080350 A1; WO 0231203 A; WO 0244336 A, provide an alternative apparatus for holding and screening samples. In one aspect, the capillary array includes a plurality of capillaries formed into an array of adjacent capillaries, wherein each capillary comprises at least one wall defining a lumen for retaining a sample. The lumen may be cylindrical, square, hexagonal or any other geometric shape so long as the walls form a lumen for retention of a liquid or sample. The capillaries of the capillary array can be held together in close proximity to form a planar structure. The capillaries can be bound together, by being fused (e.g., where the capillaries are made of glass), glued, bonded, or clamped side-by-side. Additionally, the capillary array can include interstitial material disposed between adjacent capillaries in the array, thereby forming a solid planar device containing a plurality of through-holes.

A capillary array can be formed of any number of individual capillaries, for example, a range from 100 to 4,000,000 capillaries. Further, a capillary array having about 100,000 or more individual capillaries can be formed into the standard size and shape of a Microtiter® plate for fitment into standard laboratory equipment. The lumens are filled manually or automatically using either capillary action or microinjection using a thin needle. Samples of interest may subsequently be removed from individual capillaries for further analysis or characterization. For example, a thin, needle-like probe is positioned in fluid communication with a selected capillary to either add or withdraw material from the lumen.

In a single-pot screening assay, the assay components are mixed yielding a solution of interest, prior to insertion into the capillary array. The lumen is filled by capillary action when at least a portion of the array is immersed into a solution of interest. Chemical or biological reactions and/or activity in each capillary are monitored for detectable events. A detectable event is often referred to as a “hit”, which can usually be distinguished from “non-hit” producing capillaries by optical detection. Thus, capillary arrays allow for massively parallel detection of “hits”.

In a multi-pot screening assay, a polypeptide or nucleic acid, e.g., a ligand, can be introduced into a first component, which is introduced into at least a portion of a capillary of a capillary array. An air bubble can then be introduced into the capillary behind the first component. A second component can then be introduced into the capillary, wherein the second component is separated from the first component by the air bubble. The first and second components can then be mixed by applying hydrostatic pressure to both sides

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of the capillary array to collapse the bubble. The capillary array is then monitored for a detectable event resulting from reaction or non-reaction of the two components.

In a binding screening assay, a sample of interest can be introduced as a first liquid labeled with a detectable particle into a capillary of a capillary array, wherein the lumen of the capillary is coated with a binding material for binding the detectable particle to the lumen. The first liquid may then be removed from the capillary tube, wherein the bound detectable particle is maintained within the capillary, and a second liquid may be introduced into the capillary tube. The capillary is then monitored for a detectable event resulting from reaction or non-reaction of the particle with the second liquid.

Arrays, or "Biochips"

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. For example, in one aspect of the invention, a monitored parameter is transcript expression of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme gene. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array, or "biochip." By using an "array" of nucleic acids on a microchip, some or all of the transcripts of a cell can be simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins. The present invention can be practiced with any known "array," also referred to as a "microarray" or "nucleic acid array" or "polypeptide array" or "antibody array" or "biochip," or variation thereof. Arrays are generically a plurality of "spots" or "target elements," each target element comprising a defined amount of one or more biological molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

The terms "array" or "microarray" or "biochip" or "chip" as used herein is a plurality of target elements, each target element comprising a defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.

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In practicing the methods of the invention, any known array and/or method of making and using arrays can be incorporated in whole or in part, or variations thereof, as described, for example, in U.S. Patent Nos. 6,277,628; 6,277,489; 6,261,776; 6,258,606; 6,054,270; 6,048,695; 6,045,996; 6,022,963; 6,013,440; 5,965,452; 5,959,098; 5,856,174; 5,830,645; 5,770,456; 5,632,957; 5,556,752; 5,143,854; 5,807,522; 5,800,992; 5,744,305; 5,700,637; 5,556,752; 5,434,049; see also, e.g., WO 99/51773; WO 99/09217; WO 97/46313; WO 96/17958; see also, e.g., Johnston (1998) *Curr. Biol.* 8:R171-R174; Schummer (1997) *Biotechniques* 23:1087-1092; Kern (1997) *Biotechniques* 23:120-124; Solinas-Toldo (1997) *Genes, Chromosomes & Cancer* 20:399-407; Bowtell (1999) *Nature Genetics Supp.* 21:25-32. See also published U.S. patent applications Nos. 20010018642; 20010019827; 20010016322; 20010014449; 20010014448; 20010012537; 20010008765.

Antibodies and Antibody-based screening methods

The invention provides isolated or recombinant antibodies that specifically bind to a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention. These antibodies can be used to isolate, identify or quantify the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention or related polypeptides. These antibodies can be used to isolate other polypeptides within the scope the invention or other related cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes. The antibodies can be designed to bind to an active site of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme. Thus, the invention provides methods of inhibiting cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes using the antibodies of the invention (see discussion above regarding applications for anti-cellulase, e.g., anti-endoglucanase, anti-cellobiohydrolase and/or anti-beta-glucosidase enzyme compositions of the invention).

The term "antibody" includes a peptide or polypeptide derived from, modeled after or substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof, capable of specifically binding an antigen or epitope, see, e.g. Fundamental Immunology, Third Edition, W.E. Paul, ed., Raven Press, N.Y. (1993); Wilson (1994) *J. Immunol. Methods* 175:267-273; Yarmush (1992) *J. Biochem. Biophys. Methods* 25:85-97. The term antibody includes antigen-binding portions, i.e., "antigen binding sites," (e.g., fragments, subsequences, complementarity determining regions (CDRs)) that retain capacity to bind antigen, including (i) a Fab fragment, a

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monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Single chain antibodies are also included by reference in the term "antibody."

The invention provides fragments of the enzymes of the invention (e.g., peptides) including immunogenic fragments (e.g., subsequences) of a polypeptide of the invention. The invention provides compositions comprising a polypeptide or peptide of the invention and adjuvants or carriers and the like.

The antibodies can be used in immunoprecipitation, staining, immunoaffinity columns, and the like. If desired, nucleic acid sequences encoding for specific antigens can be generated by immunization followed by isolation of polypeptide or nucleic acid, amplification or cloning and immobilization of polypeptide onto an array of the invention. Alternatively, the methods of the invention can be used to modify the structure of an antibody produced by a cell to be modified, e.g., an antibody's affinity can be increased or decreased. Furthermore, the ability to make or modify antibodies can be a phenotype engineered into a cell by the methods of the invention.

Methods of immunization, producing and isolating antibodies (polyclonal and monoclonal) are known to those of skill in the art and described in the scientific and patent literature, see, e.g., Coligan, CURRENT PROTOCOLS IN IMMUNOLOGY, Wiley/Greene, NY (1991); Stites (eds.) BASIC AND CLINICAL IMMUNOLOGY (7th ed.) Lange Medical Publications, Los Altos, CA ("Stites"); Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE (2d ed.) Academic Press, New York, NY (1986); Kohler (1975) Nature 256:495; Harlow (1988) ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York. Antibodies also can be generated *in vitro*, e.g., using recombinant antibody binding site expressing phage display libraries, in addition to the traditional *in vivo* methods using animals. See, e.g., Hoogenboom (1997) Trends Biotechnol. 15:62-70; Katz (1997) Annu. Rev. Biophys. Biomol. Struct. 26:27-45.

The polypeptides of the invention or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof, may also be used to generate antibodies which bind specifically to the polypeptides or fragments. The

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resulting antibodies may be used in immunoaffinity chromatography procedures to isolate or purify the polypeptide or to determine whether the polypeptide is present in a biological sample. In such procedures, a protein preparation, such as an extract, or a biological sample is contacted with an antibody capable of specifically binding to one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof.

In immunoaffinity procedures, the antibody is attached to a solid support, such as a bead or other column matrix. The protein preparation is placed in contact with the antibody under conditions in which the antibody specifically binds to one of the polypeptides of the invention, or fragment thereof. After a wash to remove non-specifically bound proteins, the specifically bound polypeptides are eluted.

The ability of proteins in a biological sample to bind to the antibody may be determined using any of a variety of procedures familiar to those skilled in the art. For example, binding may be determined by labeling the antibody with a detectable label such as a fluorescent agent, an enzymatic label, or a radioisotope. Alternatively, binding of the antibody to the sample may be detected using a secondary antibody having such a detectable label thereon. Particular assays include ELISA assays, sandwich assays, radioimmunoassays and Western Blots.

Polyclonal antibodies generated against the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, for example, a nonhuman. The antibody so obtained can bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies which may bind to the whole native polypeptide. Such antibodies can then be used to isolate the polypeptide from cells expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497, 1975), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* 4:72, 1983) and the EBV-hybridoma technique (Cole, *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to the polypeptides of

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the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Alternatively, transgenic mice may be used to express humanized antibodies to these polypeptides or fragments thereof.

Antibodies generated against the polypeptides of the invention, or fragments
5 comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in screening for similar polypeptides from other organisms and samples. In such techniques, polypeptides from the organism are contacted with the antibody and those polypeptides which specifically bind the antibody are detected. Any of the procedures described above may be used to detect antibody binding. One such
10 screening assay is described in "Methods for Measuring Cellulase Activities", *Methods in Enzymology*, Vol 160, pp. 87-116.

Kits

The invention provides kits comprising the compositions, e.g., nucleic acids, expression cassettes, vectors, cells, transgenic seeds or plants or plant parts, polypeptides
15 (e.g., a cellulase enzyme) and/or antibodies of the invention. The kits also can contain instructional material teaching the methodologies and industrial, medical and dietary uses of the invention, as described herein.

Whole cell engineering and measuring metabolic parameters

The methods of the invention provide whole cell evolution, or whole cell
20 engineering, of a cell to develop a new cell strain having a new phenotype, e.g., a new or modified cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity, by modifying the genetic composition of the cell. See U.S. patent application no. 20040033975.

The genetic composition can be modified by addition to the cell of a nucleic acid
25 of the invention, e.g., a coding sequence for an enzyme of the invention. See, e.g., WO0229032; WO0196551.

To detect the new phenotype, at least one metabolic parameter of a modified cell is monitored in the cell in a "real time" or "on-line" time frame. In one aspect, a plurality of cells, such as a cell culture, is monitored in "real time" or "on-line." In one aspect, a
30 plurality of metabolic parameters is monitored in "real time" or "on-line." Metabolic parameters can be monitored using the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention.

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Metabolic flux analysis (MFA) is based on a known biochemistry framework. A linearly independent metabolic matrix is constructed based on the law of mass conservation and on the pseudo-steady state hypothesis (PSSH) on the intracellular metabolites. In practicing the methods of the invention, metabolic networks are established, including the:

- identity of all pathway substrates, products and intermediary metabolites
- identity of all the chemical reactions interconverting the pathway metabolites, the stoichiometry of the pathway reactions,
- identity of all the enzymes catalyzing the reactions, the enzyme reaction kinetics,
- the regulatory interactions between pathway components, e.g. allosteric interactions, enzyme-enzyme interactions etc,
- intracellular compartmentalization of enzymes or any other supramolecular organization of the enzymes, and,
- the presence of any concentration gradients of metabolites, enzymes or effector molecules or diffusion barriers to their movement.

Once the metabolic network for a given strain is built, mathematic presentation by matrix notion can be introduced to estimate the intracellular metabolic fluxes if the on-line metabolome data is available. Metabolic phenotype relies on the changes of the whole metabolic network within a cell. Metabolic phenotype relies on the change of pathway utilization with respect to environmental conditions, genetic regulation, developmental state and the genotype, etc. In one aspect of the methods of the invention, after the on-line MFA calculation, the dynamic behavior of the cells, their phenotype and other properties are analyzed by investigating the pathway utilization. For example, if the glucose supply is increased and the oxygen decreased during the yeast fermentation, the utilization of respiratory pathways will be reduced and/or stopped, and the utilization of the fermentative pathways will dominate. Control of physiological state of cell cultures will become possible after the pathway analysis. The methods of the invention can help determine how to manipulate the fermentation by determining how to change the substrate supply, temperature, use of inducers, etc. to control the physiological state of cells to move along desirable direction. In practicing the methods of the invention, the MFA results can also be compared with transcriptome and proteome data to design experiments and protocols for metabolic engineering or gene shuffling, etc.

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In practicing the methods of the invention, any modified or new phenotype can be conferred and detected, including new or improved characteristics in the cell. Any aspect of metabolism or growth can be monitored.

Monitoring expression of an mRNA transcript

5 In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of an mRNA transcript (e.g., a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme message) or generating new (e.g., cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme) transcripts in a cell. This increased or decreased expression can be
10 traced by testing for the presence of a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention or by cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity assays. mRNA transcripts, or messages, also can be detected and quantified by any method known in the art, including, e.g., Northern blots, quantitative amplification
15 reactions, hybridization to arrays, and the like. Quantitative amplification reactions include, e.g., quantitative PCR, including, e.g., quantitative reverse transcription polymerase chain reaction, or RT-PCR; quantitative real time RT-PCR, or “real-time kinetic RT-PCR” (see, e.g., Kreuzer (2001) Br. J. Haematol. 114:313-318; Xia (2001) Transplantation 72:907-914).

20 In one aspect of the invention, the engineered phenotype is generated by knocking out expression of a homologous gene. The gene’s coding sequence or one or more transcriptional control elements can be knocked out, e.g., promoters or enhancers. Thus, the expression of a transcript can be completely ablated or only decreased.

In one aspect of the invention, the engineered phenotype comprises increasing
25 the expression of a homologous gene. This can be effected by knocking out of a negative control element, including a transcriptional regulatory element acting in cis- or trans- , or, mutagenizing a positive control element. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to
30 immobilized nucleic acids on an array.

Monitoring expression of a polypeptides, peptides and amino acids

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of a polypeptide (e.g., a cellulase, e.g., endoglucanase,

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cellobiohydrolase, mannanase and/or beta-glucosidase enzyme) or generating new polypeptides in a cell. This increased or decreased expression can be traced by determining the amount of cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme present or by cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme activity assays. Polypeptides, peptides and amino acids also can be detected and quantified by any method known in the art, including, e.g., nuclear magnetic resonance (NMR), spectrophotometry, radiography (protein radiolabeling), electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, various immunological methods, e.g. immunoprecipitation, immunodiffusion, immuno-electrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, gel electrophoresis (e.g., SDS-PAGE), staining with antibodies, fluorescent activated cell sorter (FACS), pyrolysis mass spectrometry, Fourier-Transform Infrared Spectrometry, Raman spectrometry, GC-MS, and LC-Electrospray and cap-LC-tandem-electrospray mass spectrometries, and the like. Novel bioactivities can also be screened using methods, or variations thereof, described in U.S. Patent No. 6,057,103. Furthermore, as discussed below in detail, one or more, or, all the polypeptides of a cell can be measured using a protein array.

Industrial, Energy, Pharmaceutical and other Applications

Polypeptides of the invention (e.g., having cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase) can catalyze the breakdown of cellulose. The enzymes of the invention can be highly selective catalysts. The invention provides industrial processes using enzymes of the invention, e.g., in the pharmaceutical or nutrient (diet) supplement industry, the energy industry (e.g., to make “clean” biofuels), in the food and feed industries, e.g., in methods for making food and feed products and food and feed additives. In one aspect, the invention provides processes using enzymes of the invention in the medical industry, e.g., to make pharmaceuticals or dietary aids or supplements, or food supplements and additives. In addition, the invention provides methods for using the enzymes of the invention in bioethanol, including “clean” fuel, production.

The enzymes of the invention can catalyze reactions with exquisite stereo-, regio- and chemo- selectivities. The cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention can be engineered to

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function in various solvents, operate at extreme pHs (for example, high pHs and low pHs) extreme temperatures (for example, high temperatures and low temperatures), extreme salinity levels (for example, high salinity and low salinity) and catalyze reactions with compounds that are structurally unrelated to their natural, physiological substrates.

5 *Biomass conversion and production of clean bio fuels*

The invention provides enzymes and methods for the conversion of biomass (e.g., lignocellulosic materials) to fuels (e.g., bioethanol) and chemicals. Thus, the compositions and methods of the invention provide effective and sustainable alternatives to use of petroleum-based products. The invention provides organisms expressing
10 enzymes of the invention for participation in chemical cycles involving natural biomass conversion. In one aspect, enzymes and methods for the conversion are used in enzyme ensembles for the efficient depolymerization of cellulosic and hemicellulosic polymers to metabolizable carbon moieties. As discussed above, the invention provides methods for discovering and implementing the most effective of enzymes to enable these important
15 new “biomass conversion” and alternative energy industrial processes.

In one aspect, the polypeptides of the invention, e.g., proteins having cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity, are used in processes for converting lignocellulosic biomass to ethanol. The invention also provides processes for making ethanol (“bioethanol”) from compositions
20 comprising lignocellulosic biomass. The lignocellulose biomass material can be obtained from agricultural crops, as a byproduct of food or feed production, or as lignocellulosic waste products, such as plant residues and waste paper. Examples of suitable plant residues for treatment with polypeptides of the invention include stems, leaves, hulls, husks, cobs and the like, as well as wood, wood chips, wood pulp, and sawdust. Examples
25 of paper waste suitable for treatment with polypeptides of the invention include discard photocopy paper, computer printer paper, notebook paper, notepad paper, typewriter paper, and the like, as well as newspapers, magazines, cardboard, and paper-based packaging materials.

In one aspect, the enzymes and methods of the invention can be used in
30 conjunction with more “traditional” means of making ethanol from biomass, e.g., as methods comprising hydrolyzing lignocellulosic materials by subjecting dried lignocellulosic material in a reactor to a catalyst comprised of a dilute solution of a strong acid and a metal salt; this can lower the activation energy, or the temperature, of cellulose hydrolysis to obtain higher sugar yields; see, e.g., U.S. Patent Nos. 6,660,506; 6,423,145.

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Another exemplary method that incorporated use of enzymes of the invention comprises hydrolyzing lignocellulosic material containing hemicellulose, cellulose and lignin by subjecting the material to a first stage hydrolysis step in an aqueous medium at a temperature and a pressure chosen to effect primarily depolymerization of hemicellulose without major depolymerization of cellulose to glucose. This step results in a slurry in which the liquid aqueous phase contains dissolved monosaccharides resulting from depolymerization of hemicellulose and a solid phase containing cellulose and lignin. A second stage hydrolysis step can comprise conditions such that at least a major portion of the cellulose is depolymerized, such step resulting in a liquid aqueous phase containing dissolved/ soluble depolymerization products of cellulose. See, e.g., U.S. Patent No. 5,536,325. Enzymes of the invention can be added at any stage of this exemplary process.

Another exemplary method that incorporated use of enzymes of the invention comprises processing a lignocellulose-containing biomass material by one or more stages of dilute acid hydrolysis with about 0.4% to 2% strong acid; and treating an unreacted solid lignocellulosic component of the acid hydrolyzed biomass material by alkaline delignification to produce precursors for biodegradable thermoplastics and derivatives. See, e.g., U.S. Patent No. 6,409,841. Enzymes of the invention can be added at any stage of this exemplary process.

Another exemplary method that incorporated use of enzymes of the invention comprises prehydrolyzing lignocellulosic material in a prehydrolysis reactor; adding an acidic liquid to the solid lignocellulosic material to make a mixture; heating the mixture to reaction temperature; maintaining reaction temperature for time sufficient to fractionate the lignocellulosic material into a solubilized portion containing at least about 20% of the lignin from the lignocellulosic material and a solid fraction containing cellulose; removing a solubilized portion from the solid fraction while at or near reaction temperature wherein the cellulose in the solid fraction is rendered more amenable to enzymatic digestion; and recovering a solubilized portion. See, e.g., U.S. Patent No. 5,705,369. Enzymes of the invention can be added at any stage of this exemplary process.

The invention provides methods for making motor fuel compositions (e.g., for spark ignition motors) based on liquid hydrocarbons blended with a fuel grade alcohol made by using an enzyme or a method of the invention. In one aspect, the fuels made by use of an enzyme of the invention comprise, e.g., coal gas liquid- or natural gas liquid-

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ethanol blends. In one aspect, a co-solvent is biomass-derived 2-methyltetrahydrofuran (MTHF). See, e.g., U.S. Patent No. 6,712,866.

Methods of the invention for the enzymatic degradation of lignocellulose, e.g., for production of ethanol from lignocellulosic material, can also comprise use of ultrasonic treatment of the biomass material; see, e.g., U.S. Patent No. 6,333,181.

Another exemplary process for making a biofuel comprising ethanol using enzymes of the invention comprises pretreating a starting material comprising a lignocellulosic feedstock comprising at least hemicellulose and cellulose. In one aspect, the starting material comprises potatoes, soybean (rapeseed), barley, rye, corn, oats, wheat, beets or sugar cane or a component or waste or food or feed production byproduct. The starting material ("feedstock") is reacted at conditions which disrupt the plant's fiber structure to effect at least a partial hydrolysis of the hemicellulose and cellulose.

Disruptive conditions can comprise, e.g., subjecting the starting material to an average temperature of 180°C to 270°C at pH 0.5 to 2.5 for a period of about 5 seconds to 60 minutes; or, temperature of 220°C to 270°C, at pH 0.5 to 2.5 for a period of 5 seconds to 120 seconds, or equivalent. This generates a feedstock with increased accessibility to being digested by an enzyme, e.g., a cellulase enzyme of the invention. U.S. Patent No. 6,090,595.

Exemplary conditions for cellulase hydrolysis of lignocellulosic material include reactions at temperatures between about 30°C and 48°C, and/or a pH between about 4.0 and 6.0. Other exemplary conditions include a temperature between about 30°C and 60°C and a pH between about 4.0 and 8.0.

Animal feeds and food or feed additives

In addition to providing dietary aids or supplements, or food supplements and additives for human use, the invention also provides compositions and methods for treating animal feeds and foods and food or feed additives using a polypeptide of the invention, e.g., a protein having cellulase activity, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention, and/or the antibodies of the invention. The invention provides animal feeds, foods, and additives comprising cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention and/or antibodies of the invention. The animal can be any farm animal or any animal.

The animal feed additive of the invention may be a granulated enzyme product that may readily be mixed with feed components. Alternatively, feed additives of the

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invention can form a component of a pre-mix. The granulated enzyme product of the invention may be coated or uncoated. The particle size of the enzyme granulates can be compatible with that of feed and pre-mix components. This provides a safe and convenient mean of incorporating enzymes into feeds. Alternatively, the animal feed additive of the invention may be a stabilized liquid composition. This may be an aqueous or oil-based slurry. See, e.g., U.S. Patent No. 6,245,546.

Cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the present invention, in the modification of animal feed or a food, can process the food or feed either *in vitro* (by modifying components of the feed or food) or *in vivo*. Polypeptides of the invention can be added to animal feed or food compositions.

In one aspect, an enzyme of the invention is added in combination with another enzyme, e.g., beta-galactosidases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases. These enzyme digestion products are more digestible by the animal. Thus, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention can contribute to the available energy of the feed or food, or to the digestibility of the food or feed by breaking down cellulose.

In another aspect, cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention can be supplied by expressing the enzymes directly in transgenic feed crops (as, e.g., transgenic plants, seeds and the like), such as grains, cereals, corn, soy bean, rape seed, lupin and the like. As discussed above, the invention provides transgenic plants, plant parts and plant cells comprising a nucleic acid sequence encoding a polypeptide of the invention. In one aspect, the nucleic acid is expressed such that the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme of the invention is produced in recoverable quantities. The cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase

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enzyme can be recovered from any plant or plant part. Alternatively, the plant or plant part containing the recombinant polypeptide can be used as such for improving the quality of a food or feed, e.g., improving nutritional value, palatability, etc.

5 In one aspect, the enzyme delivery matrix of the invention is in the form of discrete plural particles, pellets or granules. By "granules" is meant particles that are compressed or compacted, such as by a pelletizing, extrusion, or similar compacting to remove water from the matrix. Such compression or compacting of the particles also promotes intraparticle cohesion of the particles. For example, the granules can be prepared by pelletizing the grain-based substrate in a pellet mill. The pellets prepared
10 thereby are ground or crumbled to a granule size suitable for use as an adjuvant in animal feed. Since the matrix is itself approved for use in animal feed, it can be used as a diluent for delivery of enzymes in animal feed.

In one aspect, the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme contained in the invention enzyme delivery matrix and
15 methods is a thermostable cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme, as described herein, so as to resist inactivation of the cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme during manufacture where elevated temperatures and/or steam may be employed to prepare the palletized enzyme delivery matrix. During digestion of feed containing the
20 invention enzyme delivery matrix, aqueous digestive fluids will cause release of the active enzyme. Other types of thermostable enzymes and nutritional supplements that are thermostable can also be incorporated in the delivery matrix for release under any type of aqueous conditions.

In one aspect, a coating is applied to the enzyme matrix particles for many
25 different purposes, such as to add a flavor or nutrition supplement to animal feed, to delay release of animal feed supplements and enzymes in gastric conditions, and the like. In one aspect, the coating is applied to achieve a functional goal, for example, whenever it is desirable to slow release of the enzyme from the matrix particles or to control the conditions under which the enzyme will be released. The composition of the coating
30 material can be such that it is selectively broken down by an agent to which it is susceptible (such as heat, acid or base, enzymes or other chemicals). Alternatively, two or more coatings susceptible to different such breakdown agents may be consecutively applied to the matrix particles.

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The invention is also directed towards a process for preparing an enzyme-releasing matrix. In accordance with the invention, the process comprises providing discrete plural particles of a grain-based substrate in a particle size suitable for use as an enzyme-releasing matrix, wherein the particles comprise a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme encoded by an amino acid sequence of the invention. In one aspect, the process includes compacting or compressing the particles of enzyme-releasing matrix into granules, which most in one aspect is accomplished by pelletizing. The mold inhibitor and cohesiveness agent, when used, can be added at any suitable time, and in one aspect are mixed with the grain-based substrate in the desired proportions prior to pelletizing of the grain-based substrate. Moisture content in the pellet mill feed in one aspect is in the ranges set forth above with respect to the moisture content in the finished product, and in one aspect is about 14-15%. In one aspect, moisture is added to the feedstock in the form of an aqueous preparation of the enzyme to bring the feedstock to this moisture content. The temperature in the pellet mill in one aspect is brought to about 82°C with steam. The pellet mill may be operated under any conditions that impart sufficient work to the feedstock to provide pellets. The pelleting process itself is a cost-effective process for removing water from the enzyme-containing composition.

The compositions and methods of the invention can be practiced in conjunction with administration of prebiotics, which are high molecular weight sugars, e.g., fructo-oligosaccharides (FOS); galacto-oligosaccharides (GOS), GRAS (Generally Recognized As Safe) material. These prebiotics can be metabolized by some probiotic lactic acid bacteria (LAB). They are non-digestible by the majority of intestinal microbes.

Treating foods and food processing

The invention provides foods and feeds comprising enzymes of the invention, and methods for using enzymes of the invention in processing foods and feeds. Cellulases, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention have numerous applications in food processing industry. The invention provides methods for hydrolyzing cellulose-comprising compositions, including, e.g., a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell, or any plant or plant part, or any food or feed, a waste product and the like.

For example, the invention provides feeds or foods comprising a cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzyme the invention, e.g., in a feed, a liquid, e.g., a beverage (such as a fruit juice or a beer), a bread

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or a dough or a bread product, or a drink (e.g., a beer) or a beverage precursor (e.g., a wort).

The food treatment processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipoxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

In one aspect, the invention provides enzymes and processes for hydrolyzing liquid (liquefied) and granular starch. Such starch can be derived from any source, e.g., beet, cane sugar, potato, corn, wheat, milo, sorghum, rye or bulgher. The invention applies to any plant starch source, e.g., a grain starch source, which is useful in liquefaction (for example, to make bioethanol), including any other grain or vegetable source known to produce starch suitable for liquefaction. The methods of the invention comprise liquefying starch (e.g., making bioethanol) from any natural material, such as rice, germinated rice, corn, barley, milo, wheat, legumes, potato, beet, cane sugar and sweet potato. The liquefying process can substantially hydrolyze the starch to produce a syrup. The temperature range of the liquefaction can be any liquefaction temperature which is known to be effective in liquefying starch. For example, the temperature of the starch can be between about 80°C to about 115°C, between about 100°C to about 110°C, and from about 105°C to about 108°C. The bioethanols made using the enzymes and processes of the invention can be used as fuels or in fuels (e.g., auto fuels), e.g., as discussed below, in addition to their use in (or for making) foods and feeds, including alcoholic beverages.

Waste treatment

The invention provides enzymes for use in waste treatment. Cellulases, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention can be used in a variety of waste treatment or related industrial applications, e.g., in waste treatment related to biomass conversion to generate fuels. For example, in

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one aspect, the invention provides a solid and/or liquid waste digestion process using cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention. The methods can comprise reducing the mass and volume of substantially untreated solid waste. Solid waste can be treated with an enzymatic
5 digestive process in the presence of an enzymatic solution (including cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes of the invention) at a controlled temperature. This results in a reaction without appreciable bacterial fermentation from added microorganisms. The solid waste is converted into a liquefied waste and any residual solid waste. The resulting liquefied waste can be
10 separated from said any residual solidified waste. See e.g., U.S. Patent No. 5,709,796.

In one aspect, the compositions and methods of the invention are used for odor removal, odor prevention or odor reduction, e.g., in animal waste lagoons, e.g., on swine farms, in other animal waste management systems, or in any industrial or food processing application.

15 The enzymes and methods for the conversion of biomass (e.g., lignocellulosic materials) to fuels (e.g., bioethanol) can incorporate the treatment/ recycling of municipal solid waste material, including waste obtained directly from a municipality or municipal solid waste that was previously land-filled and subsequently recovered, or sewage sludge, e.g., in the form of sewage sludge cake which contains substantial amounts of cellulosic
20 material. Since sewage sludge cakes will normally not contain substantial amounts of recyclable materials (aluminum, glass, plastics, etc.), they can be directly treated with concentrated sulfuric acid (to reduce the heavy metal content of the cellulosic component of the waste) and processed in the ethanol production system. See, e.g., U.S. Patent Nos. 6,267,309; 5,975,439.

25 Another exemplary method using enzymes of the invention for recovering organic and inorganic matter from waste material comprises sterilizing a solid organic matter and softening it by subjecting it to heat and pressure. This exemplary process may be carried out by first agitating waste material and then subjecting it to heat and pressure, which sterilizes it and softens the organic matter contained therein. In one aspect, after heating
30 under pressure, the pressure may be suddenly released from a perforated chamber to forces the softened organic matter outwardly through perforations of the container, thus separating the organic matter from the solid inorganic matter. The softened sterilized, organic matter is then fermented in fermentation chamber, e.g., using enzymes of the invention, e.g., to form a mash. The mash may be subjected to further processing by

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centrifuge, distillation column and/or anaerobic digester to recover fuels such as ethanol and methane, and animal feed supplements. See, e.g., U.S. Patent No. 6,251,643.

Enzymes of the invention can also be used in processes, e.g., pretreatments, to reduce the odor of an industrial waste, or a waste generated from an animal production facility, and the like. For example, enzymes of the invention can be used to treat an animal waste in a waste holding facility to enhance efficient degradation of large amounts of organic matter with reduced odor. The process can also include inoculation with sulfide-utilizing bacteria and organic digesting bacteria and lytic enzymes (in addition to an enzyme of the invention). See, e.g., U.S. Patent No. 5,958,758.

Enzymes of the invention can also be used in mobile systems, e.g., batch type reactors, for bioremediation of aqueous, hazardous wastes, e.g., as described in U.S. Patent No. 5,833,857. Batch type reactors can be large vessels having circulatory capability wherein bacteria (e.g., expressing an enzyme of the invention) are maintained in an efficient state by nutrients being feed into the reactor. Such systems can be used where effluent can be delivered to the reactor or the reactor is built into a waste water treatment system. Enzymes of the invention can also be used in treatment systems for use at small or temporary remote locations, e.g., portable, high volume, highly efficient, versatile waste water treatment systems.

The waste treatment processes of the invention can include the use of any combination of other enzymes such as other cellulase, e.g., endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase enzymes, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, phytases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Detergent Compositions

The invention provides detergent compositions comprising one or more polypeptides of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) and methods of making

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and using these compositions. The invention incorporates all methods of making and using detergent compositions, see, e.g., U.S. Patent No. 6,413,928; 6,399,561; 6,365,561; 6,380,147. The detergent compositions can be a one and two part aqueous composition, a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel and/or a paste and a slurry form. The invention also provides methods capable of a rapid removal of gross food soils, films of food residue and other minor food compositions using these detergent compositions. Enzymes of the invention can facilitate the removal of starchy stains by means of catalytic hydrolysis of the starch polysaccharide. Enzymes of the invention can be used in dishwashing detergents in textile laundering detergents.

The actual active enzyme content depends upon the method of manufacture of a detergent composition and is not critical, assuming the detergent solution has the desired enzymatic activity. In one aspect, the amount of glucosidase present in the final solution ranges from about 0.001 mg to 0.5 mg per gram of the detergent composition. The particular enzyme chosen for use in the process and products of this invention depends upon the conditions of final utility, including the physical product form, use pH, use temperature, and soil types to be degraded or altered. The enzyme can be chosen to provide optimum activity and stability for any given set of utility conditions. In one aspect, the polypeptides of the present invention are active in the pH ranges of from about 4 to about 12 and in the temperature range of from about 20°C to about 95°C. The detergents of the invention can comprise cationic, semi-polar nonionic or zwitterionic surfactants; or, mixtures thereof.

Enzymes of the present invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be formulated into powdered and liquid detergents having pH between 4.0 and 12.0 at levels of about 0.01 to about 5% (preferably 0.1% to 0.5%) by weight. These detergent compositions can also include other enzymes such as known proteases, cellulases, lipases or endoglycosidases, as well as builders and stabilizers. The addition of enzymes of the invention to conventional cleaning compositions does not create any special use limitation. In other words, any temperature and pH suitable for the detergent is also suitable for the present compositions as long as the pH is within the above range, and the temperature is below the described enzyme's denaturing temperature. In addition, the polypeptides of the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and stabilizers.

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The present invention provides cleaning compositions including detergent compositions for cleaning hard surfaces, detergent compositions for cleaning fabrics, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, and contact lens cleaning solutions.

5 In one aspect, the invention provides a method for washing an object comprising contacting the object with a polypeptide of the invention under conditions sufficient for washing. A polypeptide of the invention may be included as a detergent additive. The detergent composition of the invention may, for example, be formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A
10 laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a polypeptide of the invention. Alternatively, a polypeptide of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise
15 one or more other enzymes such as a protease, a lipase, a cutinase, another glucosidase, a carbohydrase, another cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a xylanase, an oxidase, e.g., a lactase, and/or a peroxidase. The properties of the enzyme(s) of the invention are chosen to be compatible with the selected detergent (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.)
20 and the enzyme(s) is present in effective amounts. In one aspect, enzymes of the invention are used to remove malodorous materials from fabrics. Various detergent compositions and methods for making them that can be used in practicing the invention are described in, e.g., U.S. Patent Nos. 6,333,301; 6,329,333; 6,326,341; 6,297,038; 6,309,871; 6,204,232; 6,197,070; 5,856,164.

25 The detergents and related processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases,
30 peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases,

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galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Treating fabrics and textiles

The invention provides methods of treating fabrics and textiles using one or more polypeptides of the invention, e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. The polypeptides of the invention can be used in any fabric-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,077,316. For example, in one aspect, the feel and appearance of a fabric is improved by a method comprising contacting the fabric with an enzyme of the invention in a solution. In one aspect, the fabric is treated with the solution under pressure.

In one aspect, the enzymes of the invention are applied during or after the weaving of textiles, or during the desizing stage, or one or more additional fabric processing steps. During the weaving of textiles, the threads are exposed to considerable mechanical strain. Prior to weaving on mechanical looms, warp yarns are often coated with sizing starch or starch derivatives in order to increase their tensile strength and to prevent breaking. The enzymes of the invention can be applied to remove these sizing starch or starch derivatives. After the textiles have been woven, a fabric can proceed to a desizing stage. This can be followed by one or more additional fabric processing steps. Desizing is the act of removing size from textiles. After weaving, the size coating must be removed before further processing the fabric in order to ensure a homogeneous and wash-proof result. The invention provides a method of desizing comprising enzymatic hydrolysis of the size by the action of an enzyme of the invention.

The enzymes of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be used to desize fabrics, including cotton-containing fabrics, as detergent additives, e.g., in aqueous compositions. The invention provides methods for producing a stonewashed look on indigo-dyed denim fabric and garments. For the manufacture of clothes, the fabric can be cut and sewn into clothes or garments, which is afterwards finished. In particular, for the manufacture of denim jeans, different enzymatic finishing methods have been developed. The finishing of denim garment normally is initiated with an enzymatic desizing step, during which garments are subjected to the action of amylolytic enzymes in order to provide softness to the fabric and make the cotton more accessible to the subsequent enzymatic finishing steps. The invention provides methods of finishing denim garments

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(e.g., a "bio-stoning process"), enzymatic desizing and providing softness to fabrics using the Enzymes of the invention. The invention provides methods for quickly softening denim garments in a desizing and/or finishing process.

The invention also provides disinfectants comprising enzymes of the invention
5 (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity).

The fabric or textile treatment processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases,
10 amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases,
15 proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Paper or pulp treatment

The enzymes of the invention (e.g., enzymes having cellulase, endoglucanase,
20 cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using enzymes of the invention. In one aspect, the enzymes of the invention can be used to modify starch in the paper thereby converting it into a liquefied form. In another aspect, paper components of recycled photocopied paper during
25 chemical and enzymatic deinking processes. In one aspect, Enzymes of the invention can be used in combination with other enzymes, including other cellulases (including other endoglucanases, cellobiohydrolases and/or beta-glucosidases). The wood, paper, paper product or pulp can be treated by the following three processes: 1) disintegration in the presence of an enzyme of the invention, 2) disintegration with a deinking chemical and an
30 enzyme of the invention, and/or 3) disintegration after soaking with an enzyme of the invention. The recycled paper treated with an enzyme of the invention can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of an

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enzyme of the invention may be due to its behavior as surface-active agents in pulp suspension.

The invention provides methods of treating paper and paper pulp using one or more polypeptides of the invention. The polypeptides of the invention can be used in any paper- or pulp-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,241,849; 6,066,233; 5,582,681. For example, in one aspect, the invention provides a method for deinking and decolorizing a printed paper containing a dye, comprising pulping a printed paper to obtain a pulp slurry, and dislodging an ink from the pulp slurry in the presence of an enzyme of the invention (other enzymes can also be added). In another aspect, the invention provides a method for enhancing the freeness of pulp, e.g., pulp made from secondary fiber, by adding an enzymatic mixture comprising an enzyme of the invention (can also include other enzymes, e.g., pectinase enzymes) to the pulp and treating under conditions to cause a reaction to produce an enzymatically treated pulp. The freeness of the enzymatically treated pulp is increased from the initial freeness of the secondary fiber pulp without a loss in brightness.

The paper, wood or pulp treatment or recycling processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Repulping: treatment of lignocellulosic materials

The invention also provides a method for the treatment of lignocellulosic fibers, wherein the fibers are treated with a polypeptide of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity), in an amount which is efficient for improving the fiber properties. The enzymes of the invention may also be used in the production or recycling of lignocellulosic materials such as pulp, paper and cardboard, from starch reinforced waste paper and cardboard,

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especially where repulping or recycling occurs at pH above 7 and where the enzymes of the invention can facilitate the disintegration of the waste material through degradation of the reinforcing starch. The enzymes of the invention can be useful in a process for producing a papermaking pulp from starch-coated printed paper. The process may be performed as described in, e.g., WO 95/14807. An exemplary process comprises disintegrating the paper to produce a pulp, treating with a starch-degrading enzyme before, during or after the disintegrating, and separating ink particles from the pulp after disintegrating and enzyme treatment. See also U.S. Patent No. 6,309,871 and other US patents cited herein. Thus, the invention includes a method for enzymatic deinking of recycled paper pulp, wherein the polypeptide is applied in an amount which is efficient for effective de-inking of the fiber surface.

Brewing and fermenting

The invention provides methods of brewing (e.g., fermenting) beer comprising an enzyme of the invention, e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. In one exemplary process, starch-containing raw materials are disintegrated and processed to form a malt. An enzyme of the invention is used at any point in the fermentation process. For example, enzymes of the invention can be used in the processing of barley malt. The major raw material of beer brewing is barley malt. This can be a three stage process. First, the barley grain can be steeped to increase water content, e.g., to around about 40%. Second, the grain can be germinated by incubation at 15-25°C for 3 to 6 days when enzyme synthesis is stimulated under the control of gibberellins. During this time enzyme levels rise significantly. In one aspect, enzymes of the invention are added at this (or any other) stage of the process. The action of the enzyme results in an increase in fermentable reducing sugars. This can be expressed as the diastatic power, DP, which can rise from around 80 to 190 in 5 days at 12°C.

Enzymes of the invention can be used in any beer producing process, as described, e.g., in U.S. Patent No. 5,762,991; 5,536,650; 5,405,624; 5,021,246; 4,788,066.

Increasing the flow of production fluids from a subterranean formation

The invention also includes a method using an enzyme of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity), wherein the method increases the flow of production fluids from a subterranean formation by removing viscous, starch-containing, damaging fluids formed

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during production operations; these fluids can be found within the subterranean formation which surrounds a completed well bore. Thus, this method of the invention results in production fluids being able to flow from the well bore. This method of the invention also addresses the problem of damaging fluids reducing the flow of production fluids from a formation below expected flow rates. In one aspect, the invention provides for formulating an enzyme treatment (using an enzyme of the invention) by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous, starch-containing, damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack the alpha glucosidic linkages in the starch-containing fluid.

The subterranean formation enzyme treatment processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipoxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Pharmaceutical compositions and dietary supplements

The invention also provides pharmaceutical compositions and dietary supplements (e.g., dietary aids) comprising a cellulase of the invention (e.g., enzymes having endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity). The cellulase activity comprises endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. In one aspect, the pharmaceutical compositions and dietary supplements (e.g., dietary aids) are formulated for oral ingestion, e.g., to improve the digestibility of foods and feeds having a high cellulose or lignocellulosic component.

Periodontal treatment compounds can comprise an enzyme of the invention, e.g., as described in U.S. patent no. 6,776,979. Compositions and methods for the treatment or

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prophylaxis of acidic gut syndrome can comprise an enzyme of the invention, e.g., as described in U.S. patent no. 6,468,964.

In another aspect, wound dressings, implants and the like comprise antimicrobial (e.g., antibiotic-acting) enzymes, including an enzyme of the invention (including, e.g.,
5 exemplary sequences of the invention). Enzymes of the invention can also be used in alginate dressings, antimicrobial barrier dressings, burn dressings, compression bandages, diagnostic tools, gel dressings, hydro-selective dressings, hydrocellular (foam) dressings, hydrocolloid dressings, I.V dressings, incise drapes, low adherent dressings, odor
absorbing dressings, paste bandages, post operative dressings, scar management, skin
10 care, transparent film dressings and/or wound closure. Enzymes of the invention can be used in wound cleansing, wound bed preparation, to treat pressure ulcers, leg ulcers, burns, diabetic foot ulcers, scars, IV fixation, surgical wounds and minor wounds. Enzymes of the invention can be used to in sterile enzymatic debriding compositions, e.g., ointments. In various aspects, the cellulase is formulated as a tablet, gel, pill,
15 implant, liquid, spray, powder, food, feed pellet or as an encapsulated formulation.

Biodefense applications

In other aspects, cellulases of the invention (e.g., enzymes having endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be used in biodefense (e.g., destruction of spores or bacteria comprising a lignocellulosic material). Use of
20 cellulases of the invention in biodefense applications offer a significant benefit, in that they can be very rapidly developed against any currently unknown or biological warfare agents of the future. In addition, cellulases of the invention can be used for decontamination of affected environments. In aspect, the invention provides a biodefense or bio-detoxifying agent comprising a polypeptide having a cellulase activity, wherein the
25 polypeptide comprises a sequence of the invention (including, e.g., exemplary sequences of the invention), or a polypeptide encoded by a nucleic acid of the invention (including, e.g., exemplary sequences of the invention), wherein optionally the polypeptide has activity comprising endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

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The following examples are offered to illustrate, but not to limit the claimed invention.

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EXAMPLES

Example 1: GIGAMATRIXTM screen

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In one aspect, the methods of the invention use Diversa Corporation's proprietary GIGAMATRIXTM platform; see PCT Patent Publication No. WO 01/38583; U.S. patent application no. 20050046833; 20020080350; U.S. Patent No. 6,918,738; Design Patent No. D480,814. For example, in one aspect, GIGAMATRIXTM is used in methods to determine if a polypeptide has cellulase activity and is within the scope of the invention, or, to identify and isolate a polypeptide having cellulase activity.

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A GIGAMATRIXTM platform can include an ultra-high throughput screen based on a 100,000 well microplate with the dimensions of a conventional 96 well plate. In this example, the GIGAMATRIXTM screen was implemented using 2 substrates based on previously shown activity by CBHs. Methyl-umbelliferyl cellobioside (MUC) and methylumbelliferyl lactoside (MUL) were tested. Phagemid versions of the different clones were screened because the substrate diffuses into cells and fluorescence was thought to be more easily detectable. A host strain lacking, beta-galactosidase was used in order to decrease activity on the lactoside substrate. The lactoside substrate resulted in fewer hits and was deemed more specific than the cellobiose substrate. In addition, the lactoside substrate resulted in fewer beta-glucosidase hits. In order to test the feasibility of using these substrates in a screen, 14 libraries were chosen for screening based on the fact that these libraries yielded endoglucanase hits from a previous screening program. Of the libraries screened, there were a total of 50 primary hits from 11 of the libraries screened. Secondary screening consisted of plating the clones on agar plates and then colony picking into 384 well plates containing media and MUL. Active clones against MUL are differentiated from a background of inactive clones. Individual clones were then grown overnight and fluorescence was measured and the most active hits were picked for

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sequencing.

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All genomic clone inserts from hits were sequenced. In general, the hits were from several different glycosyl hydrolase families including 1, 2, 5, 6, 10 and 16. Several other hits were discovered where the open reading frame was not homologous to any known glycosyl hydrolase families. In addition, some of the hits encoded GTP cyclohydrolase genes.

Table 1. Summary of GIGAMATRIXTM hits

Enzyme No.	Open Reading Frame SEQ ID NO:	nearest relevant BLAST
1	SEQ ID NO:22 (encoded by, e.g. SEQ ID NO:21)	ORF 001 – family 5 (cellulase)
1a	SEQ ID NO:24 (encoded by SEQ ID NO:23)	ORF 003 – Family 16 + CBM
2	SEQ ID NO:26 (encoded by, e.g. SEQ ID NO:25)	ORF 001 – family 1 (β -glucosidase)
3	SEQ ID NO:92 (encoded by, e.g. SEQ ID NO:91)	ORF 001 – family 3
3a	SEQ ID NO:94 (encoded by, e.g. SEQ ID NO:93)	ORF 002 – alpha-rhamnosidase
4	SEQ ID NO:96 (encoded by, e.g. SEQ ID NO:95)	ORF 001 – family 3
4a	SEQ ID NO:98 (encoded by, e.g. SEQ ID NO:97)	ORF 003 – beta-glucuronidase
5	SEQ ID NO:128 (encoded by, e.g. SEQ ID NO:127)	ORF 004 – short chain dehydrogenase
5a	SEQ ID NO:130 (encoded by, e.g. SEQ ID NO:129)	ORF 010 – short chain dehydrogenase
6	SEQ ID NO:116 (encoded by, e.g. SEQ ID NO:115)	ORF 004 – short chain dehydrogenase
6a	SEQ ID NO:118 (encoded by, e.g. SEQ ID NO:117)	ORF 011 – short chain dehydrogenase
7	SEQ ID NO:40 (encoded by, e.g. SEQ ID NO:39)	ORF 004 – putative oxidoreductase
8	SEQ ID NO:42 (encoded by, e.g. SEQ ID NO:41)	ORF 004 – cysteinyl tRNA synthetase
8a	SEQ ID NO:44 (encoded by, e.g. SEQ ID NO:43)	ORF 011 – hypothetical protein
9	SEQ ID NO:54 (encoded by, e.g. SEQ ID NO:53)	ORF 002 – Radical SAM family
10	SEQ ID NO:134 (encoded by, e.g. SEQ ID NO:133)	ORF 006 – family 1 (β -glucosidase)
11	SEQ ID NO:58 (encoded by, e.g. SEQ ID NO:57)	ORF 001 – subtilisin like protease
12	SEQ ID NO:46 (encoded by, e.g. SEQ ID NO:45)	ORF 006 – family 1 (β -glucosidase)
13	SEQ ID NO:8 (encoded by, e.g. SEQ ID NO:7)	ORF 003 – Isocitrate dehydrogenase
13a	SEQ ID NO:10 (encoded by, e.g. SEQ ID NO:9)	ORF 004 – family 10 (xylanase)
14	SEQ ID NO:48 (encoded by, e.g. SEQ ID NO:47)	ORF 002 – family 1 (β -glucosidase)
14a	SEQ ID NO:50 (encoded by, e.g. SEQ ID NO:49)	ORF 006 – fdhd/narq oxidoreductase
15	SEQ ID NO:4 (encoded by, e.g. SEQ ID NO:3)	ORF 008 – family 1 (β -glucosidase)
15a	SEQ ID NO:6 (encoded by, e.g. SEQ ID NO:5)	ORF 012 – family 6 (cellulase)
16	SEQ ID NO:136 (encoded by, e.g. SEQ ID NO:135)	ORF 001 – cellulase (glycosyl hydrolase family 5)
17	SEQ ID NO:56 (encoded by, e.g. SEQ ID NO:55)	ORF 004 – family 1 (β -glucosidase)
18	SEQ ID NO:126 (encoded by, e.g. SEQ ID NO:125)	ORF 009 – family 1 (β -glucosidase)
19	SEQ ID NO:120 (encoded by, e.g. SEQ ID NO:119)	ORF 002 – oxidoreductase
19a	SEQ ID NO:122 (encoded by, e.g. SEQ ID NO:121)	ORF 004 – family 5 (cellulase)
20	SEQ ID NO:124 (encoded by, e.g. SEQ ID NO:123)	ORF 006 – family 1 (β -glucosidase)
21	SEQ ID NO:132 (encoded by, e.g. SEQ ID NO:131)	ORF 007 – family 5 (cellulase)
22	SEQ ID NO:38 (encoded by, e.g. SEQ ID NO:37)	ORF 011 – family 1 (β -glucosidase)
22a	SEQ ID NO:36 (encoded by, e.g. SEQ ID NO:35)	ORF 007 – family 5 (cellulase)
23	SEQ ID NO:138 (encoded by, e.g. SEQ ID NO:137)	ORF 001 – peptidase M37
24	SEQ ID NO:146 (encoded by, e.g. SEQ ID NO:145)	ORF 002 – family 1 (β -glucosidase)
25	SEQ ID NO:52 (encoded by, e.g. SEQ ID NO:51)	ORF 001 – family 5 (cellulase)

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<u>Enzyme No.</u>	<u>Open Reading Frame SEQ ID NO:</u>	<u>nearest relevant BLAST</u>
26	SEQ ID NO:20 (encoded by, e.g. SEQ ID NO:19)	ORF 008 – family 10 (xylanase)
26a	SEQ ID NO:18 (encoded by, e.g. SEQ ID NO:17)	ORF 005 – β -lactamase
27	SEQ ID NO:16 (encoded by, e.g. SEQ ID NO:15)	ORF 007 – family 1 (β -glucosidase)
27a	SEQ ID NO:14 (encoded by, e.g. SEQ ID NO:13)	ORF 005 – NADH dependent dehydrogenase
27b	SEQ ID NO:12 (encoded by, e.g. SEQ ID NO:11)	ORF 003 – NAD binding oxidoreductase
28	SEQ ID NO:28 (encoded by, e.g. SEQ ID NO:27)	ORF 002 – family 1 (β -glucosidase)
29	SEQ ID NO:114 (encoded by, e.g. SEQ ID NO:113)	ORF 003 – family 10
30	SEQ ID NO:34 (encoded by, e.g. SEQ ID NO:33)	ORF 006 – family 1 (β -glucosidase)
30a	SEQ ID NO:32 (encoded by, e.g. SEQ ID NO:31)	ORF 002 – cellodextrin phosphorylase
31	SEQ ID NO:30 (encoded by, e.g. SEQ ID NO:29)	ORF 004 – family 1 (β -glucosidase)
32	SEQ ID NO:100 (encoded by, e.g. SEQ ID NO:99)	ORF 012 – family 1 (β -glucosidase)
33	SEQ ID NO:84 (encoded by, e.g. SEQ ID NO:83)	ORF 008 – dehydrogenase
34	SEQ ID NO:102 (encoded by, e.g. SEQ ID NO:101)	ORF 003 – family 5 (cellulase)
35	SEQ ID NO:140 (encoded by, e.g. SEQ ID NO:139)	ORF 001 – threonine dehydrogenase
36	SEQ ID NO:142 (encoded by, e.g. SEQ ID NO:141)	ORF 005 – family 1 (β -glucosidase)
37	SEQ ID NO:144 (encoded by, e.g. SEQ ID NO:143)	ORF 003 – family 1 (β -glucosidase)
38	SEQ ID NO:2 (encoded by, e.g. SEQ ID NO:1)	ORF 001 – family 1 (β -glucosidase)
39	SEQ ID NO:86 (encoded by, e.g. SEQ ID NO:85)	ORF 008 – family 1 (β -glucosidase)

Abbreviations: CBM - carbohydrate binding module

Characterization enzyme and substrate activity

The 39 hits (see Table 1, above) discovered in the GIGAMATRIX™ screen were first screened against cellohexaose to determine action pattern on a cellulose oligomer.

5 Genomic clones are defined as clones that have an entire DNA insert potentially containing multiple open reading frames. For example, in Table 1, above, one such genomic clone contains two open reading frames annotated as Enzymes No. 22 and 22a, with said open reading frames having the sequences as depicted in SEQ ID NO:37 and SEQ ID NO:35, respectively. Another such genomic clone is contains three open reading

10 frames, which are annotated as Enzymes 27, 27a and 27b. Subclones are derived from genomic clones and can contain only a single open reading frame. Genomic clones were grown overnight in TB media containing antibiotic, cells were lysed and lysates were clarified by centrifugation. Subclones are grown to an OD₆₀₀=0.5 induced with an appropriate inducer and then grown an additional 3 h before lysing the cells and clarifying

15 the lysate. Genomic clones will generally have less activity than a subclone, but are a more facile way of assessing activity in a large range of clones. Initial studies were performed using thin layer chromatography (TLC) for endpoint reactions usually run for 24h. Enzymes were also tested on phosphoric acid swollen cellulose (PASC), which is crystalline cellulose that is made more amorphous through swelling by acid treatment.

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A number of cellulases which were cloned from environmental libraries were active against PASC, but released cellobiose as well as celltriose and/or glucose. The genomic clones from the GIGAMATRIX™ discovery effort were also tested against PASC and on cellulosic substrates such as cellohexaose (Seikagaku, Japan). Thin layer chromatography (TLC) experiments showed that several genomic clones were able to hydrolyze the cellohexaose, as illustrated in Figures 6 and 7. Of these clones, many were able to generate glucose as the final product which is consistent with the fact that they have sequence identity to glycosyl hydrolase family 1, which includes beta-glucosidases. Several enzymes produced cellobiose and/or larger fragments, but the exact nature of the product pattern could not be discerned from the TLC experiments, so a capillary electrophoresis (CE) method was developed.

Example 2: Capillary Electrophoresis

In some aspects, Capillary Electrophoresis (CE) is used in assays to screen for enzyme activity, e.g., CE is used in methods to determine if a polypeptide has cellulase activity and is within the scope of the invention, or, to identify and isolate a polypeptide having cellulase activity. Capillary Electrophoresis (CE) offers the advantages of faster run times and greater assay sensitivity. The CE method used 1-aminopyrene-3,6,8-trisulfonate (APTS) as the fluorophore and was optimized for use with sugars and sugar oligomers (Guttman (1996) High-resolution capillary gel electrophoresis of reducing oligosaccharides labeled with 1-aminopyrene-3,6,8-trisulfonate. Anal. Biochem 233:234-242). Enzymes that were shown to be active on cellohexaose were subjected to tests on phosphoric acid swollen cellulose as well as cellohexaose. Genes were subcloned, expressed and partially purified using a nickel-chelating column. Enzymes were incubated with substrate for 1h and the products were analyzed using a 10 cm or 48 cm capillary. Cellohexaose elutes at 2 and 9 minutes for the 10 and 48 cm capillaries respectively. The 48 cm capillary gives better separation of products in case there are low amounts of sugar or if there are contaminants in the mixture. The CE method was implemented for studies on enzymes from the GIGAMATRIX™ discovery that showed good activity on cellohexaose with TLC detection.

Enzyme 22/22a (see Table, 1 above) showed good performance on PASC (data summarized in graph form in Figure 8), releasing mainly cellobiose. In addition, enzyme 22/22a was able to release cellobiose from AVICEL® Microcrystalline Cellulose (MCC) (FMC Corporation, Philadelphia, PA) (data summarized in graph form in Figure 9).

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Sequence analysis showed that enzyme 22 and enzyme 21 are ~92% identical and belong to glycosyl hydrolase family 5. Family 5 contains mainly endoglucanases, but there are examples of cellobiohydrolases. CelO from *Clostridium thermocellum* has been characterized as a cellobiohydrolase based on activity on release of only cellobiose from amorphous and crystalline cellulose (Zverlov (2002) A newly described cellulosomal cellobiohydrolase, CelO, from *Clostridium thermocellum*: investigation of the exo-mode of hydrolysis, and binding capacity to crystalline cellulose. Microbiology 148:247-255).

All three of these enzymes, when compared to the endoglucanase from *Acidothermus cellulolyticus* have an insertion that is in close proximity to the substrate binding site. This insertion could form a loop which encloses the substrate binding site thus converting this enzyme from an endoglucanase to a cellobiohydrolase. When these enzymes were tested on cellohexaose they produced mainly cellobiose with a smaller amount of cellotriose. These results are explained by the fact that cellobiohydrolases have the capability to produce both cellobiose and cellotriose from a cellohexaose substrate (Harjunpaa (1996) Cello-oligosaccharide hydrolysis by cellobiohydrolase II from *Trichoderma reesei*. Association and rate constants derived from an analysis of progress curves. Eur. J Biochem 240:584-591).

Example 3: Sequence Based Discovery

The invention provides methods for identifying and isolating cellulases, e.g., cellobiohydrolases, using sequences of the invention. In one exemplary method, primers that were homologous to conserved regions of three glycosyl hydrolase families that contain cellobiohydrolases were used to screen either polynucleotide libraries or DNA derived from fungal samples. Primers were designed towards family 48 conserved regions and 96 libraries were screened resulting in 1 confirmed hit. In addition, primers were designed towards family 6 and family 7. Fungal libraries were screened with these primers, resulting in 1 hit for family 6 and 56 hits for family 7. One of the family 7 hits was chosen for studies to extract the full length sequence. The full-length sequence was successfully obtained and showed 73% identity to exo-cellobiohydrolase I of *Penicillium janthinellum*.

Example 4: Genetic Engineering of an Enzyme with Cellobiohydrolase Activity

This example described the genetic engineering of an exemplary enzyme of the invention. This enzyme can be used in the conversion of biomass to fuels and chemicals, and for making effective and sustainable alternatives to petroleum-based products. This

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enzyme can be expressed in organisms (e.g., microorganisms, such as bacteria) for its participation in chemical cycles involving natural biomass conversion. In one aspect, this enzyme is used in “enzyme ensembles” for the efficient depolymerization of cellulosic and hemicellulosic polymers to metabolizable carbon moieties. As discussed above, the invention provides methods for discovering and implementing the most effective of enzymes to enable these important new “biomass conversion” and alternative energy industrial processes.

Using metagenomic discovery and a non-stochastic method of directed evolution (called “DIRECTEVOLUTION[®]”, as described, e.g., in U.S. Patent No. 6,939,689, which includes Gene Site Saturation Mutagenesis (GSSM) (as discussed above, see also U.S. Patent Nos. 6,171,820 and 6,579,258) and Tunable GeneReassembly (TGR) (see, e.g., U.S. Patent No. 6,537,776) technologies. This effort focused on the discovery and optimization of an important enzyme component for cellulose reduction to glucose, cellobiohydrolase.

An enzyme discovery screen was implemented using Diversa Corporation’s GIGAMATRIX[™] high throughput expression screening platform (discussed above) to identify cellobiohydrolases using methylumbelliferyl cellobioside as substrate. A total of 100 complex environmental libraries were screened resulting in 25 confirmed cellobiohydrolase hits mainly from glycosyl hydrolase families 5 and 10. These hits were characterized for activity against AVICEL[®] Microcrystalline Cellulose (MCC) (FMC Corporation, Philadelphia, PA). Based on its performance characteristics, one enzyme, SEQ ID NO:162 (encoded by, e.g., SEQ ID NO:161) was chosen as a candidate for optimization using Gene Site Saturation Mutagenesis (GSSM) technology. However, before GSSM evolution was performed, the signal sequence (amino acids 1 through 30) was removed from SEQ ID NO:162 and a starting methionine was added. This signal-free sequence, hereinafter called the “wild-type” and represented by SEQ ID NO:164 (encoded by, e.g., SEQ ID NO:163), was the parental sequence that was optimized using GSSM technology. As discussed above, GSSM technology can rapidly mutate all amino acids in the protein to the 19 other amino acids in a sequential fashion. Mutants were screened using a fiber-based assay and potential upmutants representing single amino acid changes were identified. These upmutants were combined into a new library representing combinations of the upmutants. This library was screened resulting in identification of several candidate enzymes for commercialization.

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Research SummaryGIGAMATRIXTM screen

The GIGAMATRIXTM (GMx) screening platform is an ultra-high throughput method based on a 100,000 well microplate with the dimensions of a conventional 96 well plate (see Phase II application for details). The screen works with fluorescent substrates. The GMx screen was implemented using 2 substrates based on previously shown activity by cellulases. Methylumbelliferyl cellobioside (MUC) was used as the screening substrate. In addition, resorufin-beta-glucopyranoside was also included in the screen in order to eliminate clones that have activity on both substrates and are presumed to be beta-glucosidases.

Amplified phage or phagemid versions of the target libraries were screened. Two host strains (CEH6 & GAL631) lacking beta-galactosidase genes were used in order to decrease endogenous host activity on the substrates. 100 libraries were chosen for screening based on the fact that these libraries yielded cellulase hits from a previous screening program. Of the libraries screened, there were a total of 355 primary hits from 69 of the libraries screened.

Secondary screening consisted of plating the clones on agar plates and then colony picking into 384 well plates containing media and methylumbelliferyl cellobioside (MUC) termed a "breakout". Figure 10 illustrates in graphic form data showing a typical GIGAMATRIXTM (GMx) breakout. To generate this data, active clones against MUC (i.e., able to hydrolyze methylumbelliferyl cellobioside) are differentiated from a background of inactive clones. Individual clones were then grown overnight and fluorescence was measured and the most active hits were picked for sequencing. In Figure 10, the X axis shows sample name; Y axis is relative fluorescent units. Positive "hits" were plated onto agar plates and then colony picked into 384 well plates containing LB + antibiotic plus 50 μ M MUC and grown overnight.

Table 2. Summary of GIGAMATRIXTM (GMx) hits

<u>Enzyme</u>		
<u>No.</u>	<u>Open Reading Frame SEQ ID NO:</u>	<u>Clone Family Characterization</u>
40	SEQ ID NO:104 (encoded by, e.g., SEQ ID NO:103)	family 5 (cellulase)
41	SEQ ID NO:108 (encoded by, e.g., SEQ ID NO:107)	family 5 (cellulase)
42	SEQ ID NO:112 (encoded by, e.g., SEQ ID NO:111)	family 5 (cellulase)
H7	SEQ ID NO:60 (encoded by, e.g., SEQ ID NO:59)	family 5 (cellulase)
43	SEQ ID NO:82 (encoded by, e.g., SEQ ID NO:81)	family 5 (cellulase)
44	SEQ ID NO:78 (encoded by, e.g., SEQ ID NO:77)	family 5 (cellulase)
45	SEQ ID NO:68 (encoded by, e.g., SEQ ID NO:67)	family 5 (cellulase)- ORF 2

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45a		family 26 (mannanase) - ORF4
	SEQ ID NO:70 (encoded by, e.g., SEQ ID NO:69)	
46	SEQ ID NO:74 (encoded by, e.g., SEQ ID NO:73)	family 10 (xylanase)
47	SEQ ID NO:110 (encoded by, e.g., SEQ ID NO:109)	family 10 (xylanase)
48	SEQ ID NO:106 (encoded by, e.g., SEQ ID NO:105)	family 5 (cellulase)
49	SEQ ID NO:66 (encoded by, e.g., SEQ ID NO:65)	family 10 (xylanase)
50	SEQ ID NO:72 (encoded by, e.g., SEQ ID NO:71)	family 5 (cellulase)
51	SEQ ID NO:80 (encoded by, e.g., SEQ ID NO:79)	family 5 (cellulase)
H8	SEQ ID NO:62 (encoded by, e.g., SEQ ID NO:61)	family 5 (cellulase) ORF 1
H8a	SEQ ID NO:64 (encoded by, e.g., SEQ ID NO:63)	family 5 (cellulase) ORF 4
52	SEQ ID NO:76 (encoded by, e.g., SEQ ID NO:75)	family 5 (cellulase)
53	SEQ ID NO:160 (encoded by, e.g., SEQ ID NO:159)	family 10 (xylanase)
54	SEQ ID NO:88 (encoded by, e.g., SEQ ID NO:87)	family 5 (cellulase)
55	SEQ ID NO:148 (encoded by, e.g., SEQ ID NO:147)	family 10 (xylanase)
56	SEQ ID NO:90 (encoded by, e.g., SEQ ID NO:89)	family 5 (cellulase)
57	SEQ ID NO:152 (encoded by, e.g., SEQ ID NO:151)	family 5 (cellulase)
58	SEQ ID NO:150 (encoded by, e.g., SEQ ID NO:149)	family 5 (cellulase)
59	SEQ ID NO:154 (encoded by, e.g., SEQ ID NO:153)	family 5 (cellulase)
H6	SEQ ID NO:158 (encoded by, e.g., SEQ ID NO:157)	family 5 (cellulase)
60	SEQ ID NO:156 (encoded by, e.g., SEQ ID NO:155)	family 5 (cellulase)

All genomic clone inserts from hits were sequenced. As with Table 1 above, some genomic clones contained more than one open reading frame. For example, one such genomic clone contains two open reading frames annotated as Enzymes No. H8 and H8a, with said open reading frames having the sequences as depicted in SEQ ID NO:67 and SEQ ID NO:69, respectively. There was a total of 25 glycosyl hydrolase hits from 17 of the libraries screened. In general, the hits were from several different glycosyl hydrolase families including 5 and 10. Table 2 (above) lists the hits and their identities. Several other hits were discovered where the open reading frame was not homologous to any known glycosyl hydrolase families. In addition, some of the hits encoded GTP cyclohydrolase genes that are known false positives in this system as they create fluorescence regardless of substrate degradation. Overall the screen was successful in identifying enzymes that were active on MUC.

Characterization

Genes discovered in the GIGAMATRIXTM screen were sequenced and the data were analyzed. Open reading frames (ORFs) were annotated using a software system. The ORFs were subcloned into the appropriate vector(s) with the introduction of DNA encoding C-terminal His-tags. Construct DNA was transformed into the appropriate *E.*

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coli host(s) and expressed for characterization studies. The gene products were screened against phosphoric acid-swollen cellulose (PASC). PASC is crystalline cellulose that is made more amorphous through swelling by acid treatment. PASC was prepared from AVICEL[®] Microcrystalline Cellulose (MCC). Subclones were grown, expressed and lysed. Lysates were incubated with PASC and the reaction products were analyzed using the bicinchoninic acid (BCA) reducing sugar assay. The most active subclones were selected for larger scale growth and purification. The specific activity of these subclones was determined on PASC.

The subclones were also analyzed by capillary electrophoresis (CE). Lysates were incubated with substrate for 30 hours. The reaction products were derivatized with the fluorophore 1-aminopyrene-3,6,8-trisulfonate (APTS). The products were analyzed using a 48 cm capillary. Cellobiose elutes at 6 minutes. Figure 11 illustrates in graph form data showing the activity of selected enzymes against PASC by capillary electrophoresis (CE) analysis. Samples H9 through H1 are individual clones. In Figure 11, a number of samples had reaction product profiles representative of processive enzymes. A processive enzyme is defined as having a ratio of cellobiose / (glucose + cellotriose) ≥ 10 . Two potential processive enzymes that were the most active had specific activities on PASC of 0.35 and 0.04 U/mg, respectively.

Fungal CBHs in *Pichia*

Genes of newly discovered family 6 & 7 fungal cellobiohydrolases were transformed into *P. pastoris* and the transformations were spread onto solid agar plates. 160 colonies were selected for each construct. The samples were grown and induced and the supernatants were incubated with PASC in the presence of a β -glucosidase. The reaction products were analyzed using the glucose-oxidase assay. A glycosyl hydrolase family 6 cellobiohydrolase, was successfully heterologously expressed in *P. pastoris*.

Exo-Endo Acting Cellulase

The wild-type enzyme, a family 9 glycosyl hydrolase discovered in an enzyme screen, is a homolog of *Thermomonospora fusca* E4. E4 has been shown to have both endo- and exo-activity. Initial tests of the wild-type enzyme showed it to be active on both PASC and AVICEL[®] Microcrystalline Cellulose (MCC). HPLC analysis of the reaction products showed the primary products to be glucose and cellobiose. The wild-type enzyme is a multi-domain protein which includes a glycosyl hydrolase family 9 catalytic domain, a family 3 cellulose binding domain, and three bacterial Ig-like domains.

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that are believed to be involved in cell adhesion. Three additional subclone variants of the wild-type enzyme were tested to determine the effects of the domains on activity. The wild-type enzyme was subcloned with: 1) the catalytic domain alone (CD); 2) the catalytic and carbohydrate domain (CCD); and 3) the catalytic and carbohydrate binding domain plus the 11 downstream amino acids (CCD+11). The full-length protein and the 3 subclone variants were assayed on AVICEL[®] Microcrystalline Cellulose (MCC) and the reaction products were analyzed by the BCA reducing sugar assay, and the data is summarized in graphic form in Figure 12. The data illustrated in Figure 12 was generated by BCA of the wild-type enzyme and truncation mutants incubated with AVICEL[®] Microcrystalline Cellulose (MCC) for 74 hours, 37°C, pH 5. CBH1 is a positive control. The negative control is the host without insert.

The wild-type enzyme, the full-length protein (SEQ ID NO:164, encoded by, e.g., SEQ ID NO:163), was the most active. The full length protein was selected for GSSM evolution. The catalytic and the carbohydrate binding domain were evolved.

15 GSSM screening

GSSM technology (discussed above) was used to rapidly and sequentially mutate the amino acids of the catalytic and carbohydrate binding domain of the target protein into the 19 other amino acids. The goal of the GSSM screen was to identify mutants that increased the extent of hydrolysis on insoluble microcrystalline cellulose. A robotic screening method was developed to facilitate the GSSM screening process.

DNA from the mutation constructs was transformed into DH10b host cells. Individual colonies were picked into 96 well (shallow) plates containing 150 uL LB/Ampicillin using the automatic colony picking system. The plates were incubated for 24 hours at 37°C, 400rpm. 15uL of culture was transferred from each well into an induction plate. Each well of the induction plate contained 135 uL LB/Ampicillin with 1.1mM IPTG. The induction plates were incubated for 24 hours at 37°C, 400rpm. The plates were centrifuged and the supernatant was discarded.

The automated portion of the assay began at this point. The cells were lysed and resuspended by the robot. 150uL of lysis buffer (125uL water plus 25uL BPER containing 0.2mg/ml lysozyme and 20 unit/ml DNase I) was added to each well. 15uL lysate was transferred from each well to a reaction plate. Each well of the reaction plate contained 185uL of a reaction mix (1% AVICEL[®] Microcrystalline Cellulose (MCC), 50mM sodium acetate buffer pH5.0). The reaction plates were incubated at 37°C for 30 hours with 95% humidity. After incubation, the plates were centrifuged and 15uL

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supernatant was transferred to BCA plates. The BCA plates contained 50uL reagent A, 50uL reagent B, and 80uL 400mM Carbonate buffer, pH 10 per well. The plates were covered with rubber seals and incubated at 80°C for 30 minutes, then cooled by centrifugation and the absorbance read at A560.

5 Results

At least 80 random mutation colonies were screened for each amino acid site. An example of the primary GSSM™ screening data is graphically illustrated in Figure 13. Column 6 contained the wildtype samples and column 12 contained the host/vector negative controls. After a 30 hour incubation with AVICEL® Microcrystalline Cellulose (MCC), the signal produced from the wildtype samples was around 0.53, with a standard deviation at 0.07. The negative control had an average signal at 0.29. Samples with signal higher than the average of positive controls plus 2 times the standard deviation were deemed primary hits. From this screening plate, about ten primary hits were selected for the secondary confirmation screening.

15 Primary hits were reconfirmed in a secondary assay. This assay was the same as the primary screen. Samples were run in quadruplicate however. An example of the secondary GSSM screening data is graphically illustrated in Figure 14. Samples in wells E3-H3, A4-D4, A7-D7 on average, had higher activity than the wildtype. These 12 wells correspond to 3 hits since the samples were run in quadruplicate. These samples were the primary hits shown in wells E4, G2, and H3 in Figure 13 (plate 29805-AA89 BCA plate).

20 There were 77 hits from the secondary screening. These samples were sequenced. Thirty five of the samples had amino acid changes, 22 had transposon insertions, and the rest were wildtype or had deletions.

Hits from the secondary screen were further analyzed. The GSSM upmutants were mapped onto the crystal structure of *T. fusca* E4. Samples were prioritized based on amino acid location, amino acid change and the fold improvement score. Eight upmutants were selected from the GSSM screening and selected for gene reassembly evolution, i.e., Tunable GeneReassembly (TGR), discussed above, and also see, e.g., U.S. Patent No. 6,537,776.

30 Table 2. Up-mutants selected for site directed mutagenesis reassembly.

<u>Residue</u>	<u>OLD AA</u>	<u>NEW AA</u>
89	M	R
103	F	G

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110	P	G
114	Y	L
157	A	S
481	W	F
550	P	N
590	G	R

Blending of upmutants

Using gene reassembly (Tunable GeneReassembly (TGR)) technology, the upmutants shown in Table 2, above, were blended in order to identify the candidate with the best activity. Activity assays were the same as for the GSSM screening except reactions were further diluted to account for increased activity of upmutants over the wildtype enzyme. Figure 15 illustrates in graph form data from mixed, or “blended”, GSSM™ screening assays.

In summary, the invention provides enzymes having cellulase activity having the following sequences based on SEQ ID NO:164 (encoded by, e.g., SEQ ID NO:163):

Residue	Original Amino Acid	Codons Encoding Original Amino Acid	New Amino Acid (after GSSM Evolution)	Codons Encoding New Amino Acid
89	M	ATG	R	CGT, CGC, CGA, CGG, AGA, AGG
103	F	TTT, TTC	G	GGT, GGC, GGA, GGG
110	P	CCA, CCC, CCG, CCT	G	GGT, GGC, GGA, GGG
114	Y	TAT, TAC	L	TTA, TTG, CTT, CTC, CTA, CTG
157	A	GCT, GCC, GCA, GCG	S	TCT, TCC, TCA, TCG, AGT, AGC
481	W	TGG	F	TTT, TTC
550	P	CCA, CCC, CCG, CCT	N	AAT, AAC
590	G	GGT, GGC, GGA, GGG	R	CGT, CGC, CGA, CGG, AGA, AGG

A number of aspects of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other aspects are within the scope of the following claims.

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WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising

(a) a nucleic acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or complete sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165, over a region of at least about 20, 30, 40, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, wherein the nucleic acid encodes at least one polypeptide having a cellulase activity,

and optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or

(b) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID

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NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID
 NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID
 NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID
 NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID
 5 NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID
 NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID
 NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID
 NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID
 NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID
 10 NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID
 NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID
 NO:161, SEQ ID NO:163 or SEQ ID NO:165, wherein the nucleic acid encodes a
 polypeptide having a cellulase activity, and the stringent conditions include a wash step
 comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes,

15 and optionally the nucleic acid is at least about 20, 30, 40, 50, 60, 75, 100, 150,
 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length
 of the gene or transcript;

(c) a nucleic acid sequence encoding a polypeptide having a sequence as set forth
 in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID
 20 NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID
 NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID
 NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID
 NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID
 NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID
 25 NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID
 NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID
 NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID
 NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID
 NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID
 30 NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID
 NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID
 NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID
 NO:142, SEQ ID NO:143, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID

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NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ ID NO:166; or

(d) a nucleic acid sequence complementary to (a), (b) or (c).

2. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165.

3. The isolated or recombinant nucleic acid of claim 1, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

25 4. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises an endoglucanase activity.

5. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises a cellobiohydrolase activity.

30 6. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises an β -glucosidase or mannanase activity.

7. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises an endocellulase activity.

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8. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises hydrolyzing a glucan to produce a smaller molecular weight polysaccharide or oligomer.

5 9. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises catalyzing hydrolysis of 1,4-beta-D-glycosidic linkages.

10. The isolated or recombinant nucleic acid of claim 9, wherein the endocellulase activity comprises an endo-1,4-beta-endocellulase activity.

10 11. The isolated or recombinant nucleic acid of claim 10, wherein the 1,4-beta-D-glycosidic linkage activity comprises hydrolysis of a 1,4-beta-D-glycosidic linkage in a cellulose, a cellulose derivative, a lichenin or a cereal.

12. The isolated or recombinant nucleic acid of claim 11, wherein the cellulose derivative comprises a carboxy methyl cellulose or a hydroxy ethyl cellulose.

13. The isolated or recombinant nucleic acid of claim 11, wherein the cereal comprises a beta-D-glucan or a xyloglucan.

15 14. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises catalyzing hydrolysis of glucanase linkages.

15. The isolated or recombinant nucleic acid of claim 14, wherein the cellulase activity comprises catalyzing hydrolysis of β -1,4- and/or β -1,3- glucanase linkages.

20 16. The isolated or recombinant nucleic acid of claim 14, wherein the cellulase activity comprises catalyzing hydrolysis of endo-glucanase linkages.

17. The isolated or recombinant nucleic acid of claim 16, wherein the cellulase activity comprises catalyzing hydrolysis of endo-1,4-beta-D-glucan 4-glucano hydrolase activity.

25 18. The isolated or recombinant nucleic acid of claim 16, wherein the cellulase activity comprises catalyzing hydrolysis of internal endo- β -1,4- glucanase linkages and/or β -1,3- glucanase linkages.

19. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises catalyzing hydrolysis of internal β -1,3-glucosidic linkages.

30 20. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises hydrolyzing polysaccharides comprising glucopyranose.

21. The isolated or recombinant nucleic acid of claim 20, wherein the cellulase activity comprises hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked D-glucopyranoses.

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22. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises hydrolyzing a cellulose, a cellulose derivative or a hemicellulose.

23. The isolated or recombinant nucleic acid of claim 22 wherein the cellulase activity comprises hydrolyzing a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product.

24. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises catalyzing hydrolysis of glucan in a feed, a food product or a beverage.

25. The isolated or recombinant nucleic acid of claim 24 wherein the feed, food product or beverage comprises a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable.

26. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity comprises catalyzing hydrolysis of a glucan in a microbial cell, a fungal cell, a mammalian cell, a plant cell or any plant material comprising a cellulosic part.

27. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity is thermostable.

28. The isolated or recombinant nucleic acid of claim 27, wherein the polypeptide retains a cellulase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C, or retains a cellulase activity in a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, or between about 37°C to about 95°C, 96°C, 97°C, 98°C or 99°C.

29. The isolated or recombinant nucleic acid of claim 1, wherein the cellulase activity is thermotolerant.

30. The isolated or recombinant nucleic acid of claim 29, wherein the polypeptide retains a cellulase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C, or after exposure to a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, or between about 37°C to about 95°C, 96°C, 97°C, 98°C or 99°C.

31. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with a cellulase activity, wherein the probe comprises at least 20, 30, 40, 50, 60, 75, 100

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or 150 or more consecutive bases of a sequence as set forth in claim 1, wherein the probe identifies the nucleic acid by binding or hybridization,

wherein optionally the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about
5 50 to 150 consecutive bases,

wherein optionally the probe comprises consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15.

32. An amplification primer pair for amplifying a nucleic acid encoding a
10 polypeptide having a cellulase activity, wherein the amplification primer pair

(a) is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1, or a subsequence thereof; or

(b) comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more
15 residues of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID
20 NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID
25 NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID
30 NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member,

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wherein optionally a member of the amplification primer pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

5 33. A cellulase-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 32, wherein optionally the amplification is by polymerase chain reaction (PCR).

 34. The cellulase-encoding nucleic acid of claim 33, wherein the nucleic acid generated by amplification of a gene library, and optionally the gene library is an
10 environmental library.

 35. An isolated or recombinant cellulase encoded by the cellulase-encoding nucleic acid set forth in claim 33.

 36. A method of amplifying a nucleic acid encoding a polypeptide having a cellulase activity comprising amplification of a template nucleic acid with an
15 amplification primer pair as set forth in claim 32.

 37. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1.

 38. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1, wherein optionally the vehicle comprises an expression vector.

20 39. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1,

 wherein optionally the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome, and optionally the viral vector comprises an adenovirus vector, a retroviral vector
25 or an adeno-associated viral vector, and optionally the cloning vehicle comprises a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

 40. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1, or an expression cassette as set forth in claim 37, the vector of claim 38,
30 or a cloning vehicle as set forth in claim 39,

 wherein optionally the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

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41. A transgenic non-human animal comprising a sequence as set forth in claim 1, wherein optionally the transgenic non-human animal is a mouse or a rat.

42. A transgenic plant comprising a sequence as set forth in claim 1, wherein optionally the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

43. A transgenic seed comprising a sequence as set forth in claim 1, wherein optionally the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

44. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1, or a subsequence thereof

wherein optionally the antisense oligonucleotide has a length of between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases.

45. A method of inhibiting the translation of a cellulase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1.

46. A double-stranded interference RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1,

wherein optionally the RNAi comprises an siRNA or an miRNA, and optionally the RNAi molecule is about 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or more duplex nucleotides in length.

47. A method of inhibiting the expression of a cellulase in a cell comprising administering to the cell or expressing in the cell a double-stranded interference RNA (RNAi) molecule as set forth in claim 46.

48. An isolated or recombinant polypeptide

(i) having an amino acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or 100% sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID

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NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID
 NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID
 NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID
 NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID
 5 NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID
 NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID
 NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID
 NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID
 NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID
 10 NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID
 NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID
 NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID
 NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:146, SEQ ID
 NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID
 15 NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ ID NO:166, over a
 region of at least about 20, 25, 30, 35, 40, 45, 50, 55, 60, 75, 100, 150, 200, 250, 300 or
 more residues,

wherein optionally the sequence identities are determined by analysis with a
 sequence comparison algorithm or by a visual inspection, and optionally the sequence
 20 comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set
 to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default;

(ii) having an amino acid sequence encoded by a nucleic acid as set forth in claim
 1, wherein the polypeptide has a cellulase activity or has immunogenic activity in that it is
 capable of generating an antibody that specifically binds to a polypeptide having a
 25 sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,
 SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ
 ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID
 NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID
 NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID
 30 NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID
 NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID
 NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID
 NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID
 NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID

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NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ ID NO:166; or

(iii) having an amino acid sequence as set forth in (i) or (ii), or a polypeptide encoded by a nucleic acid as set forth in claim 1, and comprising at least one amino acid residue conservative substitution,

wherein optionally conservative substitution comprises replacement of an aliphatic amino acid with another aliphatic amino acid; replacement of a serine with a threonine or vice versa; replacement of an acidic residue with another acidic residue; replacement of a residue bearing an amide group with another residue bearing an amide group; exchange of a basic residue with another basic residue; or, replacement of an aromatic residue with another aromatic residue, or a combination thereof,

and optionally the aliphatic residue comprises Alanine, Valine, Leucine, Isoleucine or a synthetic equivalent thereof; the acidic residue comprises Aspartic acid, Glutamic acid or a synthetic equivalent thereof; the residue comprising an amide group comprises Aspartic acid, Glutamic acid or a synthetic equivalent thereof; the basic residue comprises Lysine, Arginine or a synthetic equivalent thereof; or, the aromatic residue comprises Phenylalanine, Tyrosine or a synthetic equivalent thereof.

49. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises an endoglucanase activity.

50. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises a cellobiohydrolase activity.

51. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises an β -glucosidase or mannanase activity.

52. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises an endocellulase activity.

53. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises hydrolyzing a glucan to produce a smaller molecular weight polysaccharide or oligomer.

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54. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises catalyzing hydrolysis of 1,4-beta-D-glycosidic linkages.

55. The isolated or recombinant polypeptide of claim 54, wherein the endocellulase activity comprises an endo-1,4-beta-endocellulase activity.

5 56. The isolated or recombinant polypeptide of claim 54, wherein the 1,4-beta-D-glycosidic linkage activity comprises hydrolysis of a 1,4-beta-D-glycosidic linkage in a cellulose, a cellulose derivative, a lichenin or a cereal.

57. The isolated or recombinant polypeptide of claim 56, wherein the cellulose derivative comprises a carboxy methyl cellulose or a hydroxy ethyl cellulose.

10 58. The isolated or recombinant polypeptide of claim 56, wherein the cereal comprises a beta-D-glucan or a xyloglucan.

59. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises catalyzing hydrolysis of glucanase linkages.

15 60. The isolated or recombinant polypeptide of claim 59, wherein the cellulase activity comprises catalyzing hydrolysis of β -1,4- and/or β -1,3- glucanase linkages.

61. The isolated or recombinant polypeptide of claim 59, wherein the cellulase activity comprises catalyzing hydrolysis of endo-glucanase linkages.

20 62. The isolated or recombinant polypeptide of claim 61, wherein the cellulase activity comprises catalyzing hydrolysis of endo-1,4-beta-D-glucan 4-glucano hydrolase activity.

63. The isolated or recombinant polypeptide of claim 61, wherein the cellulase activity comprises catalyzing hydrolysis of internal endo- β -1,4- glucanase linkages and/or β -1,3- glucanase linkages.

25 64. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises catalyzing hydrolysis of internal β -1,3-glucosidic linkages.

65. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises hydrolyzing polysaccharides comprising glucopyranose.

30 66. The isolated or recombinant polypeptide of claim 65, wherein the cellulase activity comprises hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked D-glucopyranoses.

67. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises hydrolyzing a cellulose, a cellulose derivative or a hemicellulose.

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68. The isolated or recombinant polypeptide of claim 67, wherein the cellulase activity comprises hydrolyzing a cellulose or a hemicellulose in a wood or paper pulp or a wood or paper product.

69. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises catalyzing hydrolysis of glucan in a feed, a food product or a beverage.

70. The isolated or recombinant polypeptide of claim 69, wherein the feed, food product or beverage comprises a cereal-based animal feed, a wort or a beer, a dough, a fruit or a vegetable.

71. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises catalyzing hydrolysis of a glucan in a microbial cell, a fungal cell, a mammalian cell, a plant cell or any plant material comprising a cellulosic part.

72. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity is thermostable.

73. The isolated or recombinant polypeptide of claim 72, wherein the polypeptide retains a cellulase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C, or retains a cellulase activity in a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, or between about 37°C to about 95°C, 96°C, 97°C, 98°C or 99°C.

74. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity is thermotolerant.

75. The isolated or recombinant polypeptide of claim 74, wherein the polypeptide retains a cellulase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C, or after exposure to a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, or between about 37°C to about 95°C, 96°C, 97°C, 98°C or 99°C.

76. The isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 48 and lacking a signal or leader sequence or a prepro sequence.

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77. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 48 and having a heterologous signal or leader sequence or a heterologous prepro sequence.

5 78. The isolated or recombinant polypeptide of claim 48, wherein the cellulase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

10 79. The isolated or recombinant polypeptide of claim 48, wherein the thermotolerance comprises retention of at least half of the specific activity of the cellulase at 37°C after being heated to an elevated temperature, or, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

15 80. The isolated or recombinant polypeptide of claim 48, wherein the polypeptide comprises at least one glycosylation site, and optionally the glycosylation is an N-linked glycosylation, and optionally the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

20 81. The isolated or recombinant polypeptide of claim 48, wherein the polypeptide retains a cellulase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0 or more acidic, or after exposure to conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0 or more acidic.

25 82. The isolated or recombinant polypeptide of claim 48, wherein the polypeptide retains a cellulase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5 or more basic, or after exposure to conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5 or more basic.

83. A protein preparation comprising a polypeptide as set forth in claim 48, wherein the protein preparation comprises a liquid, a solid or a gel.

30 84. A heterodimer comprising a polypeptide as set forth in claim 48 and a second domain, wherein optionally the second domain is a polypeptide and the heterodimer is a fusion protein, and optionally the second domain comprises an epitope, an immunogenic peptide or a tag.

85. A homodimer comprising a polypeptide as set forth in claim 48.

86. An immobilized polypeptide or an immobilized nucleic acid, wherein the polypeptide comprises a sequence as set forth in claim 48, or a subsequence thereof, or

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the nucleic acid comprises a sequence as set forth in claim 1, or a subsequence thereof, or the probe as set forth in claim 31, wherein optionally the polypeptide or nucleic acid is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

5 87. An array comprising an immobilized polypeptide as set forth in claim 86, or, an immobilized nucleic acid as set forth in claim 86.

 88. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 48, wherein optionally the antibody is a monoclonal or a polyclonal antibody.

10 89. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 48.

 90. A method of isolating or identifying a polypeptide with a cellulase activity comprising the steps of:

 (a) providing an antibody as set forth in claim 88;
15 (b) providing a sample comprising polypeptides; and
 (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having a cellulase activity.

 91. A method of making an anti-cellulase antibody comprising
20 (a) administering to a non-human animal a nucleic acid as set forth in claim 1 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-cellulase antibody, or

 (b) administering to a non-human animal a polypeptide as set forth in claim 48 or a subsequence thereof in an amount sufficient to generate a humoral immune response,
25 thereby making an anti-cellulase antibody.

 92. A method of producing a recombinant polypeptide comprising the steps of:
 (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a
30 recombinant polypeptide.

 wherein optionally the method further comprises transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

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93. A method for identifying a polypeptide having a cellulase activity comprising the following steps:

- (a) providing a polypeptide as set forth in claim 48;
- (b) providing a cellulase substrate; and
- 5 (c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a cellulase activity.

10 94. A method for identifying a cellulase substrate comprising the following steps:

- (a) providing a polypeptide as set forth in claim 48;
- (b) providing a test substrate; and
- (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction
- 15 product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a cellulase substrate.

95. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) expressing a nucleic acid or a vector comprising the nucleic acid under
- 20 conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the
- 25 polypeptide.

96. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) providing a polypeptide as set forth in claim 48;
- (b) providing a test compound;
- 30 (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

97. A method for identifying a modulator of a cellulase activity comprising the following steps:

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(a) providing a polypeptide as set forth in claim 48;

(b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the glucanase, wherein a change in the cellulase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the cellulase activity.

98. The method of claim 97, wherein the cellulase activity is measured by providing a cellulase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product,

wherein optionally a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of a cellulase activity,

and optionally an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of a cellulase activity.

99. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 48, a polypeptide encoded by a nucleic acid as set forth in claim 1,

wherein optionally the method further comprises a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon, or further comprises an identifier that identifies one or more features in said sequence and optionally the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

100. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1.

101. A method for identifying a feature in a sequence comprising the steps of:
(a) reading the sequence using a computer program which identifies one or more features

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in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 48; a polypeptide encoded by a nucleic acid as set forth in claim 1; and (b) identifying one or more features in the sequence with the computer program.

5 102. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 48 or a polypeptide encoded by a nucleic acid as set forth in claim 1; and (b) determining differences between the first sequence
10 and the second sequence with the computer program.

 wherein optionally the method further comprises a step of determining differences between the first sequence and the second sequence, or optionally the method further comprises the step of identifying polymorphisms, or optionally the method further
15 comprises use of an identifier that identifies one or more features in a sequence,
 and optionally the method comprises reading the first sequence using a computer program and identifying one or more features in the sequence.

 103. A method for isolating or recovering a nucleic acid encoding a polypeptide with a cellulase activity from an environmental sample comprising the steps of:

20 (a) providing an amplification primer pair as set forth in claim 32;
 (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

 (c) combining the nucleic acid of step (b) with the amplification primer pair of
25 step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with a cellulase activity from an environmental sample.

 104. A method for isolating or recovering a nucleic acid encoding a polypeptide with a cellulase activity from an environmental sample comprising the steps of:

30 (a) providing a polynucleotide probe comprising a sequence as set forth in claim 1, or a subsequence thereof, or a probe as set forth in claim 31;

 (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

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(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a cellulase activity from an environmental sample.

105. The method of claim 103 or claim 104, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample, and optionally the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

106. A method of generating a variant of a nucleic acid encoding a polypeptide with a cellulase activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid

wherein optionally the method further comprises expressing the variant nucleic acid to generate a variant cellulase polypeptide,

and optionally the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof

and optionally the method is iteratively repeated until a cellulase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

107. The method of claim 106, wherein the variant cellulase polypeptide: (a) is thermotolerant, and retains some activity after being exposed to an elevated temperature;

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(b) has increased glycosylation as compared to the cellulase-encoded by a template nucleic acid; or, (c) has a cellulase activity under a high temperature, wherein the cellulase-encoded by the template nucleic acid is not active under the high temperature.

108. The method of claim 106, wherein the method is iteratively repeated until
5 (a) a cellulase coding sequence having an altered codon usage from that of the template nucleic acid is produced, or, (b) a cellulase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

109. A method for modifying codons in a nucleic acid encoding a polypeptide with a cellulase activity to increase its expression in a host cell, the method comprising
10 the following steps:

(a) providing a nucleic acid encoding a polypeptide with a cellulase activity comprising a sequence as set forth in claim 1; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino
15 acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non- preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

110. A method for modifying codons in a nucleic acid encoding a cellulase
20 polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a cellulase activity comprising a sequence as set forth in claim 1; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying
25 codons in a nucleic acid encoding a cellulase.

111. A method for modifying codons in a nucleic acid encoding a cellulase polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a cellulase polypeptide comprising a
30 sequence as set forth in claim 1; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non- preferred or less preferred codon is

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a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

112. A method for modifying a codon in a nucleic acid encoding a polypeptide having a cellulase activity to decrease its expression in a host cell, the method comprising
5 the following steps:

(a) providing a nucleic acid encoding a cellulase polypeptide comprising a sequence as set forth in claim 1; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non- preferred or less preferred codon encoding the same amino acid
10 as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non- preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell,

wherein optionally the host cell is a bacterial cell, a fungal cell, an insect cell, a
15 yeast cell, a plant cell or a mammalian cell.

113. A method for producing a library of nucleic acids encoding a plurality of modified cellulase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the
20 following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID
25 NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID
30 NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID

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NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165, or a subsequence thereof, and the nucleic acid encodes a cellulase active site or a cellulase substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

10 (c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified cellulase active sites or substrate binding sites.

15 wherein optionally a mutagenic oligonucleotide or a variant nucleic acid is generated by a method comprising an optimized directed evolution system, Gene Site-Saturation Mutagenesis (GSSM), or a synthetic ligation reassembly (SLR), error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

114. A method for making a small molecule comprising the following steps:

(a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a cellulase enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1;

(b) providing a substrate for at least one of the enzymes of step (a); and

(c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

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115. A method for modifying a small molecule comprising the following steps:

(a) providing a cellulase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1;

5 (b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the cellulase enzyme, thereby modifying a small molecule by a cellulase enzymatic reaction.

10 wherein optionally step (b) comprises providing a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the cellulase enzyme;

15 and optionally the method further comprises providing a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions;

20 and optionally the method further comprises the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library, wherein optionally the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

25 116. A method for determining a functional fragment of a cellulase enzyme comprising the steps of:

(a) providing a cellulase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1; and

30 (b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a cellulase activity, thereby determining a functional fragment of a cellulase enzyme.

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wherein optionally the cellulase activity is measured by providing a cellulase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

117. A method for whole cell engineering of new or modified phenotypes by
5 using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell,
wherein the genetic composition is modified by addition to the cell of a nucleic acid
comprising a sequence as set forth in claim 1;

(b) culturing the modified cell to generate a plurality of modified cells;

10 (c) measuring at least one metabolic parameter of the cell by monitoring the cell
culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs
from a comparable measurement in an unmodified cell under similar conditions, thereby
identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

15 wherein optionally the genetic composition of the cell is modified by a method
comprising deletion of a sequence or modification of a sequence in the cell, or, knocking
out the expression of a gene,

and optionally the method further comprises selecting a cell comprising a newly
engineered phenotype,

20 and optionally the method further comprises culturing the selected cell, thereby
generating a new cell strain comprising a newly engineered phenotype.

118. An isolated or recombinant signal or leader sequence consisting of an
amino acid sequence as set forth in the amino terminal residues 1 to 14, 1 to 15, 1 to 16, 1
to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1
25 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1
to 40, 1 to 41, 1 to 42, 1 to 43 or 1 to 44, of (a) an amino acid sequence as set forth in
claim 48; or, (b) an amino acid sequence as set forth in SEQ ID NO:2, SEQ ID NO:4,
SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID
NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID
30 NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID
NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID
NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID
NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID
NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID

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NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID
NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID
NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID
NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID
5 NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID
NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID
NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID
NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164 or SEQ
10 ID NO:166.

119. A chimeric polypeptide comprising at least a first domain comprising a
signal peptide (SP) or leader sequence having an amino acid sequence as set forth in
claim 118, and at least a second domain comprising a heterologous polypeptide or
peptide, wherein the heterologous polypeptide or peptide is not naturally associated with
15 the signal peptide (SP) or leader sequence,

and optionally the heterologous polypeptide or peptide is not a cellulase, and
optionally the heterologous polypeptide or peptide is amino terminal to, carboxy terminal
to or on both ends of the signal peptide (SP) or leader sequence.

120. An isolated or recombinant nucleic acid encoding a chimeric polypeptide,
20 wherein the chimeric polypeptide comprises at least a first domain comprising signal
peptide (SP) or leader sequence having an amino acid sequence as set forth in claim 118
and at least a second domain comprising a heterologous polypeptide or peptide, wherein
the heterologous polypeptide or peptide is not naturally associated with the signal peptide
(SP) or leader sequence.

25 121. An isolated or recombinant nucleic acid comprising a sequence encoding a
polypeptide having a cellulase activity and a signal sequence, wherein the nucleic acid
comprises a sequence as set forth in claim 1.

122. The isolated or recombinant nucleic acid of claim 121, wherein the signal
sequence is derived from another cellulase or a non-cellulase enzyme.

30 123. An isolated or recombinant nucleic acid comprising a sequence encoding a
polypeptide having a cellulase activity, wherein the sequence does not contain a signal
sequence and the nucleic acid comprises a sequence as set forth in claim 1.

124. A method of increasing thermotolerance or thermostability of a cellulase
polypeptide, the method comprising glycosylating a cellulase, wherein the polypeptide

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comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, thereby increasing the thermotolerance or thermostability of the cellulase.

125. A method for overexpressing a recombinant cellulase in a cell comprising
5 expressing a vector comprising a nucleic acid sequence as set forth in claim 1, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

126. A method of making a transgenic plant comprising the following steps:
(a) introducing a heterologous nucleic acid sequence into the cell, wherein the
10 heterologous nucleic sequence comprises a sequence as set forth in claim 1, thereby producing a transformed plant cell;
(b) producing a transgenic plant from the transformed cell.

wherein optionally the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts,
15 and optionally step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

127. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:
20 (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

25 128. A method for hydrolyzing, breaking up or disrupting a glucan- or cellulose- comprising composition comprising the following steps:

(a) providing a polypeptide having a cellulase activity as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1;
(b) providing a composition comprising a cellulose or a glucan; and
30 (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the cellulase hydrolyzes, breaks up or disrupts the glucan- or cellulose- comprising composition.

wherein optionally the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell,

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and optionally the polypeptide has endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

129. A dough or a bread product comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally
5 the polypeptide has cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

130. A method of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, under conditions sufficient for conditioning the
10 dough.

131. A beverage comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

15 132. A method of beverage production comprising administration of at least one polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage,

wherein optionally the beverage or beverage precursor is a wort or a beer.

20 133. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

25 134. A method for utilizing a cellulase as a nutritional supplement in an animal diet, the method comprising:

preparing a nutritional supplement containing a cellulase enzyme comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1; and

30 administering the nutritional supplement to an animal to increase utilization of a xylan contained in a feed or a food ingested by the animal.

wherein optionally the animal is a human, or the animal is a ruminant or a monogastric animal,

and optionally the cellulase enzyme is prepared by expression of a polynucleotide encoding the cellulase in an organism selected from the group consisting of a bacterium, a

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yeast, a plant, an insect, a fungus and an animal, and optionally the organism is selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

135. An edible enzyme delivery matrix or pellet comprising a thermostable recombinant cellulase enzyme comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

136. A method for delivering a cellulase supplement to an animal, the method comprising: preparing an edible enzyme delivery matrix or pellets comprising a granulate edible carrier and a thermostable recombinant cellulase enzyme, wherein the pellets readily disperse the cellulase enzyme contained therein into aqueous media, and the recombinant cellulase enzyme comprises a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1; and, administering the edible enzyme delivery matrix or pellet to the animal.

wherein optionally the granulate edible carrier comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd,

and optionally the edible carrier comprises grain germ that is spent of oil, and optionally the cellulase enzyme is glycosylated to provide thermostability at pelletizing conditions,

and optionally the delivery matrix is formed by pelletizing a mixture comprising a grain germ and a cellulase,

and optionally the pelletizing conditions include application of steam, and optionally the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

137. A cellulose- or cellulose derivative- composition comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

138. A wood, wood pulp or wood product comprising a cellulase as set forth in claim 48, or a cellulase encoded by a nucleic acid as set forth in claim 1, wherein

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optionally the cellulase activity comprises endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

139. A paper, paper pulp or paper product comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein
5 optionally the polypeptide has cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

140. A method for reducing the amount of cellulose in a paper, a wood or wood product comprising contacting the paper, wood or wood product with a cellulase as set forth in claim 48, or a cellulase encoded by a nucleic acid as set forth in claim 1, wherein
10 optionally the cellulase activity comprises endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

141. A detergent composition comprising a cellulase as set forth in claim 48, or a cellulase encoded by a nucleic acid as set forth in claim 1,

wherein optionally the polypeptide is formulated in a non-aqueous liquid
15 composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form,

and optionally the cellulase activity comprises endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

142. A pharmaceutical composition or dietary supplement comprising a
20 cellulase as set forth in claim 48, or a cellulase encoded by a nucleic acid as set forth in claim 1,

wherein optionally the cellulase is formulated as a tablet, gel, pill, implant, liquid, spray, powder, food, feed pellet or as an encapsulated formulation

and optionally the cellulase activity comprises endoglucanase, cellobiohydrolase,
25 mannanase and/or beta-glucosidase activity.

143. A fuel comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity,

30 wherein optionally the fuel is derived from a plant material, which optionally comprises potatoes, soybean (rapeseed), barley, rye, corn, oats, wheat, beets or sugar cane,

and optionally the fuel comprises a bioethanol or a gasoline-ethanol mix.

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144. A method for making a fuel comprising contacting a composition comprising a cellulose or a fermentable sugar with a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1,

wherein optionally the composition comprising a cellulose or a fermentable sugar comprises a plant, plant product or plant derivative, and optionally the plant or plant product comprises cane sugar plants or plant products, beets or sugarbeets, wheat, corn, soybeans, potato, rice or barley,

and optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity,

and optionally the fuel comprises a bioethanol or a gasoline-ethanol mix.

145. A method for making bioethanol comprising contacting a composition comprising a cellulose or a fermentable sugar with a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1,

wherein optionally the composition comprising a cellulose or a fermentable sugar comprises a plant, plant product or plant derivative, and optionally the plant or plant product comprises cane sugar plants or plant products, beets or sugarbeets, wheat, corn, soybeans, potato, rice or barley,

and optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

146. An enzyme ensemble for depolymerization of cellulosic and hemicellulosic polymers to metabolizeable carbon moieties comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1,

wherein optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

147. A method for processing a biomass material comprising lignocellulose comprising contacting a composition comprising a cellulose or a fermentable sugar with a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1,

wherein optionally the biomass material comprising lignocellulose is derived from an agricultural crop, is a byproduct of a food or a feed production, is a lignocellulosic waste product, or is a plant residue or a waste paper or waste paper product, and optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity,

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and optionally the plant residue comprise stems, leaves, hulls, husks, cobs, wood, wood chips, wood pulp and sawdust,

and optionally the paper waste comprises discarded or used photocopy paper, computer printer paper, notebook paper, notepad paper, typewriter paper, newspapers, magazines, cardboard and paper-based packaging materials,

and optionally the processing of the biomass material generates a bioethanol.

148. A dairy product comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the dairy product comprises a milk, an ice cream, a cheese or a yogurt, and optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

149. A method for improving texture and flavor of a dairy product comprising the following steps: (a) providing a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1; (b) providing a dairy product; and (c) contacting the polypeptide of step (a) and the dairy product of step (b) under conditions wherein the cellulase can improve the texture or flavor of the dairy product.

150. A textile or fabric comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the textile or fabric comprises a cellulose-containing fiber, and optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

151. A method for treating solid or liquid animal waste products comprising the following steps:

(a) providing a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity;

(b) providing a solid or a liquid animal waste; and

(c) contacting the polypeptide of step (a) and the solid or liquid waste of step (b) under conditions wherein the protease can treat the waste.

152. A processed waste product comprising a polypeptide as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has activity comprising cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

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153. A disinfectant comprising a polypeptide having a cellulase activity, wherein the polypeptide comprises a sequence as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has activity comprising endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

154. A biodefense or bio-detoxifying agent comprising a polypeptide having a cellulase activity, wherein the polypeptide comprises a sequence as set forth in claim 48, or a polypeptide encoded by a nucleic acid as set forth in claim 1, wherein optionally the polypeptide has activity comprising endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity.

155. An isolated or recombinant nucleic acid having a sequence comprising at least one nucleotide base residue modification of SEQ ID NO:163, wherein the modification comprises one or more of the following changes:

a nucleotide at any one of positions 265 to 267 is modified to CGT, CGC, CGA, CGG, AGA or AGG;

a nucleotide at any one of positions 307 to 309 is modified to GGT, GGC, GGA or GGG;

a nucleotide at any one of positions 328 to 330 is modified to GGT, GGC, GGA or GGG;

a nucleotide at any one of positions 340 to 342 is modified to TTA, TTG, CTT, CTC, CTA or CTG,

a nucleotide at any one of positions 469 to 471 is modified to TCT, TCC, TCA, TCG, AGT or AGC;

a nucleotide at any one of positions 1441 to 1443 is modified to TTT or TTC;

a nucleotide at any one of positions 1648 to 1650 is modified to AAT or AAC; or

a nucleotide at any one of positions 1768 to 1770 is modified to CGT, CGC, CGA, CGG, AGA or AGG.

156. An isolated or recombinant polypeptide having a sequence comprising at least one amino acid residue modification of SEQ ID NO:164, wherein the modification comprises one or more of the following changes:

a methionine at amino acid position 89 is modified to arginine;

a phenylalanine at amino acid position 103 is modified to glycine;

a proline at amino acid position 110 is modified to glycine;

a tyrosine at amino acid position 114 is modified to leucine;

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an alanine at amino acid position 157 is modified to serine;
 a tryptophan at amino acid position 481 is modified to phenylalanine;
 a proline at amino acid position 550 is modified to asparagine; or
 a glycine at amino acid position 590 is modified to arginine.

- 5 157. An isolated or recombinant nucleic acid having a sequence comprising a nucleotide residue sequence modification of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163 or SEQ ID NO:165, wherein the modification comprises one or more of the following changes:
- 25 a nucleotide at the equivalent of any one of positions 265 to 267 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG;
- a nucleotide at the equivalent of any one of positions 307 to 309 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG;
- a nucleotide at the equivalent of any one of positions 328 to 330 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG;
- 30 a nucleotide at the equivalent of any one of positions 340 to 342 of SEQ ID NO:163 are changed to TTA, TTG, CTT, CTC, CTA or CTG;
- a nucleotide at the equivalent of any one of positions 469 to 471 of SEQ ID NO:163 are changed to TCT, TCC, TCA, TCG, AGT or AGC;
- a nucleotide at the equivalent of positions 1441 to 1443 of SEQ ID NO:163 are

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changed to TTT or TTC;

a nucleotide at the equivalent of any one of positions 1648 to 1650 of SEQ ID NO:163 are changed to AAT or AAC; or

a nucleotide at the equivalent of any one of positions 1768 to 1770 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG.

158. An isolated or recombinant nucleic acid having a sequence comprising a nucleotide residue sequence modification of a nucleic acid as set forth in claim 1, wherein the modification comprises one or more of the following changes:

a nucleotide at the equivalent of any one of positions 265 to 267 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG;

a nucleotide at the equivalent of any one of positions 307 to 309 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG;

a nucleotide at the equivalent of any one of positions 328 to 330 of SEQ ID NO:163 are changed to GGT, GGC, GGA or GGG;

a nucleotide at the equivalent of any one of positions 340 to 342 of SEQ ID NO:163 are changed to TTA, TTG, CTT, CTC, CTA or CTG;

a nucleotide at the equivalent of any one of positions 469 to 471 of SEQ ID NO:163 are changed to TCT, TCC, TCA, TCG, AGT or AGC;

a nucleotide at the equivalent of positions 1441 to 1443 of SEQ ID NO:163 are changed to TTT or TTC;

a nucleotide at the equivalent of any one of positions 1648 to 1650 of SEQ ID NO:163 are changed to AAT or AAC; or

a nucleotide at the equivalent of any one of positions 1768 to 1770 of SEQ ID NO:163 are changed to CGT, CGC, CGA, CGG, AGA or AGG.

159. An isolated or recombinant polypeptide having a sequence comprising an amino acid residue modification of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID

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- 10 an amino acid at the equivalent of the methionine at amino acid position 89 of SEQ ID NO:164 is changed to an arginine;
- an amino acid at the equivalent of the phenylalanine at amino acid position 103 of SEQ ID NO:164 is changed to a glycine;
- an amino acid at the equivalent of the proline at amino acid position 110 of SEQ ID NO:164 is changed to a glycine; an amino acid at the equivalent of the tyrosine at amino acid position 114 of SEQ ID NO:164 is changed to a leucine;
- 15 an amino acid at the equivalent of the alanine at amino acid position 157 of SEQ ID NO:164 is changed to a serine;
- an amino acid at the equivalent of the tryptophan at amino acid position 481 of SEQ ID NO:164 is changed to a phenylalanine;
- 20 an amino acid at the equivalent of the proline at amino acid position 550 of SEQ ID NO:164 is changed to an asparagine; or
- an amino acid at the equivalent of the glycine at amino acid position 590 of SEQ ID NO:164 is changed to an arginine.

25 160. An isolated or recombinant polypeptide having a sequence comprising an amino acid residue modification of a polypeptide as set forth in claim 48, wherein the modification comprises one or more of the following changes:

- an amino acid at the equivalent of the methionine at amino acid position 89 of SEQ ID NO:164 is changed to an arginine;
 - 30 an amino acid at the equivalent of the phenylalanine at amino acid position 103 of SEQ ID NO:164 is changed to a glycine;
 - an amino acid at the equivalent of the proline at amino acid position 110 of SEQ ID NO:164 is changed to a glycine;
-

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an amino acid at the equivalent of the tyrosine at amino acid position 114 of SEQ ID NO:164 is changed to a leucine;

an amino acid at the equivalent of the alanine at amino acid position 157 of SEQ ID NO:164 is changed to a serine;

5 an amino acid at the equivalent of the tryptophan at amino acid position 481 of SEQ ID NO:164 is changed to a phenylalanine;

an amino acid at the equivalent of the proline at amino acid position 550 of SEQ ID NO:164 is changed to an asparagine; or

10 an amino acid at the equivalent of the glycine at amino acid position 590 of SEQ ID NO:164 is changed to an arginine.

161. The isolated or recombinant polypeptide of claim 48, wherein the polypeptide having a sequence as set forth in:

- (i) SEQ ID NO:164, has alkaline endoglucanase/cellulase activity;
 - (ii) SEQ ID NO:110, has xylanase activity;
 - 15 (iii) SEQ ID NO:12, has NAD binding oxidoreductase activity;
 - (iv) SEQ ID NO:118, has short chain dehydrogenase activity;
 - (v) SEQ ID NO:14, has NADH dependent dehydrogenase activity;
 - (vi) SEQ ID NO:138, has peptidase activity;
 - (vii) SEQ ID NO:162, has alkaline endoglucanase activity,
 - 20 (viii) SEQ ID NO:42, has cysteinyl tRNA synthetase activity;
 - (viii) SEQ ID NO:32, has cellodextrin phosphorylase activity;
 - (ix) SEQ ID NO:50, has fdhd/narq oxidoreductase activity;
 - (x) SEQ ID NO:54, has a radical S-adenosylmethionine (SAM) methyltransferase activity; or
 - 25 (xi) SEQ ID NO:58, has a subtilisin-like protease activity.
-

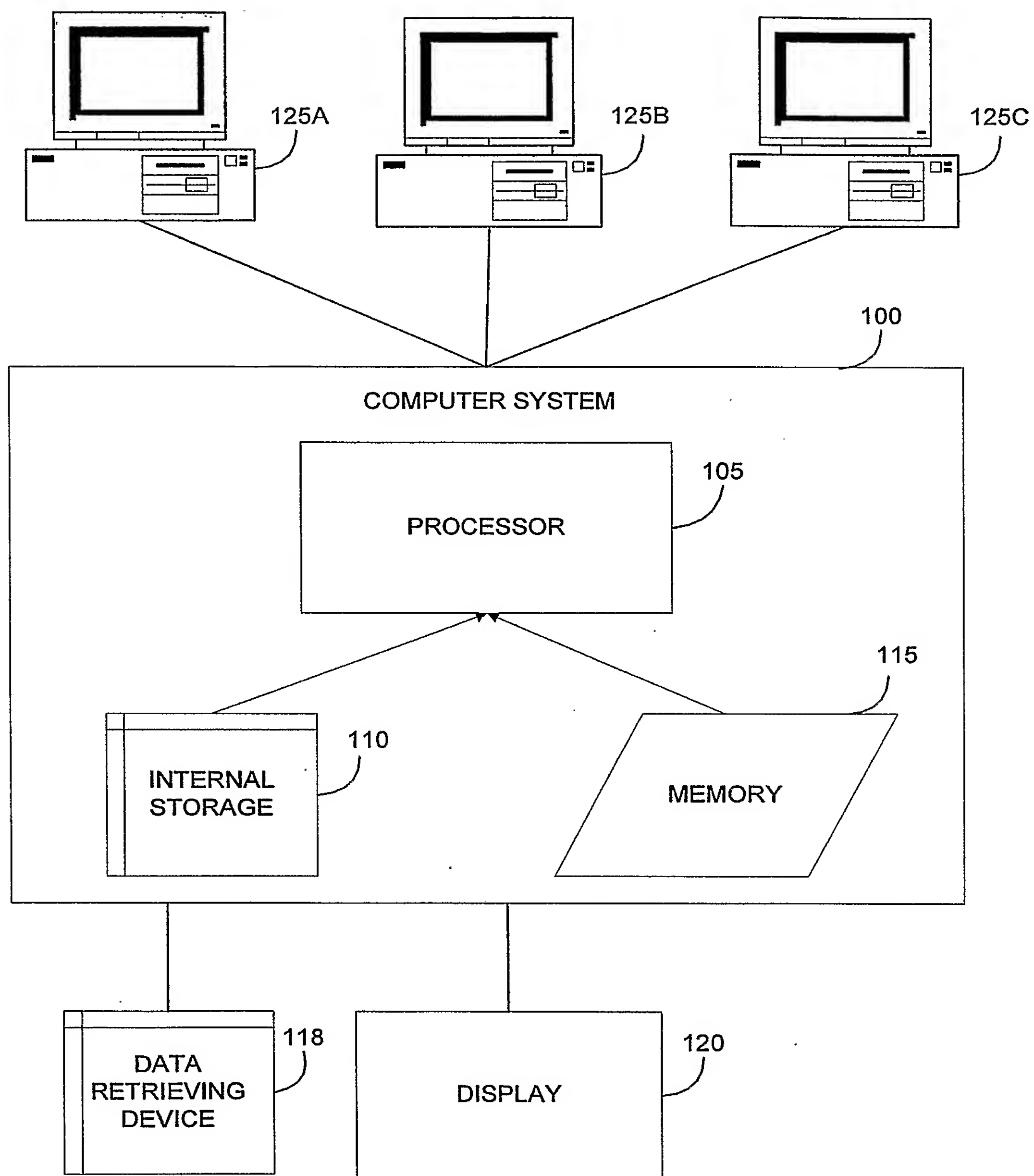


FIG. 1

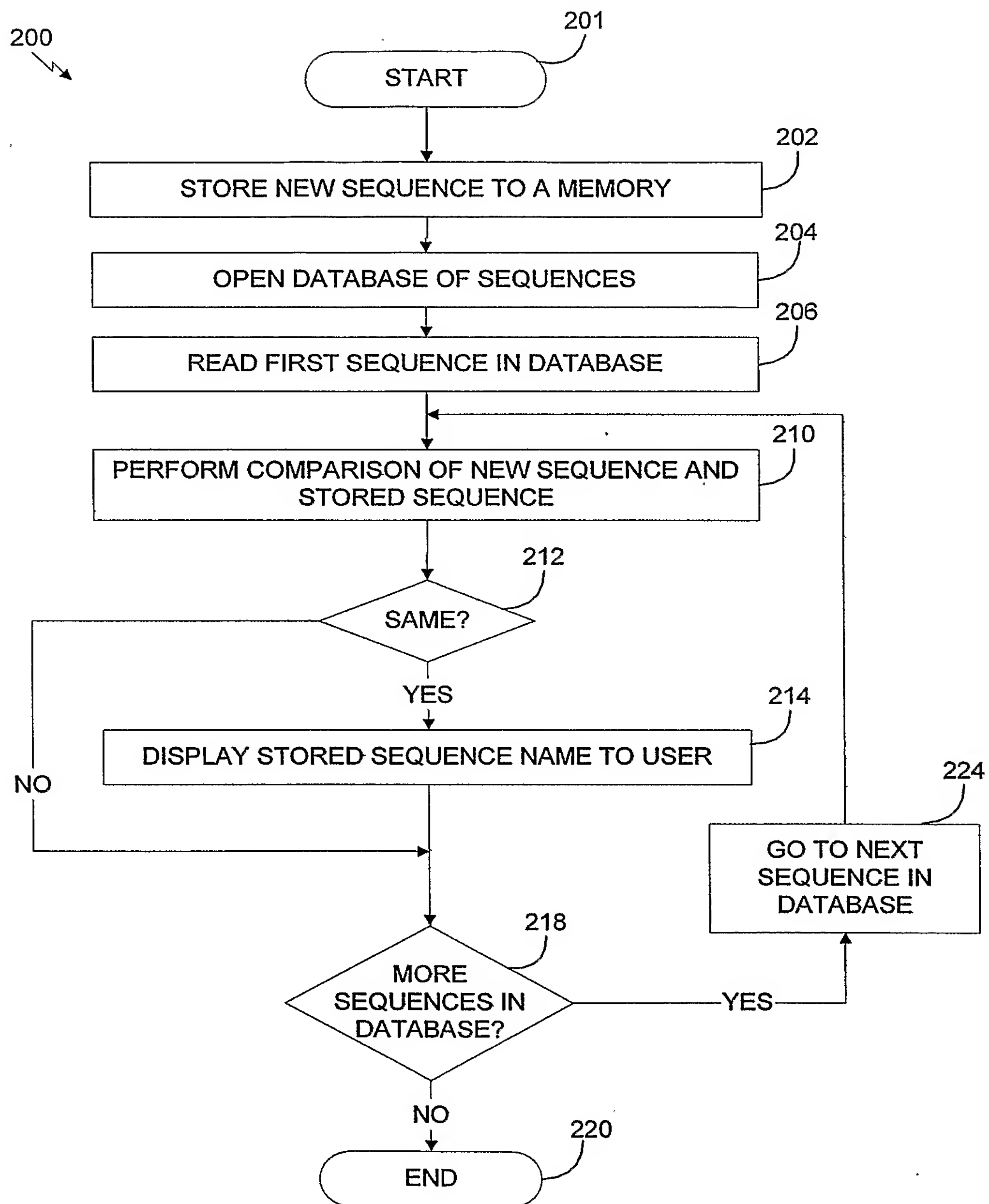


FIG. 2

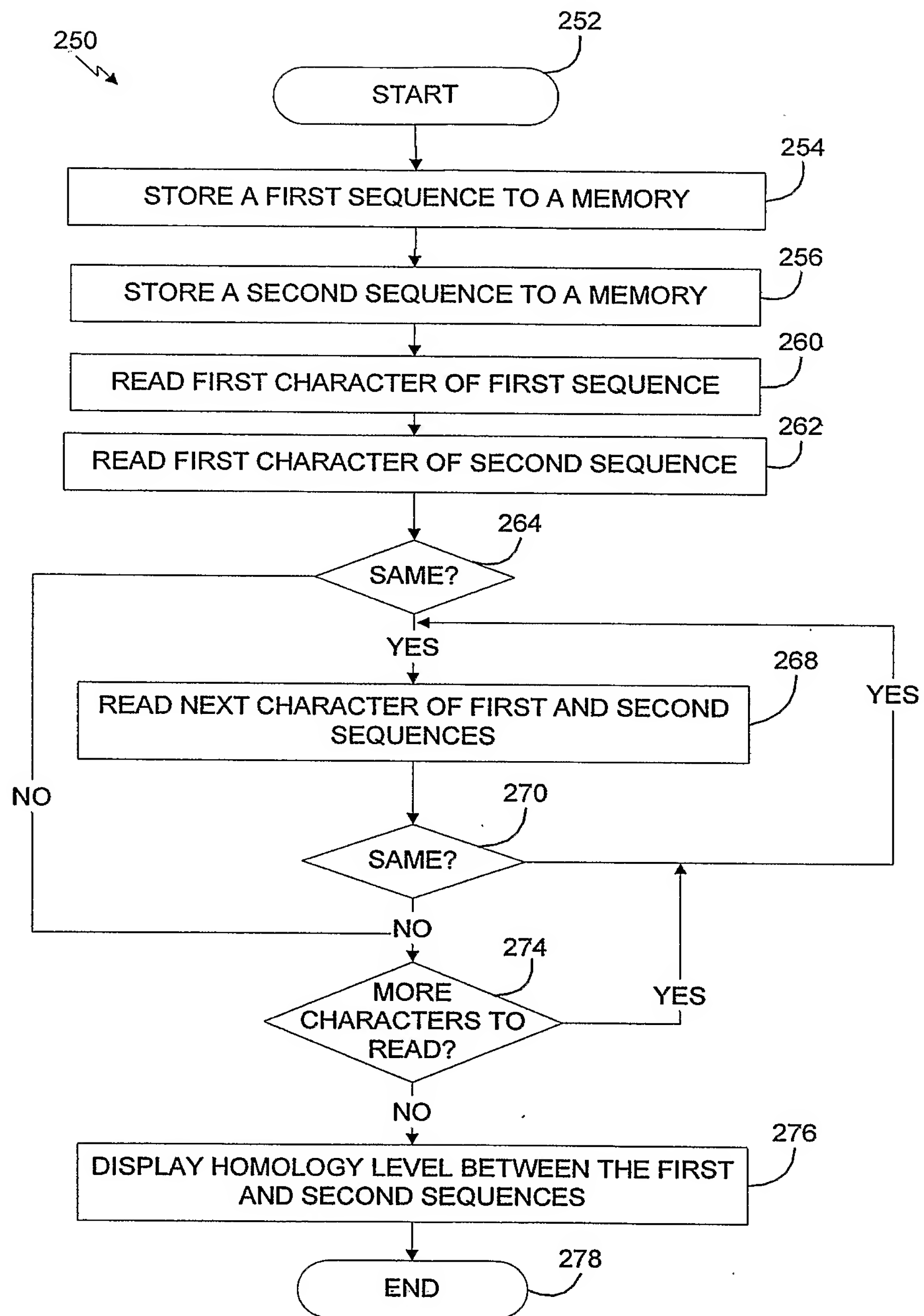


FIG. 3

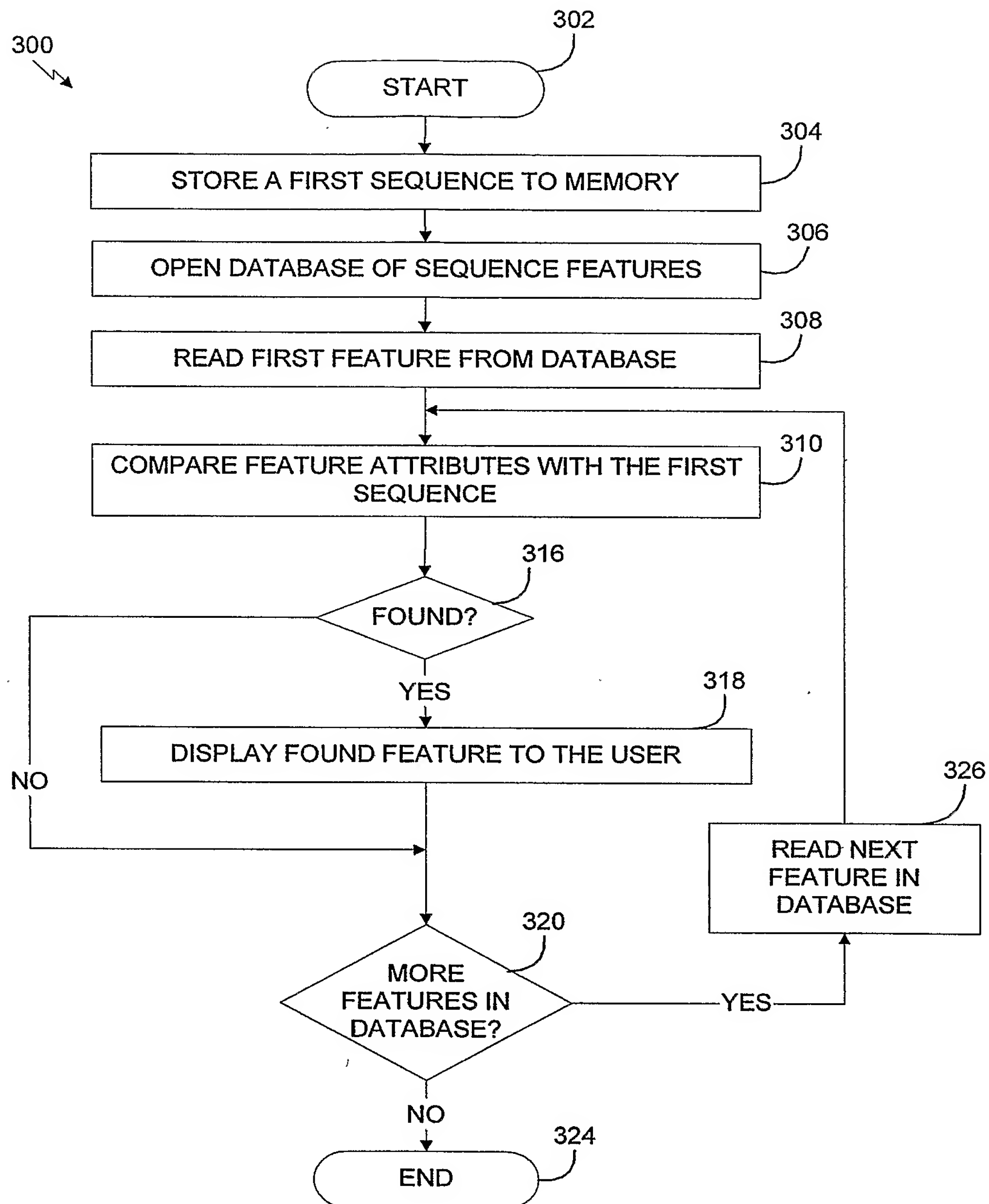


FIG. 4

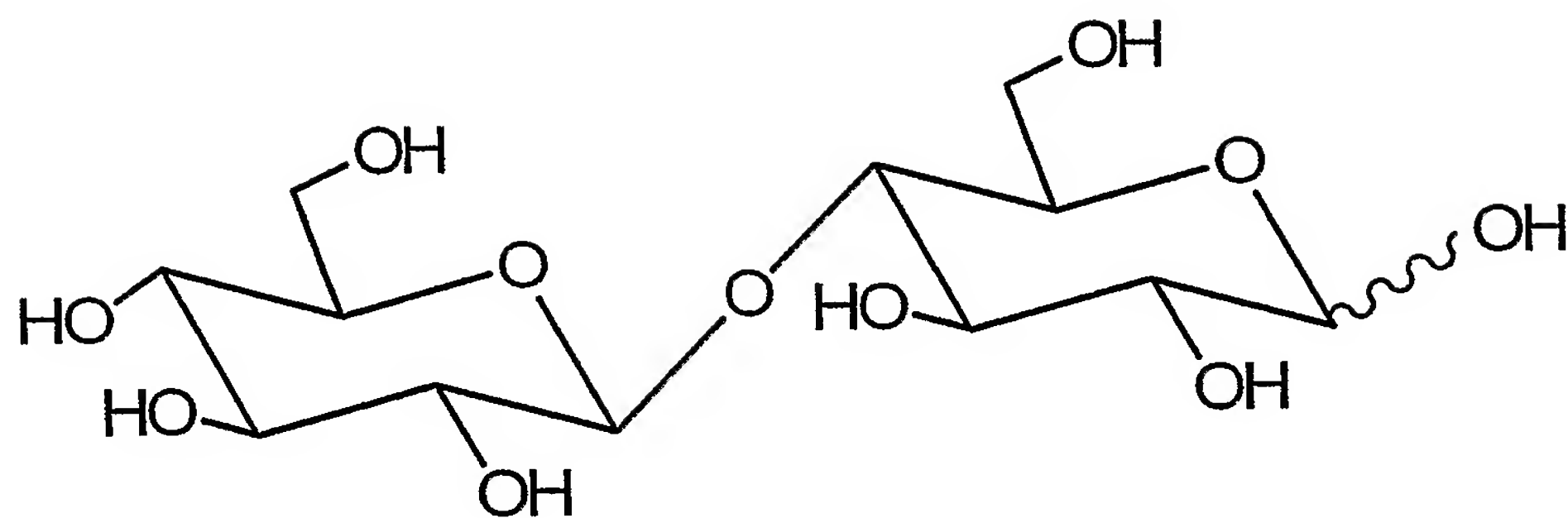
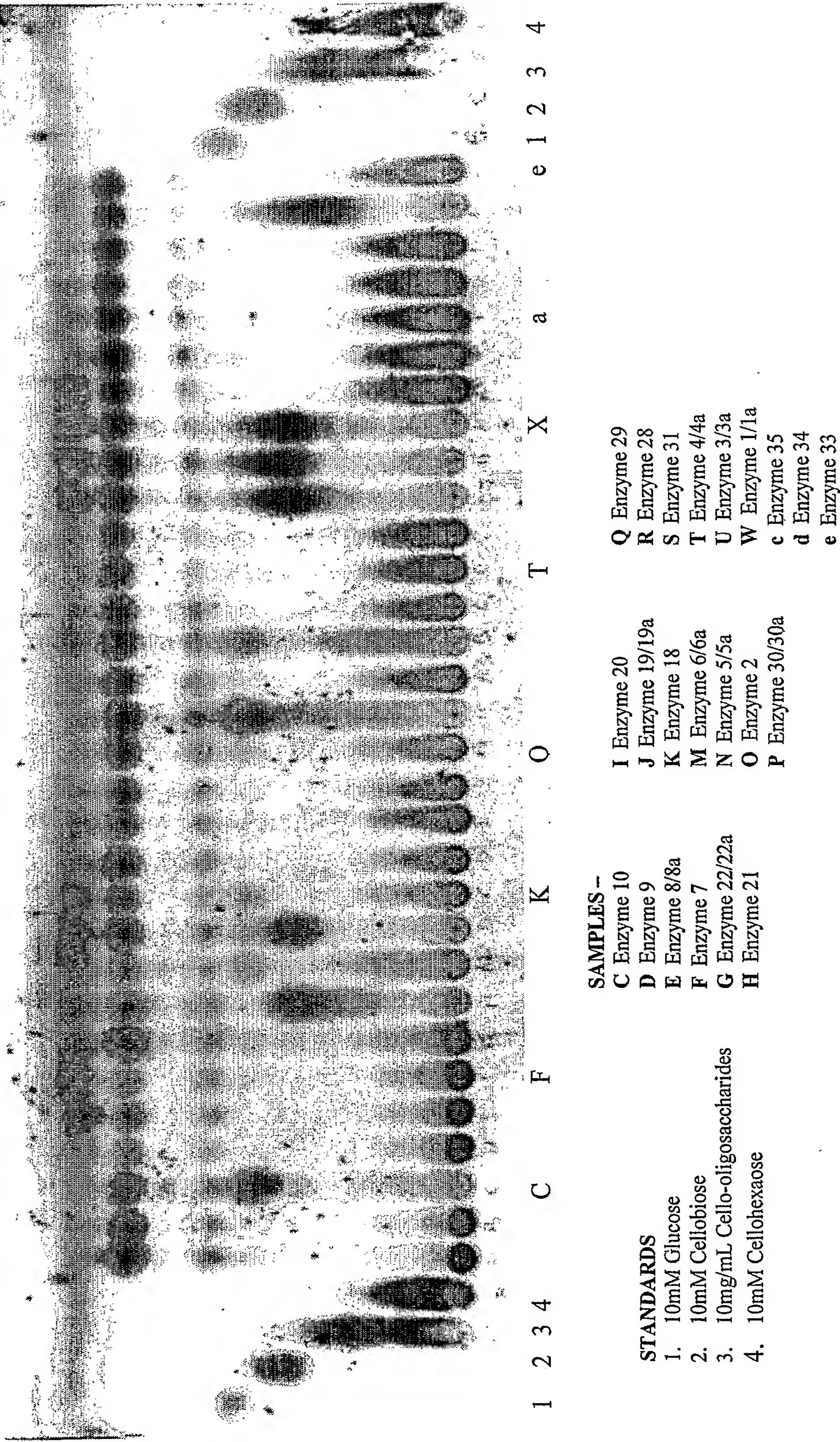


Figure 5 structure of cellobiose



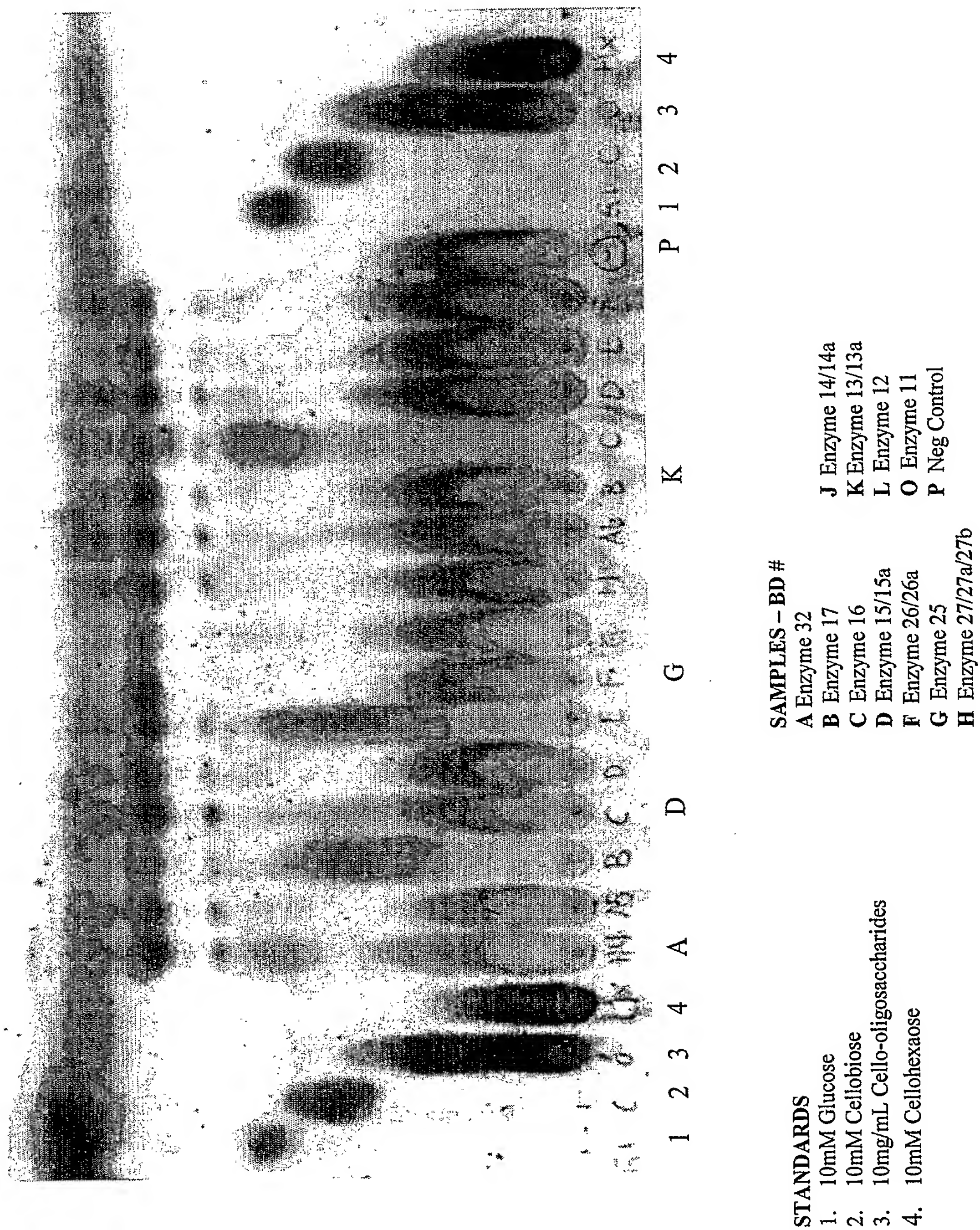


Figure 7. TLC analysis of reaction products from cellobiose

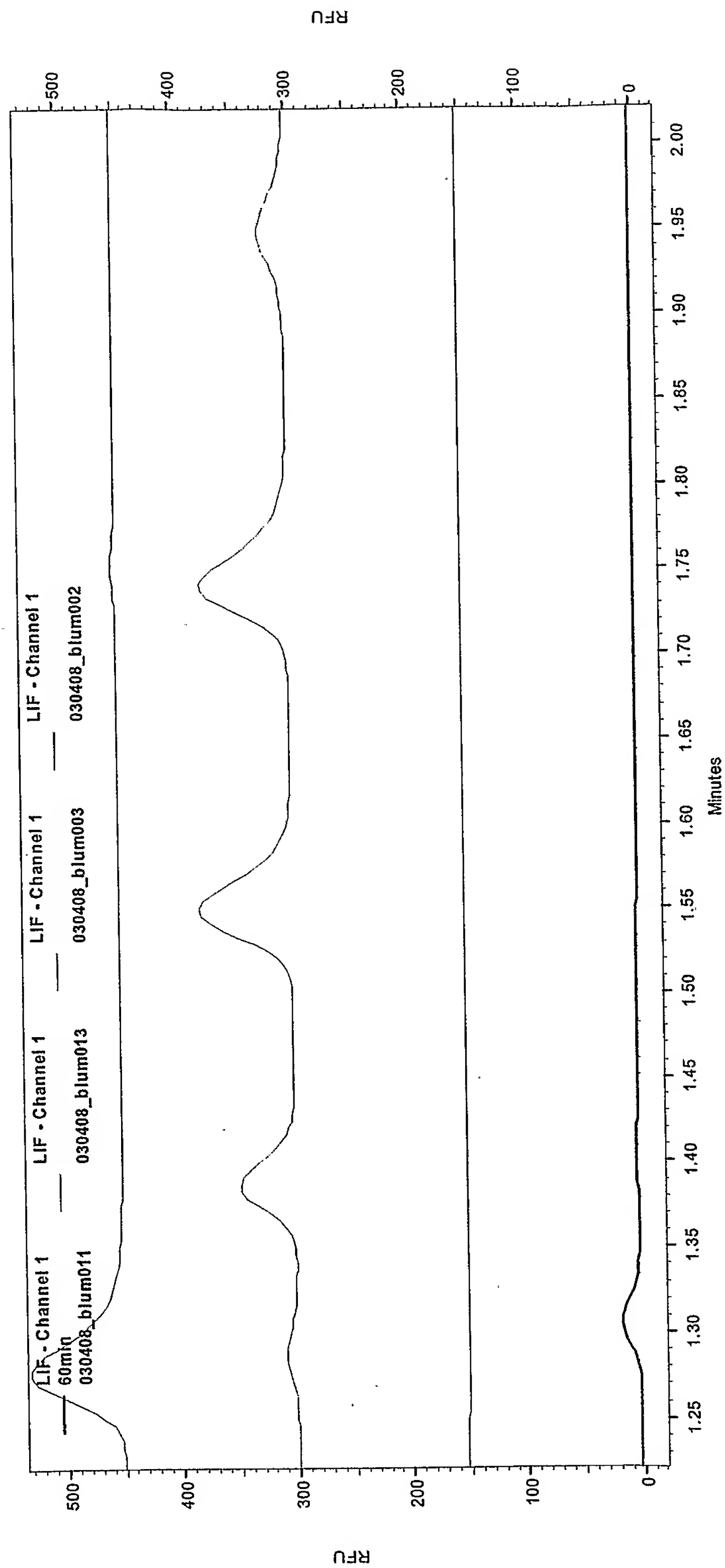


Figure 8. Release of cellobiose from PASC by enzyme 22/22a

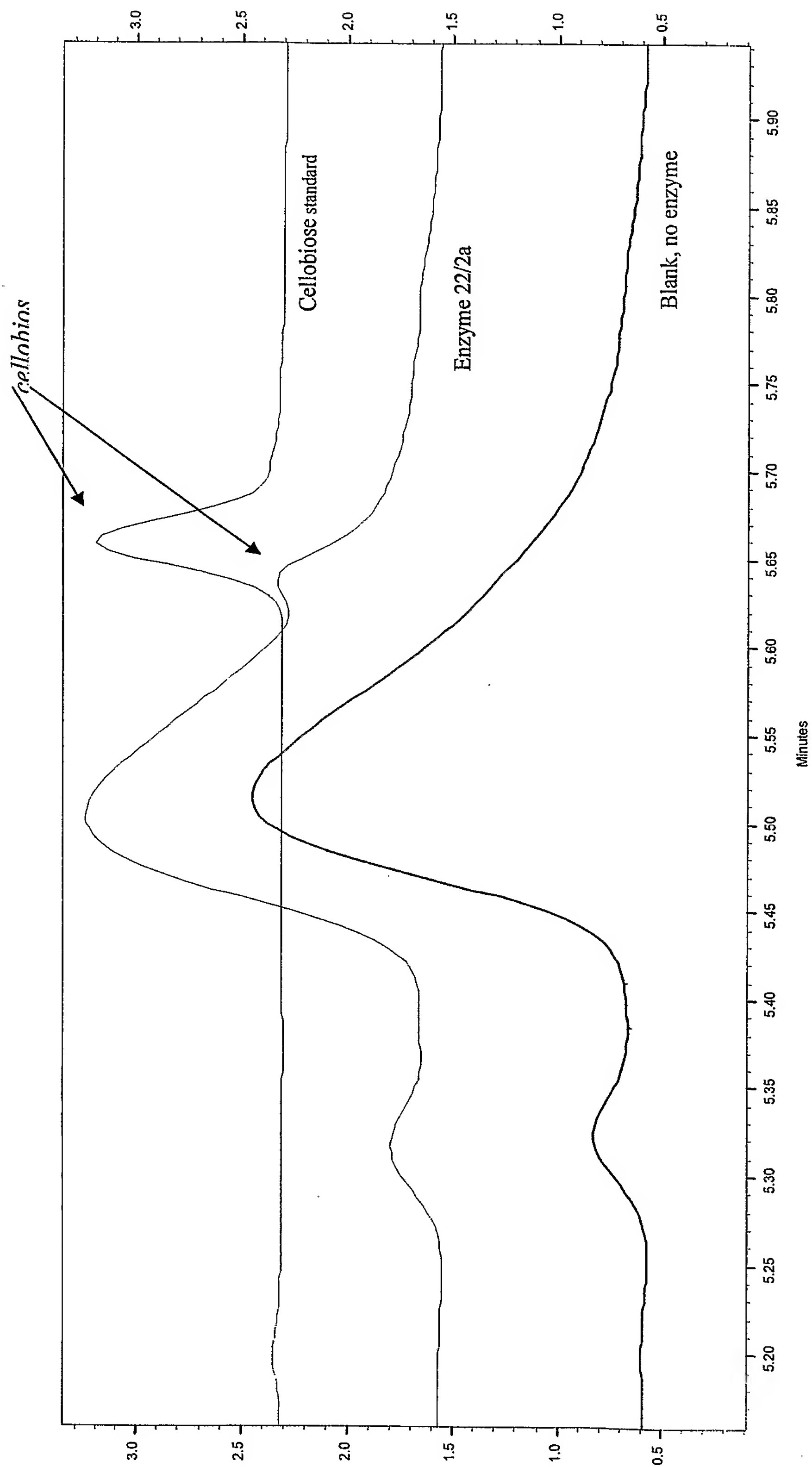


Figure 9. Release of cellobiose from Avicel MCC by CBH

Figure 10

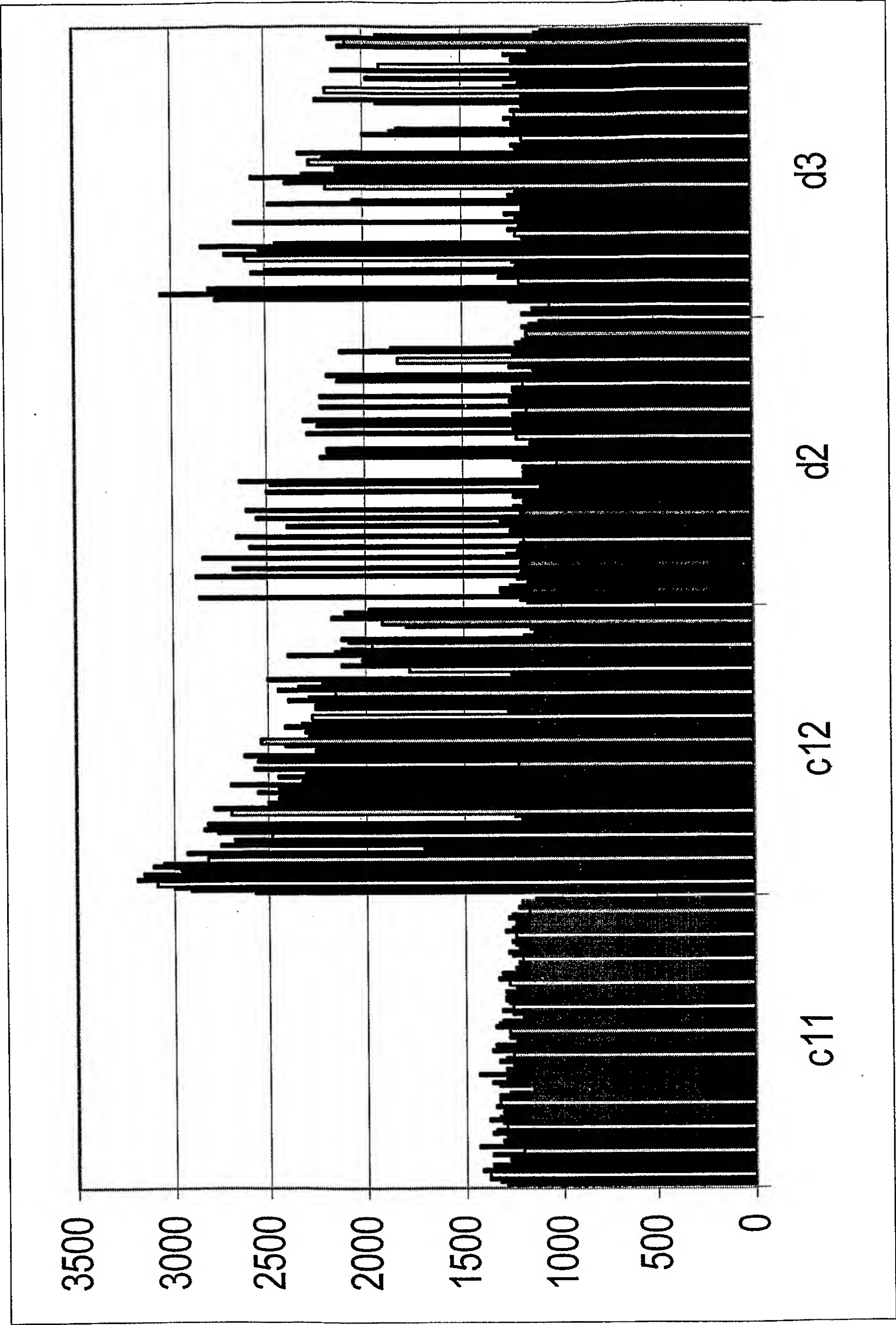


FIGURE 11

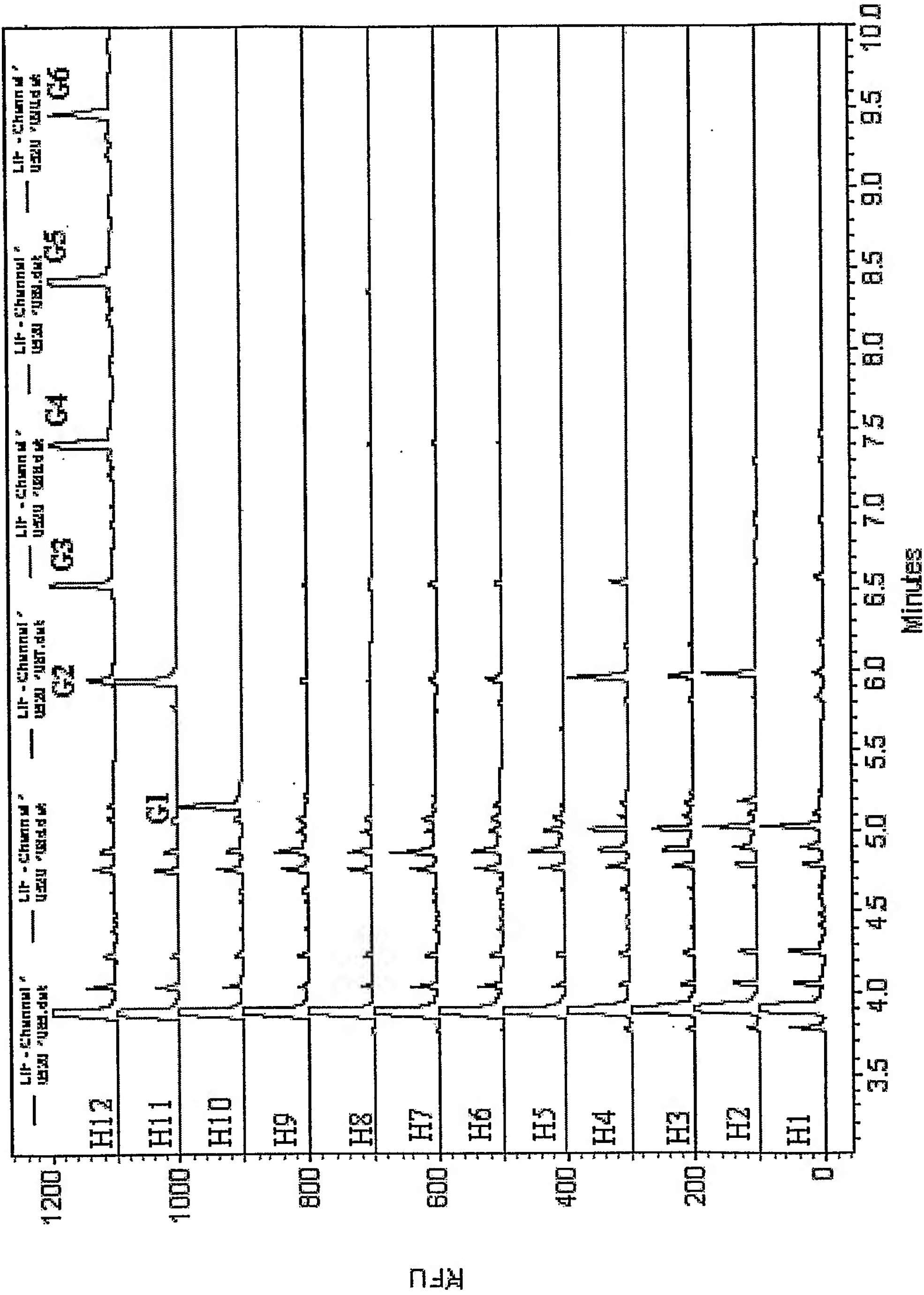


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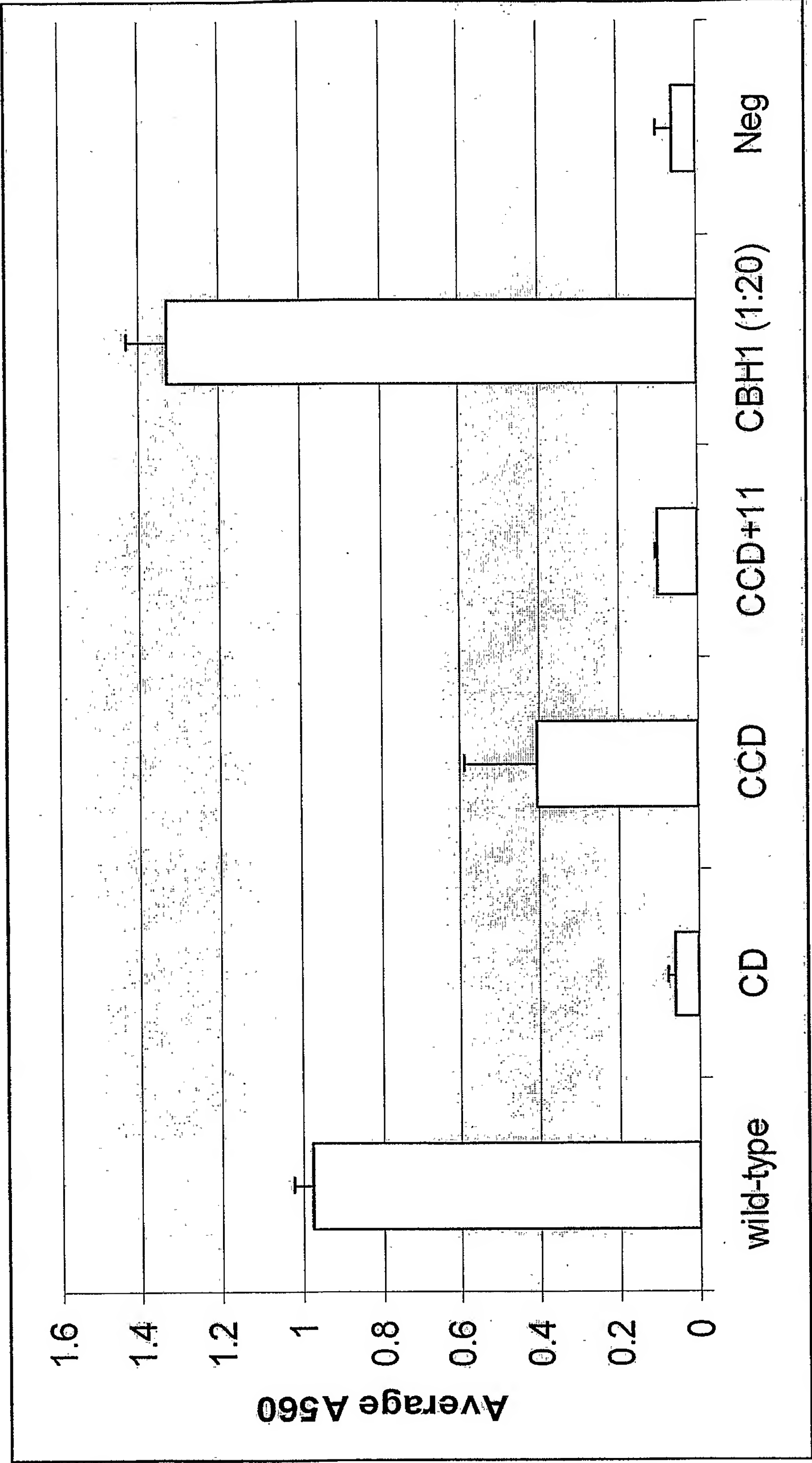


Figure 13

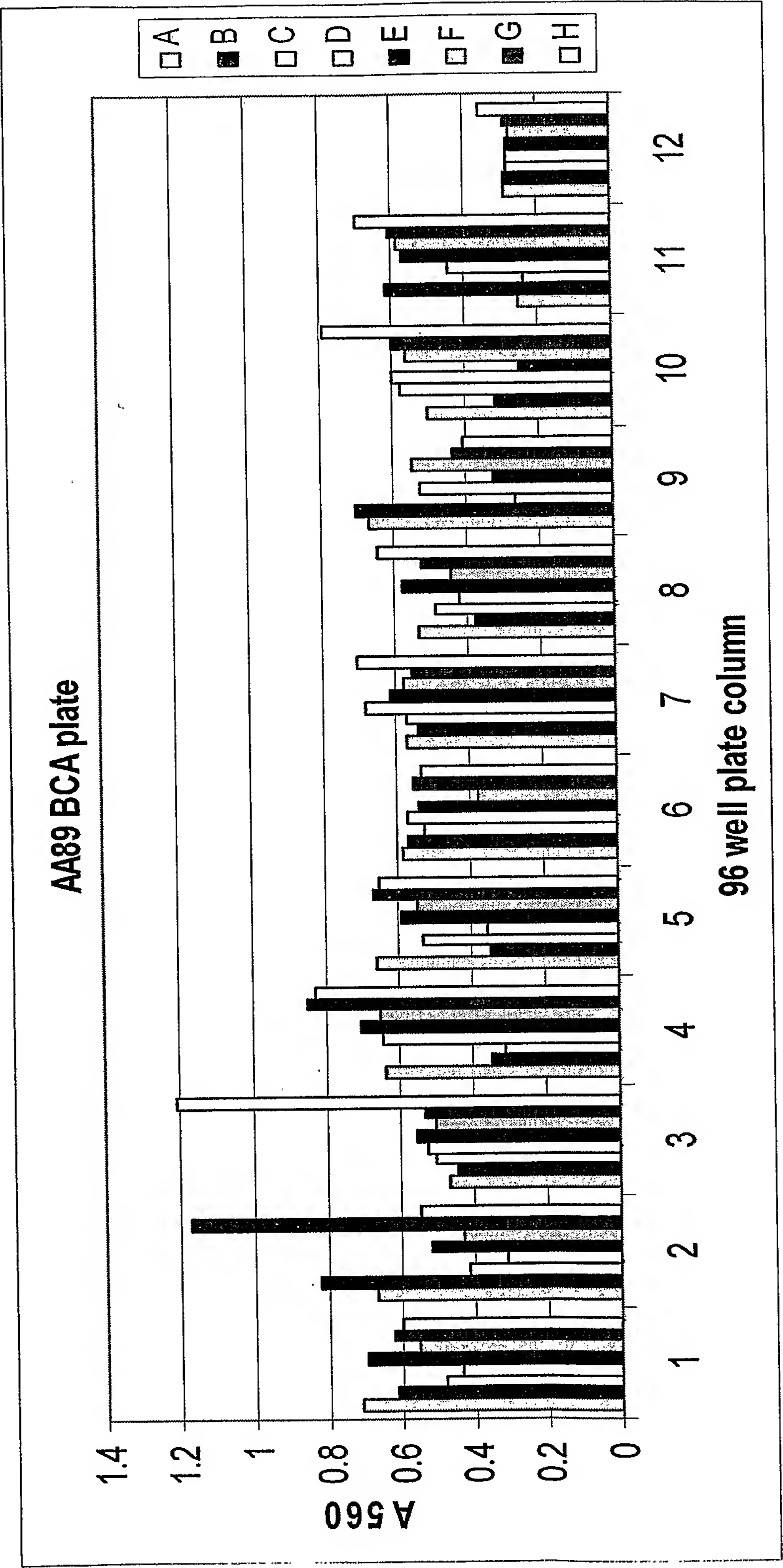


Figure 14

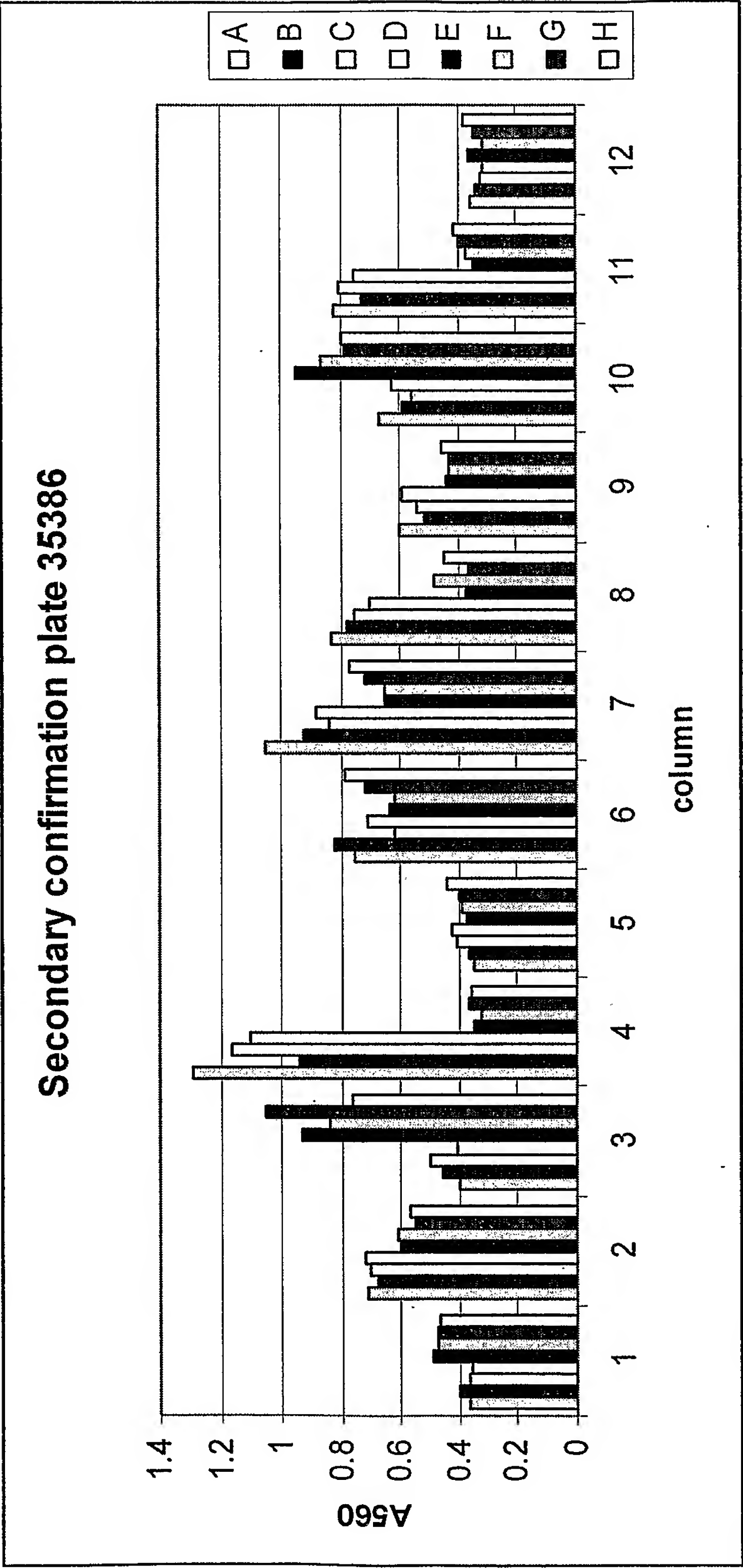
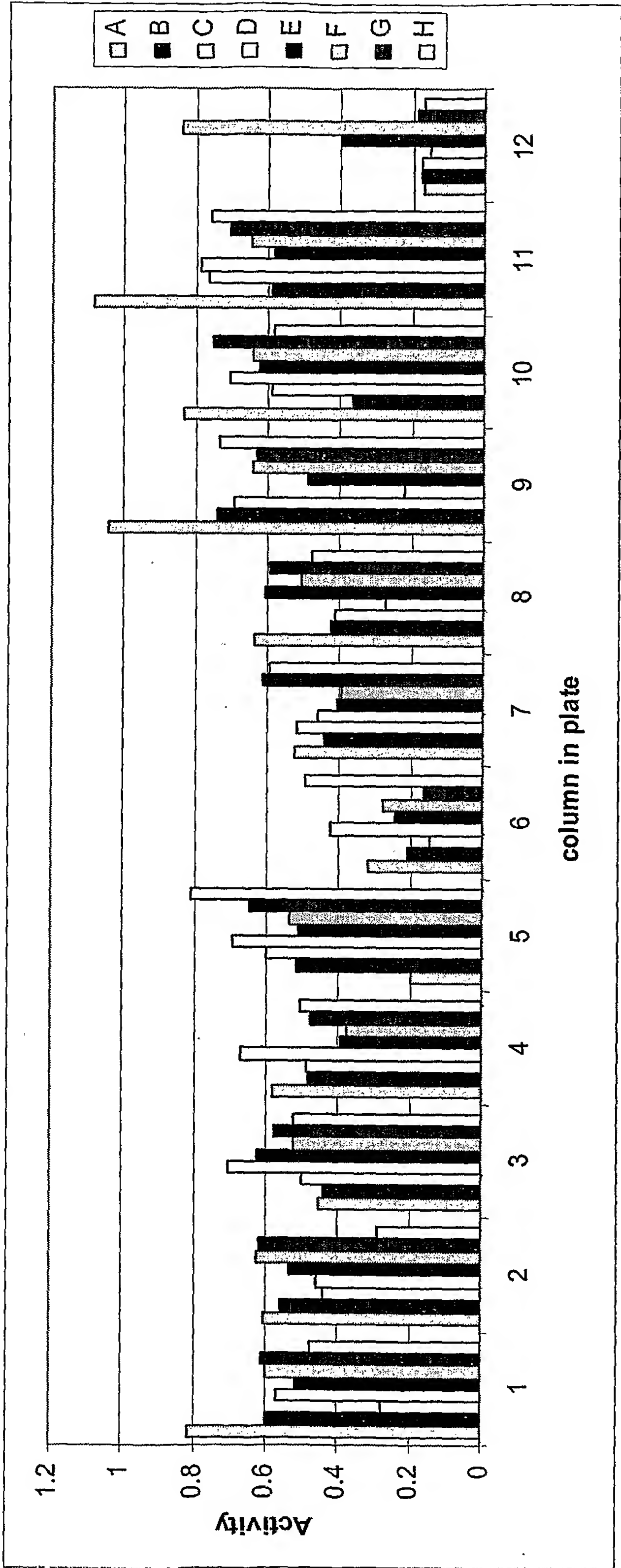


Figure 15



SEQUENCE LISTING

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BLUM, David
GEMSCH, Joslin
DYCAICO, Mark

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AND METHODS FOR MAKING AND USING THEM

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Asn Phe Glu Trp Ala Ala Gly Tyr Arg Glu Arg Phe Gly Leu Val His
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Val Asp Tyr Glu Thr Leu Val Arg Thr Pro Lys Asp Ser Ala Ala Trp
435 440 445

Tyr Arg Gln Val Ile Gln Ser Asn Gly Ala Val Leu Phe Asp
450 455 460

<210> 5

<211> 1098

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 5

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tcggccccgg ggcaggccca ggcggggcggc aagcagccgt ttcccgaaga tgcgccgatc 180

accgaaccgc ccgctccgcc ccctcgtagc ggcaatcctc tgggtgggccc caagctcttc 240
gtcgacccgg aatctttggc catgttgagc gcgaacaagc tgcggcgac cgacccggag 300
aaggcggcga ttttggatcg catcgcccag cagccccagg ctttgtggat gggcgagtgg 360
aacacgaaca tcttccgcgc ggtcgagcat ttctgggctc gcgccaaggc ggagggcgcc 420
gtgcccgtca tgatcgcta caacatcccc caccgcgact gcgggcagta ctctcagggt 480
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agcgatgcag cggtcgtcgt gctcgagccc gacgcgctcg gccacttcca ggagtgtttg 600
accgaggagc agagcgccga gcgcatgttc ctgctcagcg acgccgtcaa ggtgctgcgc 660
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gagatggccg agcgctcaa gctcgcgggc atcgagcacg cccatggctt ttctctaac 780
acctcgaact acgtgggcac cgaggagaac gccgcttacg gccacaagct cgtcgaggcc 840
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gaggccaaga acgccgagga gagctgggtg aaccgcgccg gtcgcaagat cggcaagccg 960
ccgaccaccg agacggggga tccccctatc gacggattcc tttggctgaa gcgcccgggc 1020
gagtcggacg gtcagtgcaa cggcggggccc aaggccggtg tgttctggct ggagcaggct 1080
ctccagcagg cccagtaa 1098

<210> 6
<211> 365
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(29)

<220>
<221> DOMAIN
<222> (81)...(358)
<223> Glycosyl hydrolases family 6

<220>
<221> SITE
<222> (187)...(196)
<223> Glycosyl hydrolases family 6 signature 2. Prosite id = PS00656

<220>
<221> SITE
<222> (263)...(266)
<223> N-glycosylation site. Prosite id = PS00001

<400> 6
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Lys Gly Glu Ser Gly Asp Val Ala Ser Ala Pro Gly Gln Ala Gln Ala			
	35	40	45
Gly Gly Lys Gln Pro Phe Pro Asp Asp Ala Pro Ile Thr Glu Pro Pro			
	50	55	60
Ala Pro Pro Pro Arg Ser Gly Asn Pro Leu Val Gly Ala Lys Leu Phe			
	65	70	75
Val Asp Pro Glu Ser Leu Ala Met Leu Gln Ala Asn Lys Leu Arg Arg			
	85	90	95
Thr Asp Pro Glu Lys Ala Ala Ile Leu Asp Arg Ile Ala Gln Gln Pro			
	100	105	110
Gln Ala Leu Trp Met Gly Glu Trp Asn Thr Asn Ile Phe Arg Ala Val			
	115	120	125
Glu His Phe Val Ala Arg Ala Lys Ala Glu Gly Ala Val Pro Val Met			
	130	135	140
Ile Ala Tyr Asn Ile Pro His Arg Asp Cys Gly Gln Tyr Ser Gln Gly			
	145	150	155
Gly Leu Ser Ser Lys Glu Ala Tyr Gln Arg Trp Ile Arg Asn Val Ala			
	165	170	175
Ala Gly Ile Gly Ser Asp Ala Ala Val Val Val Leu Glu Pro Asp Ala			
	180	185	190
Leu Gly His Phe Gln Glu Cys Leu Thr Glu Glu Gln Ser Ala Glu Arg			
	195	200	205
Met Phe Leu Leu Ser Asp Ala Val Lys Val Leu Arg Gln Asn Pro Lys			
	210	215	220
Thr Ala Val Tyr Leu Asp Ala Gly His Ala Arg Trp Val Pro Val Glu			
	225	230	235
Glu Met Ala Glu Arg Leu Lys Leu Ala Gly Ile Glu His Ala His Gly			
	245	250	255

Phe Ser Leu Asn Thr Ser Asn Tyr Val Gly Thr Glu Glu Asn Ala Ala
 260 265 270

Tyr Gly His Lys Leu Val Glu Ala Leu Gly Gly Asn Val Arg Phe Val
 275 280 285

Ile Asp Thr Ser Arg Asn Gly Ala Gly Pro Tyr Glu Glu Ala Lys Asn
 290 295 300

Ala Glu Glu Ser Trp Cys Asn Pro Pro Gly Arg Lys Ile Gly Lys Pro
 305 310 315 320

Pro Thr Thr Glu Thr Gly Asp Pro Leu Ile Asp Gly Phe Leu Trp Leu
 325 330 335

Lys Arg Pro Gly Glu Ser Asp Gly Gln Cys Asn Gly Gly Pro Lys Ala
 340 345 350

Gly Val Phe Trp Leu Glu Gln Ala Leu Gln Gln Ala Gln
 355 360 365

<210> 7

<211> 2649

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 7

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ctggatgttg ctggtgacag ggcataattcc ggcaagcgaa aacttctctg gaaagaggtg	180
ctggctggcg aaaaggcatt tacaaatacc gggtcctggc ttccggagga aactcttaga	240
gcatttcgtg aatatcatgt tggaattaaa gggccactca ctacgccagt tggtaggggga	300
attcgttctc tcaatgtagc cctcaggcaa gagcttgact tgtatgtttg cctgaggcca	360
gtcaaattgt ttaagggtgt accaagtcct ctaaaagatc cttccaaagt ggatatgcat	420
atthttccgcg aaaacactga agatatttat gcagggtattg aatttatgca tggtagaacg	480
gaggccctga aagttaagaa atttcttacc gaagaaatgg gaatcaagaa gtttcgggtt	540
cccgatacat cctccattgg tatcaagcct atctcactcg aaggaacaga gcgtcttgta	600
agagcttcca ttcaatatgc acttgacagg aagttgcctt ccgtaacatt ggttcataaa	660

ggcaatatca	tgaaattcac	cgaggggggca	ttcaaaaaat	gggggttatga	acttgccgaa	720
agagaatttg	gcgacagggt	ttttacatgg	tcaatgtatg	accgtatcgc	cgatgaacat	780
ggaacggaag	aagctggcaa	agtgcaatcc	gaagcgattg	caaaaggtaa	actcctgata	840
aaggatgtga	ttgctgatgc	ttttctgcag	caaatactac	tcaggcctgc	cgagtacagc	900
gttatcgcaa	ccatgaacct	gaatggcgat	tatatcagcg	atgcactggc	agctatgggtg	960
gggggtatag	gaattgctcc	cggagccaat	attaaccatc	aaactggcca	tgcagtcttt	1020
gaagcaacac	acggcacggc	tcccaaatat	gccaaccttg	atcaggtaaa	ccctggctca	1080
gtaatactaa	gtggcgcgct	gatgctcgaa	tacatgggct	ggaacgaagc	cgctcagctc	1140
attaccaatg	gattggaggc	taccattcaa	cagaaactgg	taacctatga	tttccatcgc	1200
ttaatggaag	gtgctacaaa	gttgaagact	tcagaatttg	gcgatgctgt	gatccggccg	1260
gcacgttccg	cctgggcgga	cacggctgcc	gatgccctct	ccgggcgggc	gcgtcgtgcg	1320
cggaacggcg	ggcttggtgc	cccggccgcg	gcctgtcgcc	gggggcgggg	acgggactca	1380
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cagtgcctgc	tggtagtagt	cggcctgctg	ccgcagctgc	tccttggtgg	gcttgccgct	1620
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gtaggcgctg	ctcttggcgt	tgatgccctc	gacgttgtag	tcgttgagga	acagcttggc	1860
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gctgtgccac	aggaggggtg	gcccgcgcac	ggcctggcgg	ttccgctggg	cgaactcgac	2160
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gacggccagc	gcggcggcga	gagcaaaggt	gacgatgcgg	acggatctca	tcagaggtcc	2520

ctcattcgat cgcggctccg aaagttttcg gaggattacc ggaatgtttc agggaccta 2580
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 aggcgttga 2649

<210> 8
 <211> 882
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (20)...(417)
 <223> Isocitrate/isopropylmalate dehydrogenase

<220>
 <221> SITE
 <222> (310)...(329)
 <223> Isocitrate and isopropylmalate dehydrogenases signature. Prosite id = PS00470

<220>
 <221> SITE
 <222> (868)...(871)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 8
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Asp Tyr Pro Ile Val Pro Phe Ile Glu Gly Asp Gly Thr Gly Pro Asp
 20 25 30

Ile Trp Arg Ala Ser Val Arg Val Leu Asp Val Ala Val Asp Arg Ala
 35 40 45

Tyr Ser Gly Lys Arg Lys Leu Leu Trp Lys Glu Val Leu Ala Gly Glu
 50 55 60

Lys Ala Phe Thr Asn Thr Gly Ser Trp Leu Pro Glu Glu Thr Leu Arg
 65 70 75 80

Ala Phe Arg Glu Tyr His Val Gly Ile Lys Gly Pro Leu Thr Thr Pro
 85 90 95

Val Gly Gly Gly Ile Arg Ser Leu Asn Val Ala Leu Arg Gln Glu Leu
 100 105 110

Asp Leu Tyr Val Cys Leu Arg Pro Val Lys Trp Phe Lys Gly Val Pro

115		120		125											
Ser	Pro	Leu	Lys	Asp	Pro	Ser	Lys	Val	Asp	Met	His	Ile	Phe	Arg	Glu
130						135					140				
Asn	Thr	Glu	Asp	Ile	Tyr	Ala	Gly	Ile	Glu	Phe	Met	His	Gly	Glu	Pro
145					150					155					160
Glu	Ala	Leu	Lys	Val	Lys	Lys	Phe	Leu	Thr	Glu	Glu	Met	Gly	Ile	Lys
				165					170					175	
Lys	Phe	Arg	Phe	Pro	Asp	Thr	Ser	Ser	Ile	Gly	Ile	Lys	Pro	Ile	Ser
			180					185					190		
Leu	Glu	Gly	Thr	Glu	Arg	Leu	Val	Arg	Ala	Ser	Ile	Gln	Tyr	Ala	Leu
		195					200					205			
Asp	Arg	Lys	Leu	Pro	Ser	Val	Thr	Leu	Val	His	Lys	Gly	Asn	Ile	Met
	210					215					220				
Lys	Phe	Thr	Glu	Gly	Ala	Phe	Lys	Lys	Trp	Gly	Tyr	Glu	Leu	Ala	Glu
225					230					235					240
Arg	Glu	Phe	Gly	Asp	Arg	Val	Phe	Thr	Trp	Ser	Met	Tyr	Asp	Arg	Ile
				245					250					255	
Ala	Asp	Glu	His	Gly	Thr	Glu	Glu	Ala	Gly	Lys	Val	Gln	Ser	Glu	Ala
			260					265					270		
Ile	Ala	Lys	Gly	Lys	Leu	Leu	Ile	Lys	Asp	Val	Ile	Ala	Asp	Ala	Phe
		275					280					285			
Leu	Gln	Gln	Ile	Leu	Leu	Arg	Pro	Ala	Glu	Tyr	Ser	Val	Ile	Ala	Thr
	290					295					300				
Met	Asn	Leu	Asn	Gly	Asp	Tyr	Ile	Ser	Asp	Ala	Leu	Ala	Ala	Met	Val
305					310					315					320
Gly	Gly	Ile	Gly	Ile	Ala	Pro	Gly	Ala	Asn	Ile	Asn	His	Gln	Thr	Gly
				325					330					335	
His	Ala	Val	Phe	Glu	Ala	Thr	His	Gly	Thr	Ala	Pro	Lys	Tyr	Ala	Asn
			340					345					350		
Leu	Asp	Gln	Val	Asn	Pro	Gly	Ser	Val	Ile	Leu	Ser	Gly	Ala	Leu	Met
	355					360						365			

Leu Glu Tyr Met Gly Trp Asn Glu Ala Ala Gln Leu Ile Thr Asn Gly
370 375 380

Leu Glu Ala Thr Ile Gln Gln Lys Leu Val Thr Tyr Asp Phe His Arg
385 390 395 400

Leu Met Glu Gly Ala Thr Lys Leu Lys Thr Ser Glu Phe Gly Asp Ala
405 410 415

Val Ile Arg Pro Ala Arg Ser Ala Trp Ala Asp Thr Ala Ala Asp Ala
420 425 430

Leu Ser Gly Arg Arg Arg Arg Ala Arg Asn Gly Gly Leu Val Ala Pro
435 440 445

Pro Ala Ala Cys Arg Arg Gly Arg Val Arg Asp Ser Ala Leu Ala Arg
450 455 460

Leu Leu Gln Gly Gly Leu Gln Gly Glu Glu Gly Arg Leu Ala Asp Glu
465 470 475 480

Leu Leu Arg His Asp Arg Gly Ala Ala Leu Thr Leu Glu Glu Asp Arg
485 490 495

His Pro Arg Val Leu Val Gly Glu Ala Pro Asp Gly Glu Gly Val Ala
500 505 510

Val Val His Gly Gln Ala Gly Arg Gln Cys Leu Leu Val Val Val Gly
515 520 525

Leu Leu Pro Gln Leu Leu Leu Gly Gly Leu Ala Ala Arg Arg Glu Val
530 535 540

His Ala Asp Val Asp Leu Gly Asp Gly Gly Leu Gln Thr Glu Val Gly
545 550 555 560

Glu Pro Leu Gln Val Leu Leu Gln Val Ala Arg Glu Ala Val Ala Gly
565 570 575

Ala Gln Val Ala Leu Gly Ala Glu Ser Val Glu Arg His Ala Leu Leu
580 585 590

Gln His Leu Leu Gly Glu Leu Val Val Gly Val Ala Leu Gly Val Asp
595 600 605

Ala Leu Asp Val Val Val Val Glu Glu Gln Leu Gly Leu Gly Val Gly
610 615 620

Leu Val Gly Pro Ala Glu Gly Val Arg Asp Asp Leu Arg Ala Glu Leu
625 630 635 640

Thr Tyr Pro Asp Val Leu Val Gly Ala Gln Leu Gly Leu Val Val Glu
645 650 655

Asp Leu Val Gly His Val Pro Leu Leu Asp Leu Ala Gly Val Ala Ala
660 665 670

Asp Asp Arg Val Asp Val Val Leu Glu Asp Gly Ala Gln Phe Leu Leu
675 680 685

Gly Glu Val Ala Leu Leu Gln Pro Phe Gly Val Leu Ala Val Pro Gln
690 695 700

Glu Gly Val Pro Ala His Gly Leu Ala Val Pro Leu Gly Glu Leu Asp
705 710 715 720

Asp Gly Val Gly Leu Leu Glu Ala Val Leu Val Ala Leu Gly Val Asp
725 730 735

Glu Leu Pro Leu His Leu Val Leu Gly Gly Asp Arg Val Glu Leu Leu
740 745 750

Ala Gln Asp Leu Pro Val Leu Leu Val Glu Gly Glu Gly Val Arg Val
755 760 765

Val Leu Phe Glu Val Val Ala Ala Ala Gly Arg Arg Gly Ala Tyr Glu
770 775 780

Glu Pro Phe Gly Gly Gly Pro Ala Gln Ala Val Glu Leu Gly Val Gly
785 790 795 800

Val Gly Arg Gly Leu Val Val Gly Gly Arg Leu Gly Arg Gly Arg Arg
805 810 815

Arg His Gln Arg Asp Gly Gln Arg Gly Gly Glu Ser Lys Gly Asp Asp
820 825 830

Ala Asp Gly Ser His Gln Arg Ser Leu Ile Arg Ser Arg Leu Arg Lys
835 840 845

Phe Ser Glu Asp Tyr Arg Asn Val Ser Gly Thr Leu Arg Arg Pro Glu
 850 855 860

Pro Gly Arg Gln Arg Phe Gly Pro Ala Arg Ser Lys Leu Leu Pro Thr
 865 870 875 880

Arg Arg

<210> 9
 <211> 1134
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

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 aagttcgacc gcctgcgctg ggccgcccc gaaggggttct tcataggctc cgcggcgggcc 180
 ggccggcgggcc accacctcga acaggactac ccggacccct tcaccttcga caagaagtac 240
 cggaagatcc tggggccagca gttcaactcg gtctccgcgcg agaaccagat gaagtgggag 300
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 gaatggctgg aggagggcga cttcaccaag gaggaactgc gcgccatcct caaggaccac 480
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 atcttcaacg accaggccga gctgcgcacc gacgagaaca tctggatacg tgagctcggc 600
 ccggagatcg tcgcggacgc cttccgctgg gccacgagg ccgacccccga ggccaagctg 660
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 ctggccgtga acgactgcaa ctcccttcacc atctgggggt tcaccgacaa gtactcgtgg 1020
 gtgccgggtct tcttcgaggg tgagggcagc gccacgggtca tgacggagaa gttcgtccgc 1080
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<210> 10
 <211> 377

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(26)

<220>

<221> DOMAIN

<222> (44)...(371)

<223> Glycosyl hydrolase family 10

<400> 10

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20 25 30

Glu Ala Ala Pro His Ser Asn Ala Lys Phe Asp Arg Leu Arg Trp Ala
35 40 45

Ala Pro Glu Gly Phe Phe Ile Gly Ser Ala Ala Ala Gly Gly Gly His
50 55 60

His Leu Glu Gln Asp Tyr Pro Asp Pro Phe Thr Phe Asp Lys Lys Tyr
65 70 75 80

Arg Lys Ile Leu Gly Gln Gln Phe Asn Ser Val Ser Ala Glu Asn Gln
85 90 95

Met Lys Trp Glu Phe Ile His Pro Glu Arg Asp Gln Tyr Arg Phe Glu
100 105 110

Glu Ala Asp Ala Ile Val Glu Phe Ala Gln Arg Asn Arg Gln Ala Val
115 120 125

Arg Gly His Thr Leu Leu Trp His Ser Gln Asn Pro Glu Trp Leu Glu
130 135 140

Glu Gly Asp Phe Thr Lys Glu Glu Leu Arg Ala Ile Leu Lys Asp His
145 150 155 160

Ile Asp Thr Val Val Gly Arg Tyr Ala Gly Lys Ile Gln Gln Trp Asp
165 170 175

Val Ala Asn Glu Ile Phe Asn Asp Gln Ala Glu Leu Arg Thr Asp Glu

180					185					190					
Asn	Ile	Trp	Ile	Arg	Glu	Leu	Gly	Pro	Glu	Ile	Val	Ala	Asp	Ala	Phe
		195					200					205			
Arg	Trp	Ala	His	Glu	Ala	Asp	Pro	Glu	Ala	Lys	Leu	Phe	Leu	Asn	Asp
	210					215					220				
Tyr	Asn	Val	Glu	Gly	Ile	Asn	Ala	Lys	Ser	Asp	Ala	Tyr	Tyr	Glu	Leu
225					230					235				240	
Ala	Gln	Glu	Met	Leu	Glu	Gln	Gly	Val	Pro	Leu	His	Gly	Phe	Gly	Ala
			245						250					255	
Gln	Gly	His	Leu	Ser	Thr	Arg	Tyr	Gly	Phe	Pro	Gly	Asp	Leu	Gln	Gln
		260						265					270		
Asn	Leu	Gln	Arg	Phe	Ala	Asp	Leu	Gly	Leu	Glu	Thr	Ala	Ile	Thr	Glu
	275						280					285			
Ile	Asp	Val	Arg	Met	Asp	Leu	Pro	Ala	Ser	Gly	Lys	Pro	Thr	Lys	Glu
	290					295					300				
Gln	Leu	Arg	Gln	Gln	Ala	Asp	Tyr	Tyr	Gln	Gln	Ala	Leu	Ser	Ala	Cys
305					310					315					320
Leu	Ala	Val	Asn	Asp	Cys	Asn	Ser	Phe	Thr	Ile	Trp	Gly	Phe	Thr	Asp
			325					330						335	
Lys	Tyr	Ser	Trp	Val	Pro	Val	Phe	Phe	Glu	Gly	Glu	Gly	Ser	Ala	Thr
		340					345						350		
Val	Met	Thr	Glu	Lys	Phe	Val	Arg	Lys	Pro	Ala	Phe	Phe	Ala	Leu	Gln
	355						360					365			
Ser	Thr	Leu	Lys	Glu	Ala	Arg	Lys	Arg							
	370					375									

<210> 11
 <211> 1080
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 11
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gccctagcca cacgctacgg ggtagaaaaa accacatctc gctatgagga tttactgaac 240
gatcccggcc ttgatgtcat cgatctgtgc gttcctcacg atgaacacat gcccatggcc 300
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gaagaggccg atgcaatcct cgaggccgtg aaaagcgccg gtgtaacgct gatgatggga 420
cacaaccagc gttactacgc ccatcacgcc agggctaaag cattggtcga cgccgggggc 480
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cgccgctttc ttaagcacgc cgggggtggc acgttgatcg attcgggagt gcaccgcttc 600
gacctcattc gctggatcat ggggtgaagtc gagaccgtct tcgctcaaac gggtcgcttc 660
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gccatcggga gcttctcatg cagctggagc gccaaaggcc ctgttccaga agaaacattg 780
caaattttcg gccctatgg ttcgatttat accgaagacc acacccgcac cttacgcctt 840
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ccccctccga tcaccggtat ggacggacgc gcttcccttg agctcagcat ggcttcctat 1020
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<210> 12
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (22)...(141)
 <223> Oxidoreductase family, NAD-binding Rossmann fold

<220>
 <221> DOMAIN
 <222> (153)...(260)
 <223> Oxidoreductase family, C-terminal alpha/beta domain

<400> 12
 Met Pro Trp Ser Ser Ser Thr Gly Pro Ala Pro Met Thr Ser Asn Pro
 1 5 10 15

Pro Leu Lys Arg Pro Leu Arg Ile Gly Leu Val Gly Thr Gly Ile Gly
 20 25 30

Ser Leu His Ala Ala Gly Ile Ser Arg Met Pro Gln Leu Ala Thr Leu
 35 40 45

Gly Ala Ile Cys Gly Leu Asp Thr His Ala Val Asn Ala Leu Ala Thr
 50 55 60

Arg Tyr Gly Val Glu Lys Thr Thr Ser Arg Tyr Glu Asp Leu Leu Asn
 65 70 75 80

Asp Pro Gly Leu Asp Val Ile Asp Leu Cys Val Pro His Asp Glu His
 85 90 95

Met Pro Met Ala Ile Ala Ala Ala Arg Ala Gly Lys His Leu Leu Ile
 100 105 110

Glu Lys Pro Leu Ala Arg Thr Leu Glu Glu Ala Asp Ala Ile Leu Glu
 115 120 125

Ala Val Lys Ser Ala Gly Val Thr Leu Met Met Gly His Asn Gln Arg
 130 135 140

Tyr Tyr Ala His His Ala Arg Ala Lys Ala Leu Val Asp Ala Gly Val
 145 150 155 160

Ile Gly Lys Pro Tyr Met Ile Val Ala Ser Val His Val His Gly Gln
 165 170 175

Ile Asp Gly Phe Arg Arg Phe Leu Lys His Ala Gly Gly Gly Thr Leu
 180 185 190

Ile Asp Ser Gly Val His Arg Phe Asp Leu Ile Arg Trp Ile Met Gly
 195 200 205

Glu Val Glu Thr Val Phe Ala Gln Thr Gly Arg Phe Leu Gln Met Gln
 210 215 220

Met Glu Gly Glu Asp Cys Ala Val Val Thr Leu Arg Phe Arg Ser Gly
 225 230 235 240

Ala Ile Gly Ser Phe Ser Cys Ser Trp Ser Ala Lys Gly Pro Val Pro
 245 250 255

Glu Glu Thr Leu Gln Ile Phe Gly Pro Tyr Gly Ser Ile Tyr Thr Glu
 260 265 270

Asp His Thr Arg Thr Leu Arg Leu Tyr Thr Glu Arg Pro Thr Pro Glu
 275 280 285

Leu Glu Asp Val Arg Gln Phe Val Phe Pro Val Asp Gln Ala Glu Ser
 290 295 300

Ile Arg Arg Met Ile Glu Ala His Phe Thr Ser Leu Gln Gln Gly Leu
 305 310 315 320

Pro Pro Pro Ile Thr Gly Met Asp Gly Arg Ala Ser Leu Glu Leu Ser
 325 330 335

Met Ala Ser Tyr Arg Ser Ala Gln Thr Gly Gln Pro Val His Leu Pro
 340 345 350

Leu Gln Arg Gly Asn Gln Lys
 355

<210> 13
 <211> 1038
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 13
 atgagcccgg tgcgcgttgc tgtcatcggc gccgggcaaa ttgccacagcg cgggcattta 60
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 cttgaagaaa ttggggccaa atttcacgtt caccgggtct accgcgactg gcacgccatg 180
 ctggatgccg gcggattcga agccgtcacc atttgtaccc cgcccttcct ccatgccgag 240
 atggccatcg aatgtgcccg cagaggggtg catgtactgg tagaaaaacc catggctgta 300
 aatctccaac aatgcgatca aatgatcgcc gcgtctgaac aggccggaac catcttaatg 360
 gtctcgcata accagcgctt tatggaggca catcgtctgg ccaaagaaat ccttgatgcc 420
 ggctcctcgc gcaggctcta cctggcgcac ggggtctttg gccacggcgg cccggagggt 480
 tggagcccaa cccagcaatg gtacttccga cctgaccgcg ccggcgctgg cgtgatcgct 540
 gacctggggt atcataaact tgacctgatc cgctgggtca ccgggcaaga aattaccgcg 600
 gtgggagcac tgggcgccac ctttgaaaag caaacctcgc ttgaagactc tgctgtgatg 660
 ctggttcacc ttccggaggg tactctcgcc accatccagg taagctgggt gttcaggcct 720
 gactgggaaa acagcctggc ccttcgagga gaacgggggg tgctcgccat cccactgat 780
 gcctcgcaac ccctgcgggt ctcttacata tcttcttcgg gtcaggatcat tgaaagtacg 840

catcgttgcg actccggcga tacctccggc tggttcggag cgatccgggc atttctcacc 900
 gcgatcgaaa aaagcgctcc cgctcccatt gacggaaaag aagggcgtgc tgtcatggcg 960
 gcagttctgg cggccacacg ctccattcaa aaacatacga tcatttctat aaccgaggta 1020
 gaaaccatcc atgactga 1038

<210> 14
 <211> 345
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (4)...(123)
 <223> Oxidoreductase family, NAD-binding Rossmann fold

<220>
 <221> DOMAIN
 <222> (135)...(248)
 <223> Oxidoreductase family, C-terminal alpha/beta domain

<400> 14
 Met Ser Pro Val Arg Val Ala Val Ile Gly Ala Gly Gln Ile Ala Gln
 1 5 10 15

Arg Gly His Leu Pro Gly Leu Leu Glu Ala Gly Ala Glu Ile Thr Val
 20 25 30

Leu Cys Asp Asn Ser Leu Pro Gln Leu Glu Glu Ile Gly Ala Lys Phe
 35 40 45

His Val His Arg Val Tyr Arg Asp Trp His Ala Met Leu Asp Ala Gly
 50 55 60

Gly Phe Glu Ala Val Thr Ile Cys Thr Pro Pro Phe Leu His Ala Glu
 65 70 75 80

Met Ala Ile Glu Cys Ala Arg Arg Gly Leu His Val Leu Val Glu Lys
 85 90 95

Pro Met Ala Val Asn Leu Gln Gln Cys Asp Gln Met Ile Ala Ala Ser
 100 105 110

Glu Gln Ala Gly Thr Ile Leu Met Val Ser His Asn Gln Arg Phe Met
 115 120 125

Glu Ala His Arg Leu Ala Lys Glu Ile Leu Asp Ala Gly Leu Leu Gly
 130 135 140

Arg Leu Tyr Leu Ala His Gly Val Phe Gly His Gly Gly Pro Glu Val
 145 150 155 160

Trp Ser Pro Thr Gln Gln Trp Tyr Phe Arg Pro Asp Arg Ala Gly Ala
 165 170 175

Gly Val Ile Ala Asp Leu Gly Tyr His Lys Leu Asp Leu Ile Arg Trp
 180 185 190

Leu Thr Gly Gln Glu Ile Thr Ala Val Gly Ala Leu Gly Ala Thr Phe
 195 200 205

Glu Lys Gln Thr Ser Leu Glu Asp Ser Ala Val Met Leu Val His Leu
 210 215 220

Ser Glu Gly Thr Leu Ala Thr Ile Gln Val Ser Trp Val Phe Arg Pro
 225 230 235 240

Asp Trp Glu Asn Ser Leu Val Leu Arg Gly Glu Arg Gly Val Leu Ala
 245 250 255

Ile Pro Thr Asp Ala Ser Gln Pro Leu Arg Val Ser Tyr Ile Ser Ser
 260 265 270

Ser Gly Gln Val Ile Glu Ser Thr His Arg Cys Asp Ser Gly Asp Thr
 275 280 285

Ser Gly Trp Phe Gly Ala Ile Arg Ala Phe Leu Thr Ala Ile Glu Lys
 290 295 300

Ser Ala Pro Ala Pro Ile Asp Gly Lys Glu Gly Arg Ala Val Met Ala
 305 310 315 320

Ala Val Leu Ala Ala Thr Arg Ser Ile Gln Lys His Thr Ile Ile Ser
 325 330 335

Ile Thr Glu Val Glu Thr Ile His Asp
 340 345

<210> 15

<211> 1347

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 15

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atgactgacc atcgttttcc aaaaggattc atctggggaa ccgctacggc gtctttccag      60
attgaaggcg ccacccgcga agatggccgg ggcgaatcca tctgggaccg cttctgcgcc      120
acgccgggga aaattgtcac gggcgaaacc ggcgatcctg cctgcgactc ctatcatcgt      180
taccctgaag acatcgccct gatgaaggct atgtcgctca atggttaccg cttttcaatc      240
gcctggcctc gcgtcattcc tgacggagac ggtaaagtct gtcaggccgg gctcgactac      300
tacgatcgtg tggtagatgc tctcctggcg gagaatatcc aaccttttat caccctgtac      360
cactgggacc tgccccaggc attacaggat cggggtggct ggggcaaccg tgccacgggt      420
gaggcgttca ctcgctacgt agatattgtg gtttctcgcc tgggtgaccg cgtaaagtac      480
tggaatgacac acaacgaacc ctggtgtgta tccattttga gccatgagct tggatgaacat      540
gcccccggtg tgaaggaccg aaaactggcc ctccagggtg cgcaccatgt cctcgtttct      600
cacggcctgg ccgtgcccat catccgccag cgttgtaaag aggcgcaggt tggcatcgtg      660
ttgaattttt cacctgctta cccggccacc gatagcctgg ccgaccagat ggccacccgt      720
cagcaccacg cccggtttta cctctgggtc ctcgatccca tcgcccggcg cggctacccg      780
caggatgcct gggaagggtg cggagccgat gttcccgcca tgaggcctga tgacatgcag      840
atcatcgccg ccccatcga ctccctgggc gtcaatttct acagtcgggc ggtctgccac      900
gatccggccg ggggcgaagg ttcccgggtg ctcaatgtgc gcagtaaaac cgaggccacc      960
gatcgagact gggagattta ccctcaggcg ctctacgatt tactcatctg gatccacaat     1020
ggataccagt tcagagatat ttacattacc gagaatggcg cctcatacaa cgatgtggtc     1080
tccccggatg ggaaagtgca cgatcctaaa cgtctggact atctgaaacg ccatctggcc     1140
atggctctgc gggccatcga agcgggcggt ccactgcgtg gttatttctg ctggagcttg     1200
atggacaact tcgaatgggc catgggcacc agcagccgat tcgggttggc ctacaccgac     1260
ttcactaccc agaagcgtat tctcaaagac agtgggctct ggtttggcga agtggcacgg     1320
gcaaacgcct taatcgacct tccctga                                     1347

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<210> 16

<211> 448

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (2)...(444)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (10)...(24)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (352)...(360)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 16

Met	Thr	Asp	His	Arg	Phe	Pro	Lys	Gly	Phe	Ile	Trp	Gly	Thr	Ala	Thr
1				5				10						15	

Ala	Ser	Phe	Gln	Ile	Glu	Gly	Ala	Thr	Arg	Glu	Asp	Gly	Arg	Gly	Glu
			20					25					30		

Ser	Ile	Trp	Asp	Arg	Phe	Cys	Ala	Thr	Pro	Gly	Lys	Ile	Val	Thr	Gly
		35					40					45			

Glu	Thr	Gly	Asp	Pro	Ala	Cys	Asp	Ser	Tyr	His	Arg	Tyr	Pro	Glu	Asp
	50					55					60				

Ile	Ala	Leu	Met	Lys	Ala	Met	Ser	Leu	Asn	Gly	Tyr	Arg	Phe	Ser	Ile
65					70					75					80

Ala	Trp	Pro	Arg	Val	Ile	Pro	Asp	Gly	Asp	Gly	Lys	Val	Cys	Gln	Ala
				85					90					95	

Gly	Leu	Asp	Tyr	Tyr	Asp	Arg	Val	Val	Asp	Ala	Leu	Leu	Ala	Glu	Asn
			100					105					110		

Ile	Gln	Pro	Phe	Ile	Thr	Leu	Tyr	His	Trp	Asp	Leu	Pro	Gln	Ala	Leu
		115					120					125			

Gln	Asp	Arg	Gly	Gly	Trp	Gly	Asn	Arg	Ala	Thr	Val	Glu	Ala	Phe	Thr
	130					135					140				

Arg	Tyr	Val	Asp	Ile	Val	Val	Ser	Arg	Leu	Gly	Asp	Arg	Val	Lys	Tyr
145					150					155					160

Trp	Met	Thr	His	Asn	Glu	Pro	Trp	Cys	Val	Ser	Ile	Leu	Ser	His	Glu
				165					170					175	

Leu	Gly	Glu	His	Ala	Pro	Gly	Leu	Lys	Asp	Arg	Lys	Leu	Ala	Leu	Gln
			180					185					190		

Val	Ala	His	His	Val	Leu	Val	Ser	His	Gly	Leu	Ala	Val	Pro	Ile	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195

200

205

Arg Gln Arg Cys Lys Glu Ala Gln Val Gly Ile Val Leu Asn Phe Ser
 210 215 220

Pro Ala Tyr Pro Ala Thr Asp Ser Leu Ala Asp Gln Met Ala Thr Arg
 225 230 235 240

Gln His His Ala Arg Phe Asn Leu Trp Phe Leu Asp Pro Ile Ala Gly
 245 250 255

Arg Gly Tyr Pro Gln Asp Ala Trp Glu Gly Tyr Gly Ala Asp Val Pro
 260 265 270

Ala Met Arg Pro Asp Asp Met Gln Ile Ile Ala Ala Pro Ile Asp Phe
 275 280 285

Leu Gly Val Asn Phe Tyr Ser Arg Ala Val Cys His Asp Pro Ala Gly
 290 295 300

Gly Glu Gly Ser Arg Val Leu Asn Val Arg Ser Lys Thr Glu Ala Thr
 305 310 315 320

Asp Arg Asp Trp Glu Ile Tyr Pro Gln Ala Leu Tyr Asp Leu Leu Ile
 325 330 335

Trp Ile His Asn Gly Tyr Gln Phe Arg Asp Ile Tyr Ile Thr Glu Asn
 340 345 350

Gly Ala Ser Tyr Asn Asp Val Val Ser Pro Asp Gly Lys Val His Asp
 355 360 365

Pro Lys Arg Leu Asp Tyr Leu Lys Arg His Leu Ala Met Ala Leu Arg
 370 375 380

Ala Ile Glu Ala Gly Val Pro Leu Arg Gly Tyr Phe Cys Trp Ser Leu
 385 390 395 400

Met Asp Asn Phe Glu Trp Ala Met Gly Thr Ser Ser Arg Phe Gly Leu
 405 410 415

Ala Tyr Thr Asp Phe Thr Thr Gln Lys Arg Ile Leu Lys Asp Ser Gly
 420 425 430

Leu Trp Phe Gly Glu Val Ala Arg Ala Asn Ala Leu Ile Asp Leu Pro
 435 440 445

<210> 17
<211> 1215
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 17
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gtttccacgc ctgaaaaaga gggcttctcg gcggagcgcc tcgggcggat gcaccggtat 120
ttcgagaacc tgacgaaaac cggagagcgg cctggcgcgga tcacgctgat cgtgcgcaac 180
gggcgcacatc tggactggcg cacgttcggg ctgcgcgacg tcgagaacaa tctgccgatg 240
gagaaggaca cgatcgtcca catctactcg atgacgaagc cggtagacgtc cgtggccgtg 300
atgatgctgg tggaggaggg caggctggcg ctggacgacc gggtaggacaa gttcattccc 360
gagttcaagg ggatgaagggt gtacaagggc ggcacgggtg agcggccgga gctggaggac 420
gcggcgcggc cgatcacggt gaagcatctg ctgacgcaca cgagcgggct gagctacggc 480
tggggcaacg acaacgtctc cgcgatgtac cgcaaggccg acccgctcgg cgcgccgagc 540
ctgaaagagt ttatcgacag gctgggtgaaa ctgccgctgg cattccaccc gggcgagcgt 600
tacgagtatt cgatgtcgat cgacgtgctg ggctacctgg tggaggctgt ctccggcgag 660
ccgttcgatc agttcgtgga gaagcggatc acggggccgc tgaagatgaa cgacacgcat 720
ttcagactgc cggaggcgaa gcgggcgcgg ctggcgaaga tctactcgcg gcgcgagggg 780
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ggggcggctt cgacgtatct cggggtggac cggaaagaga agctggcgat gctgctgttc 1140
ctgcaatgga tgccgtttga tcaggggacg ctgaacctgt acgagacgct ggtctaccaa 1200
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<210> 18
<211> 404
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (37)...(400)

<223> Beta-lactamase

<220>

<221> SITE

<222> (43)...(46)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (167)...(170)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (240)...(243)

<223> N-glycosylation site. Prosite id = PS00001

<400> 18

Met	Arg	Tyr	Val	Leu	Ile	Ser	Cys	Leu	Ala	Leu	Ala	Ser	Leu	Cys	Ala
1				5					10					15	

Gln	Pro	Leu	Pro	Val	Ser	Thr	Pro	Glu	Lys	Glu	Gly	Phe	Ser	Ala	Glu
			20					25					30		

Arg	Leu	Gly	Arg	Met	His	Arg	Tyr	Phe	Glu	Asn	Leu	Thr	Lys	Thr	Gly
		35					40					45			

Glu	Arg	Pro	Gly	Ala	Ile	Thr	Leu	Ile	Val	Arg	Asn	Gly	Arg	Ile	Val
	50					55					60				

Asp	Trp	Arg	Thr	Phe	Gly	Leu	Arg	Asp	Val	Glu	Asn	Asn	Leu	Pro	Met
65					70					75					80

Glu	Lys	Asp	Thr	Ile	Val	His	Ile	Tyr	Ser	Met	Thr	Lys	Pro	Val	Thr
				85					90					95	

Ser	Val	Ala	Val	Met	Met	Leu	Val	Glu	Glu	Gly	Arg	Leu	Ala	Leu	Asp
			100					105					110		

Asp	Arg	Val	Asp	Lys	Phe	Ile	Pro	Glu	Phe	Lys	Gly	Met	Lys	Val	Tyr
		115					120					125			

Lys	Gly	Gly	Thr	Val	Glu	Arg	Pro	Glu	Leu	Glu	Asp	Ala	Ala	Arg	Pro
	130					135					140				

Ile	Thr	Val	Lys	His	Leu	Leu	Thr	His	Thr	Ser	Gly	Leu	Ser	Tyr	Gly
145					150					155					160

Trp Gly Asn Asp Asn Val Ser Ala Met Tyr Arg Lys Ala Asp Pro Leu
 165 170 175

Gly Ala Pro Ser Leu Lys Glu Phe Ile Asp Arg Leu Val Lys Leu Pro
 180 185 190

Leu Ala Phe His Pro Gly Glu Arg Tyr Glu Tyr Ser Met Ser Ile Asp
 195 200 205

Val Leu Gly Tyr Leu Val Glu Ala Val Ser Gly Glu Pro Phe Asp Gln
 210 215 220

Phe Val Glu Lys Arg Ile Thr Gly Pro Leu Lys Met Asn Asp Thr His
 225 230 235 240

Phe Arg Leu Pro Glu Ala Lys Arg Ala Arg Leu Ala Lys Ile Tyr Ser
 245 250 255

Arg Arg Glu Gly Lys Leu Thr Ala Gln Arg Gly Leu Gln Thr Gly Gly
 260 265 270

Val Pro Tyr Gly Gly Met Gly Leu Tyr Ser Thr Ile Gly Asp Tyr Ala
 275 280 285

Arg Phe Ala Gln Met Leu Leu Asn Gly Gly His Leu Asp Gly Val Arg
 290 295 300

Leu Leu Gly Arg Lys Thr Val Asp Leu Met Met Met Asn His Leu Gly
 305 310 315 320

Gly Leu Ser Lys Pro Thr Ile Gly Gly Asp Asp Ser Ala Gly Phe Gly
 325 330 335

Leu Gly Gly Ala Val Arg Ile Asp Pro Ala Lys Ser Gly Arg Pro Gly
 340 345 350

Thr Glu Gly Leu Phe Gly Trp Asp Gly Ala Ala Ser Thr Tyr Phe Arg
 355 360 365

Val Asp Arg Lys Glu Lys Leu Ala Met Leu Leu Phe Leu Gln Trp Met
 370 375 380

Pro Phe Asp Gln Gly Thr Leu Asn Leu Tyr Glu Thr Leu Val Tyr Gln
 385 390 395 400

Ala Leu Val Asp

<210> 19
<211> 1794
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 19
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gggcccgttt ccctgcttgg cggagatgcg ggcgcggcgt tccgctatac cgggccatcg 120
gcggggcgcg cgagcggctc ggccgaatgg gtggcggtgg agaacatgcc gttcacgcac 180
gcctggcggc tgcgcacgaa tccgctgccg gagagcggcg gcaacgaatg ggacctgcgc 240
atccgcgcc cgcggagcggc ggctgtttcg gcaggggaca agatcctggc cgagttctgg 300
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ttccgcgtgc tgttcgagat gcgggagagc tacgccggcg gcggctacat gatcgatttc 480
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ccgcaggcca cggccgagca gcttggcctg gaccggtttt atgagggcgc ggccggcgac 600
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aagcggcacg cgttcgggtg gggcacggct gtggcgggcat cacggcttct ggggacggga 780
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gacacggcca cgcgcgcgga gcggatgctg gagatcatga accggtacgc ccggctcggg 1380
ctgccgatcg ccatcaccga gtacgatttc gccacggcgg acgaggagct gcaggcgcag 1440
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tggggcttct gggaagggag ccactggaag ccgctgggag ccatgatccg gcgcgactgg 1560
agcgagaagc cgatgtaccg cgtctggcgc gagctgatct tcgagcgctg gcagacggat 1620
gaaacaggcg tgacgccgga gcacgggtgcc atctacgtgc ggggcttcaa gggcgactac 1680
gagatcacgg tgaaggcggg cgggcaggaa gtccgggtgc cgtacacgct gaaagaagac 1740
ggccagggtgc tgtgggtgac ggtggggcggg gcttctgaag agcgcggtgca gtaa 1794

<210> 20
<211> 597
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(20)

<220>
<221> DOMAIN
<222> (235)...(533)
<223> Glycosyl hydrolase family 10

<220>
<221> SITE
<222> (467)...(477)
<223> Glycosyl hydrolases family 10 active site. Prosite id = PS00591

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1 5 10 15

Gln Ser Leu Ala Gly Pro Val Ser Leu Leu Gly Gly Asp Ala Gly Ala
20 25 30

Ala Phe Arg Tyr Thr Gly Pro Ser Ala Gly Ala Ala Ser Gly Ser Ala
35 40 45

Glu Trp Val Ala Val Glu Asn Met Pro Phe Thr His Ala Trp Arg Leu
50 55 60

Arg Thr Asn Pro Leu Pro Glu Ser Gly Gly Asn Glu Trp Asp Leu Arg
65 70 75 80

Ile Arg Ala Arg Gly Ala Ala Ala Val Ser Ala Gly Asp Lys Ile Leu
85 90 95

Ala Glu Phe Trp Met Arg Cys Val Glu Pro Glu Asn Gly Asp Cys Ile
100 105 110

Leu Arg Leu Asn Val Glu Arg Asp Gly Ser Pro Trp Thr Lys Ser Ile
 115 120 125

Ser Asn Pro Tyr Pro Val Gly Arg Glu Trp Arg Arg Phe Arg Val Leu
 130 135 140

Phe Glu Met Arg Glu Ser Tyr Ala Ala Gly Gly Tyr Met Ile Asp Phe
 145 150 155 160

Trp Met Gly Gln Gln Val Gln Thr Ala Glu Val Gly Gly Ile Ser Leu
 165 170 175

Leu Asn Tyr Gly Pro Gln Ala Thr Ala Glu Gln Leu Gly Leu Asp Arg
 180 185 190

Phe Tyr Glu Gly Ala Ala Ala Asp Ala Ala Trp Arg Gln Ala Ala Glu
 195 200 205

Gln Arg Ile Glu Glu Ile Arg Lys Ala Gly Met Ile Ile Val Ala Val
 210 215 220

Thr Pro Asp Gly Glu Pro Ile Glu Gly Ala Glu Ile Arg Ala Lys Leu
 225 230 235 240

Lys Arg His Ala Phe Gly Trp Gly Thr Ala Val Ala Ala Ser Arg Leu
 245 250 255

Leu Gly Thr Gly Thr Asp Ser Glu Arg Tyr Arg Asn Phe Ile Arg Glu
 260 265 270

Asn Phe Asn Met Ala Val Leu Glu Asn Asp Leu Lys Trp Gly Pro Phe
 275 280 285

Glu Glu Asn Arg Asn Arg Ala Met Asn Ala Leu Arg Trp Leu His Glu
 290 295 300

Asn Gly Ile Thr Trp Ile Arg Gly His Asn Leu Val Trp Pro Gly Trp
 305 310 315 320

Arg Trp Met Pro Asn Asp Val Arg Asn Leu Ala Asn Asn Pro Glu Ala
 325 330 335

Leu Arg Gln Arg Ile Leu Asp Arg Ile Arg Asp Thr Ala Thr Ala Thr
 340 345 350

Arg Gly Leu Val Val His Trp Asp Val Val Asn Glu Pro Val Ala Glu
355 360 365

Arg Asp Val Leu Asn Ile Leu Gly Asp Glu Val Met Ala Asp Trp Phe
370 375 380

Arg Ala Ala Lys Glu Cys Asp Pro Glu Ala Arg Met Phe Ile Asn Glu
385 390 395 400

Tyr Asp Ile Leu Ala Ala Asn Gly Ala Asn Leu Arg Lys Gln Asn Ala
405 410 415

Tyr Tyr Arg Met Ile Glu Met Leu Leu Lys Leu Glu Ala Pro Val Glu
420 425 430

Gly Ile Gly Phe Gln Gly His Phe Asp Thr Ala Thr Pro Pro Glu Arg
435 440 445

Met Leu Glu Ile Met Asn Arg Tyr Ala Arg Leu Gly Leu Pro Ile Ala
450 455 460

Ile Thr Glu Tyr Asp Phe Ala Thr Ala Asp Glu Glu Leu Gln Ala Gln
465 470 475 480

Phe Thr Arg Asp Leu Met Ile Leu Ala Phe Ser His Pro Ala Val Ser
485 490 495

Asp Phe Leu Met Trp Gly Phe Trp Glu Gly Ser His Trp Lys Pro Leu
500 505 510

Gly Ala Met Ile Arg Arg Asp Trp Ser Glu Lys Pro Met Tyr Arg Val
515 520 525

Trp Arg Glu Leu Ile Phe Glu Arg Trp Gln Thr Asp Glu Thr Gly Val
530 535 540

Thr Pro Glu His Gly Ala Ile Tyr Val Arg Gly Phe Lys Gly Asp Tyr
545 550 555 560

Glu Ile Thr Val Lys Ala Gly Gly Gln Glu Val Arg Val Pro Tyr Thr
565 570 575

Leu Lys Glu Asp Gly Gln Val Leu Trp Val Thr Val Gly Gly Ala Ser
580 585 590

Glu Glu Arg Val Gln

595

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<212> DNA
<213> Clostridium thermocellum

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ggagaatata aagaagatgg gctttcttat attgaccggg gccttgagtg gtgtaaaaaa 240
tacaatttgg ggcttgtggt ggatatgcat cacgctcccg ggtaccgctt tcaagatttt 300
aagacaagca ccttgtttga agatccgaac cagcaaaaaga gatttggtga catatggaga 360
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gagcttaaaa accttgcaga tattgatgat gattacatag ttacaatttt ccattttttac 600
aatccttttt tctttacgca tcagaaagcc cactgggtcgg aaagtgccat ggcgtacaac 660
aggactgtaa aatatccggg acaatatgag ggaattgaag agtttgtgaa aaataatcct 720
aagtacagtt ttatgatgga attgaataac ctgaagctga ataaagagct ttgcgcaaaa 780
gatttaaaac cagcaattga gttcagggaa aagaaaaaat gcaaactata ttgcggggag 840
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agaaaaactt ga 1032

<210> 22
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<213> Clostridium thermocellum

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<223> N-glycosylation site. Prosite id = PS00001

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			20					25					30		

Asp	Ile	Glu	Thr	Ile	Ala	Glu	Ala	Gly	Phe	Asp	His	Val	Arg	Leu	Pro
		35					40					45			

Phe	Asp	Tyr	Pro	Ile	Ile	Glu	Ser	Asp	Asp	Asn	Val	Gly	Glu	Tyr	Lys
	50					55					60				

Glu	Asp	Gly	Leu	Ser	Tyr	Ile	Asp	Arg	Cys	Leu	Glu	Trp	Cys	Lys	Lys
65					70					75					80

Tyr	Asn	Leu	Gly	Leu	Val	Leu	Asp	Met	His	His	Ala	Pro	Gly	Tyr	Arg
				85					90					95	

Phe	Gln	Asp	Phe	Lys	Thr	Ser	Thr	Leu	Phe	Glu	Asp	Pro	Asn	Gln	Gln
			100					105					110		

Lys	Arg	Phe	Val	Asp	Ile	Trp	Arg	Phe	Leu	Ala	Lys	Arg	Tyr	Ile	Asn
		115					120					125			

Glu	Arg	Glu	His	Ile	Ala	Phe	Glu	Leu	Leu	Asn	Glu	Val	Val	Glu	Pro
	130					135					140				

Asp	Ser	Thr	Arg	Trp	Asn	Lys	Leu	Met	Leu	Glu	Cys	Val	Lys	Ala	Ile
145					150					155					160

Arg	Glu	Ile	Asp	Ser	Thr	Arg	Trp	Leu	Tyr	Ile	Gly	Gly	Asn	Asn	Tyr
				165					170					175	

Asn	Ser	Pro	Asp	Glu	Leu	Lys	Asn	Leu	Ala	Asp	Ile	Asp	Asp	Asp	Tyr
			180					185					190		

Ile	Val	Tyr	Asn	Phe	His	Phe	Tyr	Asn	Pro	Phe	Phe	Phe	Thr	His	Gln
		195					200					205			

Lys Ala His Trp Ser Glu Ser Ala Met Ala Tyr Asn Arg Thr Val Lys
 210 215 220
 Tyr Pro Gly Gln Tyr Glu Gly Ile Glu Glu Phe Val Lys Asn Asn Pro
 225 230 235 240
 Lys Tyr Ser Phe Met Met Glu Leu Asn Asn Leu Lys Leu Asn Lys Glu
 245 250 255
 Leu Leu Arg Lys Asp Leu Lys Pro Ala Ile Glu Phe Arg Glu Lys Lys
 260 265 270
 Lys Cys Lys Leu Tyr Cys Gly Glu Phe Gly Val Ile Ala Ile Ala Asp
 275 280 285
 Leu Glu Ser Arg Ile Lys Trp His Glu Asp Tyr Ile Ser Leu Leu Glu
 290 295 300
 Glu Tyr Asp Ile Gly Gly Ala Val Trp Asn Tyr Lys Lys Met Asp Phe
 305 310 315 320
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 325 330 335
 Ile Leu Ala Arg Arg Lys Thr
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<210> 23
 <211> 3966
 <212> DNA
 <213> Clostridium thermocellum

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 gacaattata ttacaagaca agaagccgtt gttataatcg cgaaagtttt tgaacttcaa 420
 agcggcagca attatacaag caagttttaa gatggaagtc tggtaaagga atacgcaaaa 480
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aacaccgaag	gagttatfff	aaaagatacc	gtaataaacg	gggatttgta	tcttgctcag	720
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cagtaa 3966

<210> 24

<211> 1321

<212> PRT

<213> Clostridium thermocellum

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<221> SIGNAL
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Ser	Ala	Trp	Ser	Pro	Ile	Ser	Val	Gln	Ala	Ser	Asp	Gly	Ile	Asn	Asp
			20					25					30		

Ile	Arg	Gly	His	Trp	Ala	Glu	Glu	Asp	Leu	Asn	Lys	Trp	Met	Glu	Lys
		35					40					45			

Gly	Ile	Leu	Val	Gly	Tyr	Gln	Asp	Gly	Thr	Ile	Arg	Pro	Asp	Asn	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Ile Thr Arg Ala Glu Phe Val Thr Leu Ile Asn Lys Val Phe Gly Leu
 65 70 75 80

Tyr Glu Leu Ser Arg Glu Gln Phe Ala Asp Val Glu Asp Ser Lys Trp
 85 90 95

Tyr Ser Arg Glu Ile Leu Lys Ala Arg Ala Ala Gly Tyr Ile Ala Gly
 100 105 110

Tyr Gly Ser Asn Val Phe Lys Pro Asp Asn Tyr Ile Thr Arg Gln Glu
 115 120 125

Ala Val Val Ile Ile Ala Lys Val Phe Glu Leu Gln Ser Gly Ser Asn
 130 135 140

Tyr Thr Ser Lys Phe Lys Asp Gly Ser Leu Val Lys Glu Tyr Ala Lys
 145 150 155 160

Asp Ser Val Ser Ala Leu Val Glu Lys Gly Tyr Ile Ala Gly Tyr Glu
 165 170 175

Asp Gly Thr Phe Arg Pro Asp Asn Tyr Ile Thr Arg Ala Glu Thr Ile
 180 185 190

Lys Ile Leu Asn Lys Ile Ile Pro Ser Leu Tyr Asn Glu Lys Gly Asp
 195 200 205

Tyr Lys Asn Glu Glu Val Ala Gly Asn Ala Leu Ile Asn Thr Glu Gly
 210 215 220

Val Ile Leu Lys Asp Thr Val Ile Asn Gly Asp Leu Tyr Leu Ala Gln
 225 230 235 240

Gly Ile Gln Asn Gly Asp Val Thr Leu Asp Gly Val Asn Val Lys Gly
 245 250 255

Thr Val Phe Val Asn Gly Gly Gly Ser Asp Ser Ile His Phe Ile Asn
 260 265 270

Thr Lys Ile Asn Arg Val Val Val Asn Lys Thr Gly Val Arg Ile Val
 275 280 285

Thr Ser Gly Asn Thr Ser Val Glu Ser Val Val Val Lys Ser Gly Ala
 290 295 300

Lys Leu Glu Glu Lys Glu Leu Thr Gly Asp Gly Phe Lys Asn Val Thr
 305 310 315 320

Val Asp Ser Gln Leu Ser Ala Gly Asn Glu Ile Ile Phe Val Gly Asp
 325 330 335

Phe Glu Gln Val Asp Val Leu Ala Asp Asp Ala Leu Leu Glu Thr Lys
 340 345 350

Glu Ala Lys Met Lys Leu Arg Ile Phe Gly Gln Arg Ile Lys Val Asn
 355 360 365

Gly Lys Ala Ile Glu Lys Ser Ser Lys Asn Tyr Ile Val Asn Gly Glu
 370 375 380

Leu Ile Ser Thr Glu Glu Glu Pro Gly Pro Ser Asp Ala Pro Gly Ala
 385 390 395 400

Glu Asp Asp Gln Asn Ser Gly Ser Pro Gly Ser Ser Thr Asn Pro Ala
 405 410 415

Pro Thr Lys Asn Pro Asn Glu Glu Trp Arg Leu Val Trp Ser Asp Glu
 420 425 430

Phe Asn Gly Ser Glu Ile Asn Met Ala Asn Trp Ser Tyr Asp Asp Pro
 435 440 445

Thr Asn Gly Arg Trp Asn Gly Glu Val Gln Ser Tyr Thr Gln Asn Asn
 450 455 460

Ala Tyr Ile Lys Asp Gly Ala Leu Val Ile Glu Ala Arg Lys Glu Asp
 465 470 475 480

Ile Thr Glu Pro Ser Gly Glu Thr Tyr His Tyr Thr Ser Ser Lys Leu
 485 490 495

Ile Thr Lys Gly Lys Lys Ser Trp Lys Tyr Gly Lys Phe Glu Ile Arg
 500 505 510

Ala Lys Met Pro Gln Gly Gln Gly Ile Trp Pro Ala Ile Trp Met Met
 515 520 525

Pro Glu Asp Glu Pro Phe Tyr Gly Thr Trp Pro Lys Cys Gly Glu Ile
 530 535 540

Asp Ile Met Glu Leu Leu Gly His Glu Pro Asp Lys Ile Tyr Gly Thr
 545 550 555 560

Ile His Phe Gly Glu Pro His Lys Glu Ser Gln Gly Thr Tyr Thr Leu
 565 570 575

Pro Glu Gly Gln Thr Phe Ala Asp Asp Phe His Val Tyr Ser Ile Glu
 580 585 590

Trp Glu Pro Gly Glu Ile Arg Trp Tyr Ile Asp Gly Lys Leu Tyr His
 595 600 605

Val Ala Asn Asp Trp Tyr Ser Arg Asp Pro Tyr Leu Ala Asp Asp Tyr
 610 615 620

Thr Tyr Pro Ala Pro Phe Asp Gln Asn Phe Phe Leu Ile Leu Asn Ile
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Ser Val Gly Gly Gly Trp Pro Gly Tyr Pro Asp Glu Thr Thr Val Phe
 645 650 655

Pro Gln Gln Met Val Val Asp Tyr Val Arg Val Tyr Gln Lys Asp Lys
 660 665 670

Tyr Pro His Arg Glu Lys Pro Ala Lys Glu Glu Val Lys Pro Arg Glu
 675 680 685

Pro Leu Glu Asp Gly Asn Tyr Ile Tyr Asn Gly Gly Phe Asp Val Asp
 690 695 700

Asp Ser Ala Ala Val Gly Val Asp Gly Val Pro Tyr Thr Ser Tyr Trp
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Thr Phe Leu Thr Ala Ser Gly Gly Ala Ala Thr Val Asn Val Glu Glu
 725 730 735

Gly Val Met His Val Gln Ile Glu Asn Gly Gly Thr Thr Asp Tyr Gly
 740 745 750

Val Gln Leu Leu Gln Ala Pro Ile His Leu Glu Lys Gly Ala Lys Tyr
 755 760 765

Lys Ala Ser Phe Asp Met Lys Ala Glu Asn Pro Arg Gln Val Lys Leu
 770 775 780

Lys Ile Gly Gly Asp Gly Asp Arg Gly Trp Lys Asp Tyr Ala Ala Ile
 785 790 795 800

Pro Pro Phe Thr Val Ser Thr Glu Met Thr Asn Tyr Glu Phe Glu Phe
 805 810 815

Thr Met Lys Asp Asp Thr Asp Val Lys Ala Arg Phe Glu Phe Asn Met
 820 825 830

Gly Leu Asp Asp Asn Asp Val Trp Ile Asp Asn Val Lys Leu Ile Lys
 835 840 845

Thr Glu Asp Ala Pro Val Ile Asp Pro Ser Glu Ile Ala Arg Pro Pro
 850 855 860

Leu Leu Ser Gly Asn Tyr Ile Tyr Asn Gly Thr Phe Asp Gln Gly Pro
 865 870 875 880

Asn Arg Met Gly Phe Trp Asn Phe Val Val Asp Ser Thr Ala Lys Ala
 885 890 895

Thr Tyr Tyr Ile Gly Ser Asp Val Asn Glu Arg Arg Phe Glu Thr Arg
 900 905 910

Ile Glu Lys Gly Gly Thr Ser Arg Gly Ala Ile Arg Leu Val Gln Pro
 915 920 925

Gly Ile Asn Ile Glu Asn Gly Lys Thr Tyr Lys Val Ser Phe Glu Ala
 930 935 940

Ser Ala Ala Asn Thr Arg Thr Ile Glu Val Glu Ile Ala Ser Asn Leu
 945 950 955 960

His Asn Ser Ser Ile Phe Ala Thr Thr Phe Glu Ile Ser Lys Glu Ser
 965 970 975

Lys Ile Tyr Glu Phe Glu Phe Thr Met Asp Lys Asp Ser Asp Lys Asn
 980 985 990

Gly Glu Leu Arg Phe Asn Leu Gly Gly Ser Asn Val Asn Val Tyr Ile
 995 1000 1005

Asp Asn Val Val Met Lys Arg Val Ser Thr Asp Glu Val Glu Gly
 1010 1015 1020

Asn Leu Ile Leu Asn Gly Val Phe Asn Gly Leu Ala Gly Trp Gly

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1040		1045		1050
Glu Gln Phe Arg Ala Ile Ile Ser Ser Val Gly Asn Glu Gly Trp				
1055		1060		1065
Asn Val Gln Leu Tyr Gln Asp Asn Val Pro Leu Glu Gln Gly Gln				
1070		1075		1080
Thr Tyr Glu Val Ser Phe Asp Ala Lys Ser Thr Ile Asp Arg Lys				
1085		1090		1095
Ile Ile Val Gln Leu Gln Arg Asn Gly Thr Ser Asp Asn Asn Trp				
1100		1105		1110
Asp Ser Tyr Phe Tyr Gln Glu Val Glu Leu Thr Asn Glu Leu Lys				
1115		1120		1125
Thr Phe Lys Tyr Glu Phe Thr Met Ser Lys Pro Thr Asp Ser Ala				
1130		1135		1140
Ser Arg Phe Asn Phe Ala Leu Gly Asn Thr Glu Asn Lys Thr Tyr				
1145		1150		1155
Ala Pro His Glu Ile Ile Ile Asp Asn Val Val Val Arg Lys Val				
1160		1165		1170
Ala Thr Pro Ser Ala Leu Ile Leu Asn Gly Thr Phe Asp Asp Gly				
1175		1180		1185
Met Asp His Trp Leu Leu Tyr Trp Gly Asp Gly Glu Gly Asn Cys				
1190		1195		1200
Asp Val Thr Asp Gly Glu Leu Glu Ile Asn Ile Thr Lys Val Gly				
1205		1210		1215
Thr Ala Asp Tyr Met Pro Gln Ile Lys Gln Glu Asn Ile Ala Leu				
1220		1225		1230
Gln Glu Gly Val Thr Tyr Thr Leu Ser Leu Lys Ala Arg Ala Leu				
1235		1240		1245
Glu Ala Arg Ser Ile Lys Val Asp Ile Leu Asp Ser Ser Tyr Asn				
1250		1255		1260

Trp Tyr Gly Gly Thr Ile Phe Asp Leu Thr Thr Glu Asp Ala Val
 1265 1270 1275

Tyr Thr Phe Thr Phe Thr Gln Ser Lys Ser Ile Asn Asn Gly Val
 1280 1285 1290

Leu Thr Ile Asn Leu Gly Thr Ile Glu Gly Lys Thr Ser Ala Ala
 1295 1300 1305

Thr Thr Val Tyr Leu Asp Asp Ile Leu Leu Glu Gln Gln
 1310 1315 1320

<210> 25

<211> 1347

<212> DNA

<213> Clostridium thermocellum

<400> 25

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atgtcaaaga taactttccc aaaagatttc atatgggggtt ctgcaacagc agcatatcag      60
attgaagggtg catacaacga agacggcaaa ggtgaatcta tatgggaccg tttttcccac      120
acgccaggaa atatagcaga cggacatacc ggcgatgttg catgcgacca ctatcatcgt      180
tatgaagaag atatcaaaat aatgaaagaa atcgggtatta aatcatacag gttttccatc      240
tcatggccca gaatctttcc tgaaggaaca ggtaaattaa atcaaaaggg actggatttt      300
tacaaaaggc tcacaaatct gcttctggaa aacggaatta tgccctgcaat cactctttat      360
cactgggacc ttccccaaaa gcttcaggat aaaggcggat ggaaaaaccg ggacaccacc      420
gattatttta cagaatactc tgaagtaata tttaaaaatc tcggagatat cgttccaata      480
tggtttactc acaatgaacc cgggtgttgtt tctttgcttg gccacttttt aggaattcat      540
gcccttggga taaaagacct ccgcacttca ttggaagtct cgcacaatct tcttttgtcc      600
cacggcaagg ccgtgaaact gtttagagaa atgaatattg acgccc aaat tggaatagct      660
ctcaatttat cttaccatta tcccgcattc gaaaaagctg aggatattga agcagcggaa      720
ttgtcatttt ctctggcggg aagggtggtat ctggatcctg tgctaaaagg ccggtatcct      780
gaaaacgcat tgaaacttta taaaaagaag ggtattgagc tttctttccc tgaagatgac      840
ctgaaactta tcagtcagcc aatagacttc atagcattca acaattattc ttcggaattt      900
ataaaatatg atccgtccag tgagtcaggt ttttcacctg caaactccat attagaaaag      960
ttcgaaaaaa cagatatggg ctggatcata taccctgaag gcttgtatga tctgcttatg     1020
ctccttgaca gggattatgg aaagccaaac attggttatca gcgaaaacgg agccgccttc     1080
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 gttcacgtaa attttgatac gttggaaaga aaaataaagg atagcggcta ctggtacaaa 1320
 gaagtaatca aaaacaacgg ttttttaa 1347

<210> 26
 <211> 448
 <212> PRT
 <213> Clostridium thermocellum

<220>
 <221> DOMAIN
 <222> (2)...(448)
 <223> Glycosyl hydrolase family 1

<220>
 <221> SITE
 <222> (10)...(24)
 <223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>
 <221> SITE
 <222> (225)...(228)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (299)...(302)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (356)...(364)
 <223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 26
 Met Ser Lys Ile Thr Phe Pro Lys Asp Phe Ile Trp Gly Ser Ala Thr
 1 5 10 15

Ala Ala Tyr Gln Ile Glu Gly Ala Tyr Asn Glu Asp Gly Lys Gly Glu
 20 25 30

Ser Ile Trp Asp Arg Phe Ser His Thr Pro Gly Asn Ile Ala Asp Gly
 35 40 45

His Thr Gly Asp Val Ala Cys Asp His Tyr His Arg Tyr Glu Glu Asp
 50 55 60

Ile Lys Ile Met Lys Glu Ile Gly Ile Lys Ser Tyr Arg Phe Ser Ile
 65 70 75 80

Ser Trp Pro Arg Ile Phe Pro Glu Gly Thr Gly Lys Leu Asn Gln Lys
85 90 95

Gly Leu Asp Phe Tyr Lys Arg Leu Thr Asn Leu Leu Leu Glu Asn Gly
100 105 110

Ile Met Pro Ala Ile Thr Leu Tyr His Trp Asp Leu Pro Gln Lys Leu
115 120 125

Gln Asp Lys Gly Gly Trp Lys Asn Arg Asp Thr Thr Asp Tyr Phe Thr
130 135 140

Glu Tyr Ser Glu Val Ile Phe Lys Asn Leu Gly Asp Ile Val Pro Ile
145 150 155 160

Trp Phe Thr His Asn Glu Pro Gly Val Val Ser Leu Leu Gly His Phe
165 170 175

Leu Gly Ile His Ala Pro Gly Ile Lys Asp Leu Arg Thr Ser Leu Glu
180 185 190

Val Ser His Asn Leu Leu Leu Ser His Gly Lys Ala Val Lys Leu Phe
195 200 205

Arg Glu Met Asn Ile Asp Ala Gln Ile Gly Ile Ala Leu Asn Leu Ser
210 215 220

Tyr His Tyr Pro Ala Ser Glu Lys Ala Glu Asp Ile Glu Ala Ala Glu
225 230 235 240

Leu Ser Phe Ser Leu Ala Gly Arg Trp Tyr Leu Asp Pro Val Leu Lys
245 250 255

Gly Arg Tyr Pro Glu Asn Ala Leu Lys Leu Tyr Lys Lys Lys Gly Ile
260 265 270

Glu Leu Ser Phe Pro Glu Asp Asp Leu Lys Leu Ile Ser Gln Pro Ile
275 280 285

Asp Phe Ile Ala Phe Asn Asn Tyr Ser Ser Glu Phe Ile Lys Tyr Asp
290 295 300

Pro Ser Ser Glu Ser Gly Phe Ser Pro Ala Asn Ser Ile Leu Glu Lys
305 310 315 320

Phe Glu Lys Thr Asp Met Gly Trp Ile Ile Tyr Pro Glu Gly Leu Tyr

325	330	335
Asp Leu Leu Met Leu Leu Asp Arg Asp Tyr Gly Lys Pro Asn Ile Val		
340	345	350
Ile Ser Glu Asn Gly Ala Ala Phe Lys Asp Glu Ile Gly Ser Asn Gly		
355	360	365
Lys Ile Glu Asp Thr Lys Arg Ile Gln Tyr Leu Lys Asp Tyr Leu Thr		
370	375	380
Gln Ala His Arg Ala Ile Gln Asp Gly Val Asn Leu Lys Ala Tyr Tyr		
385	390	395
Leu Trp Ser Leu Leu Asp Asn Phe Glu Trp Ala Tyr Gly Tyr Asn Lys		
405	410	415
Arg Phe Gly Ile Val His Val Asn Phe Asp Thr Leu Glu Arg Lys Ile		
420	425	430
Lys Asp Ser Gly Tyr Trp Tyr Lys Glu Val Ile Lys Asn Asn Gly Phe		
435	440	445

<210> 27
 <211> 1362
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 27
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 cacacgcccg gtaagatcag gaacaacgat acgggcgatg tagcaaatga ccattatcgc 180
 ctctggaaaa aagacattgg ctgatgaag aagatcgggt tgaaggctta tcgattttcc 240
 atttcgtggc cgcgtattct tcctgctgga agaggcaagg tcaatcaaag agggctggat 300
 ttttacaaca agatcgtaga tgagctgctg aaagcagata tcatcccatt tgttactctc 360
 aatcactggg acctgcccc aaaaactggaa gatgagggcg gctggccggc ccgttctact 420
 gccgatgctt ttattgaata cacagatgtg atcaccgcgt cccttggcga ccgcgcaaag 480
 aattggatca ctcaaatga acctgccgtc gttgcctgga tgggatactc cactggccaa 540
 cacgcacccg gactgaagga ctatgggctt ggtgcccgcg ccgcgcatca cctgttgctc 600
 tcacatggac aggctgtacc ggtcattcgc agcaatagcg cgggggcaga agtgggaatt 660

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acgctcgata ttagctggcg gatcgctgcc tcaaacagcc gcgccgaccg ggagctggtc      720
cgtgaggatg atgggaggtg gttccgctgg tttgccgacc cgctttacgg gcgcggatat      780
ccctccgata aggtgtctga tttcactaag ttgggagcac tgcccaacgg acttgatttt      840
gtgcaggcag gcgacatgga cacgatcgcg acaccgactg attttatggg gctaaactac      900
tactcccgaa atgtctaccg cgcggaagggt gcagataatg atccgcaaac tgttttccca      960
caaccgaaga tgcccgaaca ctggaccgag atgggctggg aaattttacc ggatgggctg     1020
accaacattc tgggacgcgt ctatttcaac tatcagccgc gcaaactata cgtcacagaa     1080
aacggcgcca gttactccac gcctcctgat gataagggga atgtcgcgga tgaactccgc     1140
atccattatc tgaggacaca ttttgcagct gcctatcggg ccattcaa at gggcgtgcct     1200
ctggcaggat acttcgtctg gtccctcatg gacaactttg agtggtcatg gggctatatg     1260
caacgctttg gactcatctg ggtggattat gagaccctaa aacgcacttt aaaggatagc     1320
gcaaaatggg ataagcgcgt gatcaagaag aatgggctct aa                        1362

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<210> 28
 <211> 453
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (3)...(453)
 <223> Glycosyl hydrolase family 1

<220>
 <221> SITE
 <222> (11)...(25)
 <223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>
 <221> SITE
 <222> (49)...(52)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (361)...(369)
 <223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 28
 Met Ala Asn Lys Ile Thr Phe Pro Glu Asn Phe Leu Trp Gly Ala Ala
 1 5 10 15

Thr Ala Ser Tyr Gln Ile Glu Gly Ala Trp Asn Lys His Gly Lys Gly
 20 25 30

Glu Ser Thr Trp Asp Arg Phe Ser His Thr Pro Gly Lys Ile Arg Asn
35 40 45

Asn Asp Thr Gly Asp Val Ala Asn Asp His Tyr Arg Leu Trp Lys Lys
50 55 60

Asp Ile Gly Leu Met Lys Lys Ile Gly Leu Lys Ala Tyr Arg Phe Ser
65 70 75 80

Ile Ser Trp Pro Arg Ile Leu Pro Ala Gly Arg Gly Lys Val Asn Gln
85 90 95

Arg Gly Leu Asp Phe Tyr Asn Lys Ile Val Asp Glu Leu Leu Lys Ala
100 105 110

Asp Ile Ile Pro Phe Val Thr Leu Asn His Trp Asp Leu Pro Gln Lys
115 120 125

Leu Glu Asp Glu Gly Gly Trp Pro Ala Arg Ser Thr Ala Asp Ala Phe
130 135 140

Ile Glu Tyr Thr Asp Val Ile Thr Arg Ser Leu Gly Asp Arg Ala Lys
145 150 155 160

Asn Trp Ile Thr His Asn Glu Pro Ala Val Val Ala Trp Met Gly Tyr
165 170 175

Ser Thr Gly Gln His Ala Pro Gly Leu Lys Asp Tyr Gly Leu Gly Ala
180 185 190

Arg Ala Ala His His Leu Leu Leu Ser His Gly Gln Ala Val Pro Val
195 200 205

Ile Arg Ser Asn Ser Ala Gly Ala Glu Val Gly Ile Thr Leu Asp Ile
210 215 220

Ser Trp Arg Ile Ala Ala Ser Asn Ser Arg Ala Asp Arg Glu Leu Val
225 230 235 240

Arg Glu Asp Asp Gly Arg Trp Phe Arg Trp Phe Ala Asp Pro Leu Tyr
245 250 255

Gly Arg Gly Tyr Pro Ser Asp Lys Val Ser Asp Phe Thr Lys Leu Gly
260 265 270

Ala Leu Pro Asn Gly Leu Asp Phe Val Gln Ala Gly Asp Met Asp Thr
275 280 285

Ile Ala Thr Pro Thr Asp Phe Met Gly Leu Asn Tyr Tyr Ser Arg Asn
290 295 300

Val Tyr Arg Ala Asp Gly Ala Asp Asn Asp Pro Gln Thr Val Phe Pro
305 310 315 320

Gln Pro Lys Met Pro Glu His Trp Thr Glu Met Gly Trp Glu Ile Tyr
325 330 335

Pro Asp Gly Leu Thr Asn Ile Leu Gly Arg Val Tyr Phe Asn Tyr Gln
340 345 350

Pro Arg Lys Leu Tyr Val Thr Glu Asn Gly Ala Ser Tyr Ser Thr Pro
355 360 365

Pro Asp Asp Lys Gly Asn Val Ala Asp Glu Leu Arg Ile His Tyr Leu
370 375 380

Arg Thr His Phe Ala Ala Ala Tyr Arg Ala Ile Gln Met Gly Val Pro
385 390 395 400

Leu Ala Gly Tyr Phe Val Trp Ser Leu Met Asp Asn Phe Glu Trp Ser
405 410 415

Trp Gly Tyr Met Gln Arg Phe Gly Leu Ile Trp Val Asp Tyr Glu Thr
420 425 430

Gln Lys Arg Thr Leu Lys Asp Ser Ala Lys Trp Tyr Lys Arg Val Ile
435 440 445

Lys Lys Asn Gly Leu
450

<210> 29
<211> 1362
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 29
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cagatcgaag gtgcgtggga caaacatggc aagggtgaat ccatctggga tcgcttttcg 120

catacccctg gcaagatcag aaataatgat acgggcgatg ttgccaatga tcattatcgt 180
ctctggaaaa aagacattgg cttgatgaag aagatcggct tgaaggcata tcgtttttcc 240
atttcgtggc cgcgtgttct tcccgcggga cgcggcaaag tcaatcagaa gggactggat 300
ttctataaca ggctggtaga tgctctgttg aaagaagata tcatcccatt tgtgactctc 360
aatcactggg acctgcccc aagctggag gaggaaggcg gttggccggg tcgctccacc 420
gcagatgcct ttgtggaata cacagacgtg gtcacacggt ccctcggcga ccgcgtaaag 480
aattggatca cgcataatga gcctgccgtc gttgcctgga tgggatattc cacagggtcaa 540
cacgcacccg gtttgaagga ctatgggctt ggtgtgcgcg ccgcgcatca tctgctgctc 600
tcccacgggc aggcggtgcc agtcatccgc agtaacagcg ccgatgcaga agtgggcatt 660
acgctggata ttagctggcg gattcctgcc tccaatagcc gagcagaccg ggaattggtc 720
cgtaaagatg acggactatg gttccgctgg ttcgccgatc cgctttatgg gcgcggatac 780
ccctcggata aagtcaccga ttttaciaaag atcggcgcg cgcgcaatgg tctggacttt 840
atgcaagccg gtgatatgga tgcgatcgcc acgccaaccg atttcatggg gctgaactat 900
tattttccga atgtctaccg cgcgaatggc gaagacaatg atccgcaggt cgttttccca 960
caaccaaaaga tgcccgaaca ctggacggag atgggctggg aaatctatcc ggatggactg 1020
acgaacatcc tgggacgcgt ttattttcaat taccagccac ataaactgta tatcacagag 1080
aacggcgcgga gctactccac cccgcccgat gaaaagggga atgtcgccga tgagctccgc 1140
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ctggcaggat actttgtctg gtccctcatg gacaactttg agtggtcctg gggatatatg 1260
cagcgctttg ggctcatctg ggtggactac gagacacaga aacgcaccct gaaggatagc 1320
gccaagtggg acaaacgtgt gatcaggaag aatgggtttt ag 1362

<210> 30

<211> 453

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (3)...(453)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (11)...(25)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (49)...(52)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (361)...(369)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 30

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Thr	Ala	Ser	Tyr	Gln	Ile	Glu	Gly	Ala	Trp	Asp	Lys	His	Gly	Lys	Gly
			20					25					30		

Glu	Ser	Ile	Trp	Asp	Arg	Phe	Ser	His	Thr	Pro	Gly	Lys	Ile	Arg	Asn
		35					40					45			

Asn	Asp	Thr	Gly	Asp	Val	Ala	Asn	Asp	His	Tyr	Arg	Leu	Trp	Lys	Lys
	50					55					60				

Asp	Ile	Gly	Leu	Met	Lys	Lys	Ile	Gly	Leu	Lys	Ala	Tyr	Arg	Phe	Ser
65					70					75					80

Ile	Ser	Trp	Pro	Arg	Val	Leu	Pro	Ala	Gly	Arg	Gly	Lys	Val	Asn	Gln
				85					90					95	

Lys	Gly	Leu	Asp	Phe	Tyr	Asn	Arg	Leu	Val	Asp	Ala	Leu	Leu	Lys	Glu
			100					105					110		

Asp	Ile	Ile	Pro	Phe	Val	Thr	Leu	Asn	His	Trp	Asp	Leu	Pro	Gln	Lys
		115					120					125			

Leu	Glu	Glu	Glu	Gly	Gly	Trp	Pro	Val	Arg	Ser	Thr	Ala	Asp	Ala	Phe
	130					135					140				

Val	Glu	Tyr	Thr	Asp	Val	Val	Thr	Arg	Ser	Leu	Gly	Asp	Arg	Val	Lys
145					150					155					160

Asn	Trp	Ile	Thr	His	Asn	Glu	Pro	Ala	Val	Val	Ala	Trp	Met	Gly	Tyr
				165					170					175	

Ser	Thr	Gly	Gln	His	Ala	Pro	Gly	Leu	Lys	Asp	Tyr	Gly	Leu	Gly	Val
			180					185					190		

Arg	Ala	Ala	His	His	Leu	Leu	Leu	Ser	His	Gly	Gln	Ala	Val	Pro	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195	200	205
Ile Arg Ser Asn Ser Ala Asp Ala Glu Val Gly Ile Thr Leu Asp Ile 210	215	220
Ser Trp Arg Ile Pro Ala Ser Asn Ser Arg Ala Asp Arg Glu Leu Val 225	230	235 240
Arg Lys Asp Asp Gly Leu Trp Phe Arg Trp Phe Ala Asp Pro Leu Tyr 245	250	255
Gly Arg Gly Tyr Pro Ser Asp Lys Val Thr Asp Phe Thr Lys Ile Gly 260	265	270
Ala Leu Pro Asn Gly Leu Asp Phe Met Gln Ala Gly Asp Met Asp Ala 275	280	285
Ile Ala Thr Pro Thr Asp Phe Met Gly Leu Asn Tyr Tyr Phe Arg Asn 290	295	300
Val Tyr Arg Ala Asn Gly Glu Asp Asn Asp Pro Gln Val Val Phe Pro 305	310	315 320
Gln Pro Lys Met Pro Glu His Trp Thr Glu Met Gly Trp Glu Ile Tyr 325	330	335
Pro Asp Gly Leu Thr Asn Ile Leu Gly Arg Val Tyr Phe Asn Tyr Gln 340	345	350
Pro His Lys Leu Tyr Ile Thr Glu Asn Gly Ala Ser Tyr Ser Thr Pro 355	360	365
Pro Asp Glu Lys Gly Asn Val Ala Asp Glu Leu Arg Thr His Tyr Leu 370	375	380
Arg Thr His Phe Ala Ala Ala Tyr Arg Ala Ile Gln Met Gly Val Pro 385	390	395 400
Leu Ala Gly Tyr Phe Val Trp Ser Leu Met Asp Asn Phe Glu Trp Ser 405	410	415
Trp Gly Tyr Met Gln Arg Phe Gly Leu Ile Trp Val Asp Tyr Glu Thr 420	425	430
Gln Lys Arg Thr Leu Lys Asp Ser Ala Lys Trp Tyr Lys Arg Val Ile 435	440	445

Arg Lys Asn Gly Phe
450

<210> 31
<211> 1167
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 31
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aaggacccgg tcgagggcgt gtctgtgctg gatcacgtta aacgggcctt gacctttacc 180
cgcaacaaca tcgggaaaca tgggtctgcct ctctcggct ttgcggattg gaacgacacg 240
atcaatctgg cgaagggcgc cgagtctctt ttcacgtcgc atctatatgg acgcgcgctg 300
ctggagttta ttgatctgct cacatatctt ggcaagaacg atgaagccga tgaatggcag 360
cgagcccacg ttgagatgca gtcccgcgtc gaaaaacatg cctgggatgg cgaatgggat 420
ttcatgtact ttgaccacga cggcagcccg gttgggtctc acacgaatca gtatggaaag 480
atccatctca acggacagag ctgggctgtg ctttcgggct ttgcctctcc gcagcgcgcc 540
cgccaggcca tggactcggg ttacaagcat ctcaacacaa agcacggcat caagctctcc 600
acgccgggct acaatggcta tgaccccaac tacggcggcg tgaccaccta cccaccggga 660
gcaaaggaaa acggcggcat cttcctgcac ccgaatccct gggccatgat cgcagagacc 720
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tgctatcagg ctgccacaca gtggatcctc ggaatccgcg ccgactatga agggctgcgc 960
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gtgaacgtgg aagttacctt aggataa 1167

<210> 32
<211> 388
<212> PRT
<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SITE

<222> (79)...(82)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (349)...(352)

<223> N-glycosylation site. Prosite id = PS00001

<400> 32

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1 5 10 15

Leu Cys Val Thr Ala Tyr Ile Lys Glu Thr Gly Asp Phe Ala Phe Leu
20 25 30

Asp Glu Lys Val His Phe Tyr Glu Lys Asp Pro Val Glu Gly Val Ser
35 40 45

Val Leu Asp His Val Lys Arg Ala Leu Thr Phe Thr Arg Asn Asn Ile
50 55 60

Gly Lys His Gly Leu Pro Leu Leu Gly Phe Ala Asp Trp Asn Asp Thr
65 70 75 80

Ile Asn Leu Ala Lys Gly Ala Glu Ser Leu Phe Thr Ser His Leu Tyr
85 90 95

Gly Arg Ala Leu Leu Glu Phe Ile Asp Leu Leu Thr Tyr Leu Gly Lys
100 105 110

Asn Asp Glu Ala Asp Glu Trp Gln Arg Ala His Val Glu Met Gln Ser
115 120 125

Arg Val Glu Lys His Ala Trp Asp Gly Glu Trp Tyr Phe Met Tyr Phe
130 135 140

Asp His Asp Gly Ser Pro Val Gly Ser His Thr Asn Gln Tyr Gly Lys
145 150 155 160

Ile His Leu Asn Gly Gln Ser Trp Ala Val Leu Ser Gly Phe Ala Ser
165 170 175

Pro Gln Arg Ala Arg Gln Ala Met Asp Ser Val Tyr Lys His Leu Asn
180 185 190

Thr Lys His Gly Ile Lys Leu Ser Thr Pro Gly Tyr Asn Gly Tyr Asp
 195 200 205

Pro Asn Tyr Gly Gly Val Thr Thr Tyr Pro Pro Gly Ala Lys Glu Asn
 210 215 220

Gly Gly Ile Phe Leu His Pro Asn Pro Trp Ala Met Ile Ala Glu Thr
 225 230 235 240

Met Leu Gly Asp Gly Asp Arg Ala Tyr Glu Tyr Tyr Ser Gln Ile Asn
 245 250 255

Pro Ala Gly Lys Asn Asp Asp Ile Asp Leu Tyr Glu Val Glu Pro Tyr
 260 265 270

Val Tyr Ala Gln Asn Ile Leu Gly Asp Glu His Pro Gln Phe Gly Leu
 275 280 285

Gly Arg Asn Ser Trp Leu Ser Gly Thr Ala Ser Trp Cys Tyr Gln Ala
 290 295 300

Ala Thr Gln Trp Ile Leu Gly Ile Arg Ala Asp Tyr Glu Gly Leu Arg
 305 310 315 320

Ile Asp Pro Cys Ile Pro Ser Lys Trp Asp Gly Phe Lys Ala Thr Arg
 325 330 335

Leu Tyr Arg Gly Val Lys Tyr Asn Ile Thr Val Thr Asn Pro Lys His
 340 345 350

Ile Cys Lys Gly Val Glu Lys Val Leu Val Asn Gly Lys Pro Val Glu
 355 360 365

Gly Asn Val Val Arg Ala Asp Val Gly Leu Arg Glu Val Asn Val Glu
 370 375 380

Val Thr Leu Gly
 385

<210> 33
 <211> 1362
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 33

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cagatcgagg gggcttggga taaacatggg aagggcgagt cgacctggga ccgtttttacg 120
catacacctg gaaagatcaa aaacaatgat acgggcgatg tagcagatga ccattatcga 180
ttatggaaaa aagatatcgg cttgatgaag aagctcggct tgaaggctta tcgttttttcg 240
acttcctggc cgcgggtgct gccggccggg cgcggtaaga gcaatcaaaa aggactcgat 300
ttctacagca agctgggttg tgagttgcta aaagcaaata tcatcccatt cgtgacattg 360
aatcactggg acatcccaca aaagttggag gacgaggggtg gctggggccgt gcgctcaacg 420
gctgaggcat ttgtggaata tgccgatctc atgtcgcgca cgcttggaga ccgcgtcaag 480
aactggatca cgcacaacga accggccgtc gtcgcctgga tgggatacgg gatgggcatc 540
cacgcgccgg gcttaacgga tttctcgatt gcgggtgccg tctcgcatca tctgctcctt 600
tcgcacggat gggccgtgcc tgtgattcgc ggtaacagcc cggatgccga ggtgggcatt 660
accctcaaca ttcaatgggg cgaagcagca tccaacagcc gggccgacct aaacgccctg 720
cgctgaacg atggacagtg gttccgctgg tttgccgatc cggtttatgg ccgcggctat 780
ccttccgacg tgggtggctga tttcgagaaa atgggcgcgc tgccgaacgg catgaatttc 840
gtgcaacctg gcgatatgga tgtcatcgcc acgccaaccg atttcctcgg gctcaattat 900
tattcccgcc atgtgcatcg cgtcaacaca ccggataacg atcaacaggt tgtgtttgcc 960
aaacagcagg gtcccgagaa ctggaccgag atgggctggg agatccatcc tgatggattg 1020
gccggaatth tatccagagc gtattttcaat taccagccgc gcaaagtata tgtgactgaa 1080
aacggtgcca gctattccac cgcgcccgat gagaatggta ttgtcaacga cattcacgcg 1140
gtcaattatc tacggacgca cttcgcggct gcccatcgcg ccctgcaggc gggcgtgcca 1200
ttggcaggat acttcgtctg gtcaatgctc gataacttcg aatggagtca cgggtacagc 1260
cagcgctttg gcatcgttta tgtggactat caaaccagaa agcgttactt gaaagacagc 1320
gccaagtggg acaaagggtg catcaaaaag aatgggttct aa 1362

<210> 34

<211> 453

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (3)...(453)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (11)...(25)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (49)...(52)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (332)...(335)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (361)...(369)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 34

Met	Ala	Asn	Lys	Ile	Leu	Phe	Pro	Glu	Asn	Phe	Leu	Trp	Gly	Thr	Ala
1				5					10					15	

Thr	Ala	Ser	Tyr	Gln	Ile	Glu	Gly	Ala	Trp	Asp	Lys	His	Gly	Lys	Gly
			20					25					30		

Glu	Ser	Thr	Trp	Asp	Arg	Phe	Thr	His	Thr	Pro	Gly	Lys	Ile	Lys	Asn
		35					40					45			

Asn	Asp	Thr	Gly	Asp	Val	Ala	Asp	Asp	His	Tyr	Arg	Leu	Trp	Lys	Lys
	50					55					60				

Asp	Ile	Gly	Leu	Met	Lys	Lys	Leu	Gly	Leu	Lys	Ala	Tyr	Arg	Phe	Ser
65					70					75					80

Thr	Ser	Trp	Pro	Arg	Val	Leu	Pro	Ala	Gly	Arg	Gly	Lys	Ser	Asn	Gln
				85					90					95	

Lys	Gly	Leu	Asp	Phe	Tyr	Ser	Lys	Leu	Val	Asp	Glu	Leu	Leu	Lys	Ala
		100						105					110		

Asn	Ile	Ile	Pro	Phe	Val	Thr	Leu	Asn	His	Trp	Asp	Ile	Pro	Gln	Lys
		115					120					125			

Leu	Glu	Asp	Glu	Gly	Gly	Trp	Ala	Val	Arg	Ser	Thr	Ala	Glu	Ala	Phe
	130					135					140				

Val	Glu	Tyr	Ala	Asp	Leu	Met	Ser	Arg	Thr	Leu	Gly	Asp	Arg	Val	Lys
145					150					155					160

Asn	Trp	Ile	Thr	His	Asn	Glu	Pro	Ala	Val	Val	Ala	Trp	Met	Gly	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

165

170

175

Gly Met Gly Ile His Ala Pro Gly Leu Thr Asp Phe Ser Ile Ala Val
 180 185 190

Pro Val Ser His His Leu Leu Leu Ser His Gly Trp Ala Val Pro Val
 195 200 205

Ile Arg Gly Asn Ser Pro Asp Ala Glu Val Gly Ile Thr Leu Asn Ile
 210 215 220

Gln Trp Gly Glu Ala Ala Ser Asn Ser Arg Ala Asp Leu Asn Ala Leu
 225 230 235 240

Arg Leu Asn Asp Gly Gln Trp Phe Arg Trp Phe Ala Asp Pro Val Tyr
 245 250 255

Gly Arg Gly Tyr Pro Ser Asp Val Val Ala Asp Phe Glu Lys Met Gly
 260 265 270

Ala Leu Pro Asn Gly Met Asn Phe Val Gln Pro Gly Asp Met Asp Val
 275 280 285

Ile Ala Thr Pro Thr Asp Phe Leu Gly Leu Asn Tyr Tyr Ser Arg His
 290 295 300

Val His Arg Val Asn Thr Pro Asp Asn Asp Gln Gln Val Val Phe Ala
 305 310 315 320

Lys Gln Gln Gly Pro Glu Asn Trp Thr Glu Met Gly Trp Glu Ile His
 325 330 335

Pro Asp Gly Leu Ala Gly Ile Leu Ser Arg Ala Tyr Phe Asn Tyr Gln
 340 345 350

Pro Arg Lys Val Tyr Val Thr Glu Asn Gly Ala Ser Tyr Ser Thr Ala
 355 360 365

Pro Asp Glu Asn Gly Ile Val Asn Asp Ile His Arg Val Asn Tyr Leu
 370 375 380

Arg Thr His Phe Ala Ala Ala His Arg Ala Leu Gln Ala Gly Val Pro
 385 390 395 400

Leu Ala Gly Tyr Phe Val Trp Ser Met Leu Asp Asn Phe Glu Trp Ser
 405 410 415

His Gly Tyr Ser Gln Arg Phe Gly Ile Val Tyr Val Asp Tyr Gln Thr
 420 425 430

Gln Lys Arg Tyr Leu Lys Asp Ser Ala Lys Trp Tyr Lys Gly Val Ile
 435 440 445

Lys Lys Asn Gly Phe
 450

<210> 35

<211> 1116

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 35

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tggctctctc	aagtgaatga	aaacattccc	gaccgttcca	cctatgtgac	ggagcgggat	180
ttgcaatttc	tgcgggcagc	cggtttcgac	catgtgcgtc	tgccaatcga	tgaggtcgaa	240
ctctgggatg	aagagggcaa	tcagatcgag	gaggcctggc	aatacatgca	taactttctc	300
cgttggagcc	gaaagaacga	tctccgggtc	attctcgacc	tgcacacggt	attgtcccac	360
cacttcaacg	cggtaaatat	gggagaggtc	aatacactct	tcaatgatcc	cagggaacag	420
gaaaagttcc	tcaacctatg	ggaacaaatc	atggatgccg	tgggtcacca	tccgaatgag	480
tttctcgcct	atgaaatgct	caatgaggcg	gtcgcggaag	atgatgaaga	ctggaatctg	540
ctcctcaacc	gcgccattgt	ccgcatccgg	gaccgtgagc	cttatcgggt	gctgattgcg	600
gggtcgaact	ggtggcagca	tgccgaccgg	gtccccaacc	tgaggctccc	gaaaggagac	660
cccaatatca	tcatcagttt	tcatttttat	tccccttttc	tcttcaccca	ctaccgcagt	720
agctggactg	cgatgcaggc	gtaccagggc	ttcgtccaat	accctggcaa	aaccatacct	780
tccatacatc	tcgaaggcat	gaactaccgc	gagtccttcg	ttcatatgtg	ggaagcgcac	840
aatcgggtact	atgacatcca	ttccatgtat	gccgaaatgg	tcccggcggt	gcgtttttgcc	900
gaaaagttgg	gacttcggct	ctattgcgga	gaattcgggg	ccatgaagac	cgttgatcgc	960
gcccagatgc	tgcagtggta	tcgggatgtt	gtcactgtat	ttaataaatt	gggtattccc	1020
tatactgcct	gggattatca	gggaaccttc	ggaatccgcg	atgagctgac	cggtgagccc	1080
gatcatgaaa	tgatcgatat	tctcctcggg	cgctga			1116

<210> 36
 <211> 371
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SIGNAL
 <222> (1)...(23)

<220>
 <221> DOMAIN
 <222> (39)...(350)
 <223> Cellulase (glycosyl hydrolase family 5)

<220>
 <221> SITE
 <222> (37)...(40)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 36
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 1 5 10 15

Ile Cys Pro Ala Leu Gln Ala Glu Pro Val Glu Thr Tyr Phe Pro Leu
 20 25 30

Ser Arg Gly Ile Asn Met Ser His Trp Leu Ser Gln Val Asn Glu Asn
 35 40 45

Ile Pro Asp Arg Ser Thr Tyr Val Thr Glu Arg Asp Leu Gln Phe Leu
 50 55 60

Arg Ala Ala Gly Phe Asp His Val Arg Leu Pro Ile Asp Glu Val Glu
 65 70 75 80

Leu Trp Asp Glu Glu Gly Asn Gln Ile Glu Glu Ala Trp Gln Tyr Met
 85 90 95

His Asn Phe Leu Arg Trp Ser Arg Lys Asn Asp Leu Arg Val Ile Leu
 100 105 110

Asp Leu His Thr Val Leu Ser His His Phe Asn Ala Val Asn Met Gly
 115 120 125

Glu Val Asn Thr Leu Phe Asn Asp Pro Arg Glu Gln Glu Lys Phe Leu
 130 135 140

Asn Leu Trp Glu Gln Ile Met Asp Ala Val Gly His His Pro Asn Glu
 145 150 155 160

Phe Leu Ala Tyr Glu Met Leu Asn Glu Ala Val Ala Glu Asp Asp Glu
165 170 175

Asp Trp Asn Leu Leu Leu Asn Arg Ala Ile Val Arg Ile Arg Asp Arg
180 185 190

Glu Pro Tyr Arg Val Leu Ile Ala Gly Ser Asn Trp Trp Gln His Ala
195 200 205

Asp Arg Val Pro Asn Leu Arg Leu Pro Lys Gly Asp Pro Asn Ile Ile
210 215 220

Ile Ser Phe His Phe Tyr Ser Pro Phe Leu Phe Thr His Tyr Arg Ser
225 230 235 240

Ser Trp Thr Ala Met Gln Ala Tyr Gln Gly Phe Val Gln Tyr Pro Gly
245 250 255

Lys Thr Ile Pro Ser Ile His Leu Glu Gly Met Asn Tyr Pro Glu Ser
260 265 270

Phe Val His Met Trp Glu Ala His Asn Arg Tyr Tyr Asp Ile His Ser
275 280 285

Met Tyr Ala Glu Met Val Pro Ala Val Arg Phe Ala Glu Lys Leu Gly
290 295 300

Leu Arg Leu Tyr Cys Gly Glu Phe Gly Ala Met Lys Thr Val Asp Arg
305 310 315 320

Ala Gln Met Leu Gln Trp Tyr Arg Asp Val Val Thr Val Phe Asn Lys
325 330 335

Leu Gly Ile Pro Tyr Thr Ala Trp Asp Tyr Gln Gly Thr Phe Gly Ile
340 345 350

Arg Asp Glu Leu Thr Gly Glu Pro Asp His Glu Met Ile Asp Ile Leu
355 360 365

Leu Gly Arg
370

<210> 37

<211> 1383

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 37

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gcggtttatc ggatgcacaa cggggatatg gcctgcgac attatcatcg gtatcgaacg	180
gatatcgagc tgatgcagaa gatcggccta gaggttacc gcttttccat aaactggccc	240
cgggttctgc cggaagggac cgggtgccgc aatgaagcag gtctggactt ttacgaccgg	300
ctggtggacg cactgttga agcgggaatt cagccttga tcaccttta tcactgggaa	360
ctccctggg ctctccacct gcgcgggggt tggctcaatc gggacatgcc cgaccacatt	420
gagaactacg ccgccttggc gccaggtgc ctcggtgacc gggtgaaaaa ctggattact	480
ttgaatgagc ctcaggtttt catcgggctt ggctatgcca gcgggggttca tgcccccggc	540
tataagttgt ccttgccgga gtgcctggtc ggttcccacc atgccgtgct ttcccaccac	600
cgggcagtca aggcgatccg ggccaactgc gaaggcagcg tccagatcgg ctcagccccg	660
gtgggtgttg tctgccgacc ggaaacggag tcggcagcag acattgaggc tgcccgccag	720
gccacctacc atatcaacac tcccagcacc cacactcccg acaatctgat cggctgcctc	780
tggaacagca cttggtggat agatccaatg gttctgggga agtatccgga acacgggctg	840
aaagcctttg aaagctatct gccggacaac attcaggccg aactggatgc cgtattcgaa	900
ccgacggact ttgtcggttc caacatctac cacggccgca cggtgccggc caagcaggat	960
ggtggttttg agtttatcga ctttccgccc ggcagcccc gcaccaccat gggctgggac	1020
atcccccg acatcctcta ctggggagga aagtatcttt acgaacgcta tggcaagccg	1080
atgtttatca cggaaaacgg cattgccgtc ccggaactgg tgaatgatga aggccaggtc	1140
gaggataccg tccgtgagca atacatgaag ctgcacctgc gtgggctgca gcgggcccgc	1200
gatgaaggca tcccctatgc cggatacttc cactggtccc tgctcgacaa cttcgagtgg	1260
gaacaaggct actcccagcg ctttggcatg gtctacgtcg actaccagac ccaggaacgt	1320
atcctcaaac gttcgggcca gcatttcgct gccatcgtcc gggaaatcac cggaaccgcc	1380
taa	1383

<210> 38

<211> 460

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (1)...(458)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (7)...(21)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (266)...(269)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (366)...(374)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 38

Met	Ser	Lys	Leu	Pro	Lys	Phe	Leu	Phe	Gly	Ala	Gly	Thr	Ser	Ser	Tyr
1				5					10					15	

Gln	Ile	Glu	Gly	Ala	Trp	Asn	Ile	Asp	Gly	Lys	Gly	Pro	Ser	Ile	Trp
		20						25					30		

Asp	Phe	His	Thr	Arg	His	Pro	Gly	Ala	Val	Tyr	Arg	Met	His	Asn	Gly
		35					40					45			

Asp	Met	Ala	Cys	Asp	His	Tyr	His	Arg	Tyr	Arg	Thr	Asp	Ile	Glu	Leu
	50					55					60				

Met	Gln	Lys	Ile	Gly	Leu	Glu	Ala	Tyr	Arg	Phe	Ser	Ile	Asn	Trp	Pro
65				70						75				80	

Arg	Val	Leu	Pro	Glu	Gly	Thr	Gly	Ala	Ala	Asn	Glu	Ala	Gly	Leu	Asp
				85				90						95	

Phe	Tyr	Asp	Arg	Leu	Val	Asp	Ala	Leu	Leu	Glu	Ala	Gly	Ile	Gln	Pro
			100					105					110		

Trp	Ile	Thr	Leu	Tyr	His	Trp	Glu	Leu	Pro	Trp	Ala	Leu	His	Leu	Arg
		115					120					125			

Gly	Gly	Trp	Leu	Asn	Arg	Asp	Met	Pro	Asp	His	Ile	Glu	Asn	Tyr	Ala
	130					135					140				

Ala	Leu	Val	Ala	Arg	Cys	Leu	Gly	Asp	Arg	Val	Lys	Asn	Trp	Ile	Thr
145					150					155					160

Leu Asn Glu Pro Gln Val Phe Ile Gly Leu Gly Tyr Ala Ser Gly Val
 165 170 175

His Ala Pro Gly Tyr Lys Leu Ser Leu Arg Glu Cys Leu Val Gly Ser
 180 185 190

His His Ala Val Leu Ser His His Arg Ala Val Lys Ala Ile Arg Ala
 195 200 205

Asn Cys Glu Gly Ser Val Gln Ile Gly Ser Ala Pro Val Gly Val Val
 210 215 220

Cys Arg Pro Glu Thr Glu Ser Ala Ala Asp Ile Glu Ala Ala Arg Gln
 225 230 235 240

Ala Thr Tyr His Ile Asn Thr Pro Ser Thr His Thr Pro Asp Asn Leu
 245 250 255

Ile Gly Cys Leu Trp Asn Ser Thr Trp Trp Ile Asp Pro Met Val Leu
 260 265 270

Gly Lys Tyr Pro Glu His Gly Leu Lys Ala Phe Glu Ser Tyr Leu Pro
 275 280 285

Asp Asn Ile Gln Ala Glu Leu Asp Ala Val Phe Glu Pro Thr Asp Phe
 290 295 300

Val Gly Ser Asn Ile Tyr His Gly Arg Thr Val Arg Ala Lys Gln Asp
 305 310 315 320

Gly Gly Phe Glu Phe Ile Asp Leu Pro Pro Gly Ser Pro Arg Thr Thr
 325 330 335

Met Gly Trp Asp Ile Thr Pro Asp Ile Leu Tyr Trp Gly Gly Lys Tyr
 340 345 350

Leu Tyr Glu Arg Tyr Gly Lys Pro Met Phe Ile Thr Glu Asn Gly Ile
 355 360 365

Ala Val Pro Glu Leu Val Asn Asp Glu Gly Gln Val Glu Asp Thr Val
 370 375 380

Arg Glu Gln Tyr Met Lys Leu His Leu Arg Gly Leu Gln Arg Ala Arg
 385 390 395 400

Asp Glu Gly Ile Pro Tyr Ala Gly Tyr Phe His Trp Ser Leu Leu Asp
 405 410 415

Asn Phe Glu Trp Glu Gln Gly Tyr Ser Gln Arg Phe Gly Met Val Tyr
 420 425 430

Val Asp Tyr Gln Thr Gln Glu Arg Ile Leu Lys Arg Ser Gly Gln His
 435 440 445

Phe Ala Ala Ile Val Arg Glu Ile Thr Gly Thr Ala
 450 455 460

<210> 39
 <211> 1521
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 39
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 ctcgagatca ccgagatctg cgatcgacc ctgcgcgccc gcggcccggc gctgctgttc 180
 gagaacgtca agggggcacga catgcctctg ctgggcaacc tcttcggcac gccgaagcgg 240
 gttgccctcg gcatgggcca ggactccgtg gccgccctgc gcgaagtggg cgagctgctc 300
 gccttcctca aggagccgga gcctcccaag ggctttcgcg acgcctggga caagctgccg 360
 atcttcaagc aggtgatgag catggggccg aagaaggctc gctcggcgcc ggtgcaggaa 420
 aaggtgtacg agggcgacga ggtcgacctc gaccgcctgc cgatccagca ctgctggccc 480
 ggcgacgccc cgcccctggt cacctggccc ctggtgatca cccgcggggc ccacaagaag 540
 cgccagaacc tcggcatcta ccgccagcag aagctgtcga agaaccggct gatcatgcgc 600
 tggctctccc accgcggcgg ggcgctggac ttcttgaggt tccagaaggc ccaccccggc 660
 gagcccttcc cgggtggcggg ggcgctgggc gccgaccgga cgaccatcct cggcgcggtg 720
 accccgggtgc cggattcgct ctccgagtac gccttcgccc ggctgctgcg cggctcgcgc 780
 accgagctgg tcaagtgcgg ccacgccgac ctggacgtgc cggcctcggc ggagatcatc 840
 ctggaggggt tcatctaccc ggatgacatg gccccgagg gccctacgg cgaccatacc 900
 ggctactaca acgaggtgga taccttcccg gtcttcacgg tgacgcgtat gaccatgcgc 960
 cgcgatgcc a tctatcactc cacctacacc ggccggccgc ccgacgagcc ggcgatcctt 1020
 gggctggcgc tcaacgaggt gttcgtgccg atcctgcgcc gccagttccc ggagatcgtc 1080

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gacttctacc tgccgcccga gggctgctcc taccgcatgg cggtggtgac catgaagaag 1140
cagtacccgg gccacgcca gcggtgatg atgggcgtgt ggagcttcct gcgccagttc 1200
atgtacacca agttcgtggg ggtgctcgac gacgacgtca gcgcccgga ctgggaggac 1260
gtgatctggg ccatcaccac ccgcatggac ccggcccggg acaccgtggg ggtggagAAC 1320
acccccatcg actacctgga cttcgctcgc ccggtctccg gcctcggttc caagatgggc 1380
ctggatgcca ccagcaagtg gcccggcgag accgaccgcg agtggggggg gcccatcgtc 1440
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cccgacaaca cgacccctg a 1521

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<210> 40
 <211> 506
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (21)...(445)
 <223> 3-octaprenyl-4-hydroxybenzoate carboxy-lyase

<220>
 <221> SITE
 <222> (5)...(8)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 40
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 1 5 10 15

Pro Val Glu Phe Ile Ser Ala Leu Glu Ala Arg Gly Glu Leu Gln Arg
 20 25 30

Ile Thr Ala Glu Val Asp Pro Tyr Leu Glu Ile Thr Glu Ile Cys Asp
 35 40 45

Arg Thr Leu Arg Ala Gly Gly Pro Ala Leu Leu Phe Glu Asn Val Lys
 50 55 60

Gly His Asp Met Pro Leu Leu Gly Asn Leu Phe Gly Thr Pro Lys Arg
 65 70 75 80

Val Ala Leu Gly Met Gly Gln Asp Ser Val Ala Ala Leu Arg Glu Val
 85 90 95

Gly Glu Leu Leu Ala Phe Leu Lys Glu Pro Glu Pro Pro Lys Gly Phe

100					105					110					
Arg	Asp	Ala	Trp	Asp	Lys	Leu	Pro	Ile	Phe	Lys	Gln	Val	Met	Ser	Met
		115					120					125			
Gly	Pro	Lys	Lys	Val	Arg	Ser	Ala	Pro	Val	Gln	Glu	Lys	Val	Tyr	Glu
	130					135					140				
Gly	Asp	Glu	Val	Asp	Leu	Asp	Arg	Leu	Pro	Ile	Gln	His	Cys	Trp	Pro
145					150					155					160
Gly	Asp	Ala	Ala	Pro	Leu	Val	Thr	Trp	Pro	Leu	Val	Ile	Thr	Arg	Gly
				165					170					175	
Pro	His	Lys	Lys	Arg	Gln	Asn	Leu	Gly	Ile	Tyr	Arg	Gln	Gln	Lys	Leu
			180					185					190		
Ser	Lys	Asn	Arg	Leu	Ile	Met	Arg	Trp	Leu	Ser	His	Arg	Gly	Gly	Ala
		195					200					205			
Leu	Asp	Phe	Leu	Glu	Phe	Gln	Lys	Ala	His	Pro	Gly	Glu	Pro	Phe	Pro
	210					215					220				
Val	Ala	Val	Ala	Leu	Gly	Ala	Asp	Pro	Ala	Thr	Ile	Leu	Gly	Ala	Val
225					230					235					240
Thr	Pro	Val	Pro	Asp	Ser	Leu	Ser	Glu	Tyr	Ala	Phe	Ala	Gly	Leu	Leu
				245					250					255	
Arg	Gly	Ser	Arg	Thr	Glu	Leu	Val	Lys	Cys	Gly	His	Ala	Asp	Leu	Asp
			260					265					270		
Val	Pro	Ala	Ser	Ala	Glu	Ile	Ile	Leu	Glu	Gly	Phe	Ile	Tyr	Pro	Asp
		275					280					285			
Asp	Met	Ala	Pro	Glu	Gly	Pro	Tyr	Gly	Asp	His	Thr	Gly	Tyr	Tyr	Asn
	290					295					300				
Glu	Val	Asp	Thr	Phe	Pro	Val	Phe	Thr	Val	Thr	Arg	Met	Thr	Met	Arg
305					310					315					320
Arg	Asp	Ala	Ile	Tyr	His	Ser	Thr	Tyr	Thr	Gly	Arg	Pro	Pro	Asp	Glu
			325						330					335	
Pro	Ala	Ile	Leu	Gly	Leu	Ala	Leu	Asn	Glu	Val	Phe	Val	Pro	Ile	Leu
			340					345					350		

Arg Arg Gln Phe Pro Glu Ile Val Asp Phe Tyr Leu Pro Pro Glu Gly
355 360 365

Cys Ser Tyr Arg Met Ala Val Val Thr Met Lys Lys Gln Tyr Pro Gly
370 375 380

His Ala Lys Arg Val Met Met Gly Val Trp Ser Phe Leu Arg Gln Phe
385 390 395 400

Met Tyr Thr Lys Phe Val Val Val Leu Asp Asp Asp Val Ser Ala Arg
405 410 415

Asp Trp Glu Asp Val Ile Trp Ala Ile Thr Thr Arg Met Asp Pro Ala
420 425 430

Arg Asp Thr Val Val Val Glu Asn Thr Pro Ile Asp Tyr Leu Asp Phe
435 440 445

Ala Ser Pro Val Ser Gly Leu Gly Ser Lys Met Gly Leu Asp Ala Thr
450 455 460

Ser Lys Trp Pro Gly Glu Thr Asp Arg Glu Trp Gly Val Pro Ile Val
465 470 475 480

Met Asp Glu Ala Val Lys Ala Arg Val Ser Glu Arg Trp Asn Glu Leu
485 490 495

Gly Ile Glu Leu Pro Asp Asn Thr Thr Pro
500 505

<210> 41
<211> 1410
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 41
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ggcaattttcc gcaccttcat cattcaggac gtgctgcgac gcgttatcga agggtcgggc 180
ctcaaaacga gacacgtacg caacatcacc gatgtggacg acaaaaccat ccgccaatcg 240
caagcgggaag gaaaatctct gaaaatcttc acagggtact ggctggaacg gttccacgcc 300

gattgcgacg cgctgaatct gctgcgcccg cacgtcgagc ccggcgccgt tgaccatata 360
ccggcgcaaa tccggatgat cgaacaactg atcgaaaaag gccacgccta cgtggcggac 420
gacaactcgg tctattatcg cgttgcttcg ttogaagcgt acggccgggt gtcacgcctg 480
caagaacgac acatcaccac cggctgcgcc gaacacgcgc ataccgacga tgaatacgag 540
cgcgaaatcgg ccgcccactt cgccttgtgg aaagcgcata aatccgagga cggcccgaac 600
gcgtggccga gcccgtgggg cgacggacga cccggctggc acatcgagtg cagcgccatg 660
tccgtcgagt atctgggcga gacattcgat ctgcacggcg gcggcggtga cctgaccttc 720
ccccaccacg aaaacgaaat cgcgcaaagc gaagccgcca ccggcaagcc cttcgcgcgt 780
atctgggttc attccgcgca tctcatggtc gaaggccaca agatgtccaa gagcctcggc 840
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gcgcaaagcg ccttacgccg cctgcgtcag ctcaaccacg atctccagca ggccggcggc 1020
aagacggtcg cgcccgtga tacttcgtgg gggccgttcg aaccggtgta cgacgcgctt 1080
gccgacaacc tgaacacgcc cgacgccctc ggccgcttat tctccgccct gcacagcata 1140
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ttcctgcggg tcatggacct ttctcggttc agcctggacg cgccgccgac cgccgaagcg 1260
cccgaagaag tgcgtgcgct ggcgacgacg cgatgggacg ctaaacaagc gcgcgatttc 1320
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aaagacggct acgaactcgt ccaagagtaa 1410

<210> 42

<211> 469

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (16)...(323)

<223> tRNA synthetases class I (C) catalytic domain

<220>

<221> SITE

<222> (69)...(72)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (316)...(319)

<223> N-glycosylation site. Prosite id = PS00001

<400> 42

Met Lys Thr Pro Ser Ile Tyr Asp Thr Met Thr Arg Ser Val Gln Pro
 1 5 10 15

Leu Thr Pro Ala Asp Gly Asp Thr Phe Arg Phe Tyr Cys Cys Gly Pro
 20 25 30

Thr Val Tyr Gly Pro Ala His Val Gly Asn Phe Arg Thr Phe Ile Ile
 35 40 45

Gln Asp Val Leu Arg Arg Val Ile Glu Gly Ser Gly Leu Lys Thr Arg
 50 55 60

His Val Arg Asn Ile Thr Asp Val Asp Asp Lys Thr Ile Arg Gln Ser
 65 70 75 80

Gln Ala Glu Gly Lys Ser Leu Lys Ile Phe Thr Gly Tyr Trp Leu Glu
 85 90 95

Arg Phe His Ala Asp Cys Asp Ala Leu Asn Leu Leu Arg Pro His Val
 100 105 110

Glu Pro Gly Ala Val Asp His Ile Pro Ala Gln Ile Arg Met Ile Glu
 115 120 125

Gln Leu Ile Glu Lys Gly His Ala Tyr Val Ala Asp Asp Asn Ser Val
 130 135 140

Tyr Tyr Arg Val Ala Ser Phe Glu Ala Tyr Gly Arg Leu Ser Arg Leu
 145 150 155 160

Gln Glu Arg His Ile Thr Thr Gly Cys Ala Glu His Ala His Thr Asp
 165 170 175

Asp Glu Tyr Glu Arg Glu Ser Ala Ala Asp Phe Ala Leu Trp Lys Ala
 180 185 190

His Lys Ser Glu Asp Gly Pro Asn Ala Trp Pro Ser Pro Trp Gly Asp
 195 200 205

Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ala Met Ser Val Glu Tyr
 210 215 220

Leu Gly Glu Thr Phe Asp Leu His Gly Gly Gly Val Asp Leu Thr Phe
 225 230 235 240

Pro His His Glu Asn Glu Ile Ala Gln Ser Glu Ala Ala Thr Gly Lys
245 250 255

Pro Phe Ala Arg Ile Trp Phe His Ser Ala His Leu Met Val Glu Gly
260 265 270

His Lys Met Ser Lys Ser Leu Gly Asn Leu Phe Thr Leu Asp Asp Ile
275 280 285

Arg Ala Arg Gly Phe Asp Ala Met Thr Leu Arg Tyr Val Leu Leu Ser
290 295 300

Gly Asn Tyr Arg Gln Pro Leu Asn Phe Thr Trp Asp Ser Leu Asn Ala
305 310 315 320

Ala Gln Ser Ala Leu Arg Arg Leu Arg Gln Leu Asn His Asp Leu Gln
325 330 335

Gln Ala Ala Gly Lys Thr Val Ala Pro Ala Asp Thr Ser Trp Gly Pro
340 345 350

Phe Glu Pro Val Tyr Asp Ala Leu Ala Asp Asn Leu Asn Thr Pro Asp
355 360 365

Ala Leu Gly Arg Leu Phe Ser Ala Leu His Ser Ile Glu Arg Ala Leu
370 375 380

Asn Gly Lys Glu Arg Thr Ala Glu Glu Ala Ala Leu Ala Arg Ala Gln
385 390 395 400

Phe Leu Arg Val Met Asp Leu Phe Gly Phe Ser Leu Asp Ala Pro Pro
405 410 415

Thr Ala Glu Ala Pro Glu Glu Val Arg Ala Leu Ala Gln Gln Arg Trp
420 425 430

Asp Ala Lys Gln Ala Arg Asp Phe Val Arg Ala Asp Ala Leu Arg Lys
435 440 445

Gln Val Thr Asp Leu Gly Trp Thr Ile Arg Asp Ala Lys Asp Gly Tyr
450 455 460

Glu Leu Val Gln Glu
465

<211> 984
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 43
atgacgactg aaaccaaata caaactgtac ttgcataaag tgaacggcca gaaaggactg 60
gacctgcgcc agacctatca gcgcgacttc accgtgaccg aggcgtatcg cgatacgctg 120
ccggatatgc agaacgcttc cgaggcggtg cagggggcca atgtcgccat ccagaaagtc 180
ggcgtatcca atttcaagct gccactcaag taccgcaccc acacggggcga accgaccacg 240
ctggaaacca gcgtaaccgg cagcgtatcc ctgaagccgg gcctgaaggg catcaacatg 300
tcccgcgtca tgcggacctt ctacgacttc caggacgacg tggtcacgct cgacacgctg 360
gcccgatatac tggaagcgta caaacgggat gtcgacagca acgacgcaca tcttcggctg 420
agtttctcct acccgctgct tcaaaaaagt ctgcgcagcg aattattcgg ctggcaatat 480
taccaggctg cattcgaggg acggatcgat gccgaaaata gagtccgcac gttcattcat 540
tttgacttcg tgtattcctc cgctgtccc tggtcggctg aactggccga acacgcgcgg 600
gaagtgcgcg gcctatacag catccccac tcgcaacgca gcaaggcgcg cgtcttcgtg 660
gaagttcagc ccggcgccga actcaccatc gaagacgtgc acatgcactg cctgaacgcg 720
ctccaaacgg aaacgcaagt gatgggtcaaa cgcgaaagac agcaggcggt cgctgaaatg 780
aacggcgccg ccatcaaatt cgtcgaagac gccgcccgtc tgatctatga gcagttcgac 840
caggatccgc gcatcaagga ttctgaaatc gcctgcgcgc atctggaatc cttgcactcg 900
cacgacgccg tatcggtcat cgccaaaggc gtgcccggcg gcttccgcgc cgacttctcg 960
gacttcaaga gtctgatctg ctaa 984

<210> 44
<211> 327
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (39)...(308)
<223> Uncharacterized ACR, COG1469

<220>
<221> SITE
<222> (45)...(48)
<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (100)...(103)

<223> N-glycosylation site. Prosite id = PS00001

<400> 44

Met	Thr	Thr	Glu	Thr	Lys	Ser	Lys	Leu	Tyr	Leu	His	Lys	Val	Asn	Gly
1				5					10					15	

Gln	Lys	Gly	Leu	Asp	Leu	Arg	Gln	Thr	Tyr	Gln	Arg	Asp	Phe	Thr	Val
			20					25					30		

Thr	Glu	Ala	Tyr	Arg	Asp	Thr	Leu	Pro	Asp	Met	Gln	Asn	Ala	Ser	Glu
		35					40					45			

Ala	Leu	Gln	Gly	Ala	Asn	Val	Ala	Ile	Gln	Lys	Val	Gly	Val	Ser	Asn
	50					55					60				

Phe	Lys	Leu	Pro	Leu	Lys	Tyr	Arg	Thr	His	Thr	Gly	Glu	Pro	Thr	Thr
65					70					75					80

Leu	Glu	Thr	Ser	Val	Thr	Gly	Ser	Val	Ser	Leu	Lys	Pro	Gly	Leu	Lys
				85					90					95	

Gly	Ile	Asn	Met	Ser	Arg	Val	Met	Arg	Thr	Phe	Tyr	Asp	Phe	Gln	Asp
			100					105					110		

Asp	Val	Phe	Thr	Leu	Asp	Thr	Leu	Ala	Arg	Ile	Leu	Glu	Ala	Tyr	Lys
		115					120					125			

Arg	Asp	Val	Asp	Ser	Asn	Asp	Ala	His	Leu	Arg	Leu	Ser	Phe	Ser	Tyr
	130					135					140				

Pro	Leu	Leu	Gln	Lys	Ser	Leu	Arg	Ser	Glu	Leu	Phe	Gly	Trp	Gln	Tyr
145					150					155					160

Tyr	Gln	Val	Ala	Phe	Glu	Gly	Arg	Ile	Asp	Ala	Glu	Asn	Arg	Val	Arg
			165						170					175	

Thr	Phe	Ile	His	Phe	Asp	Phe	Val	Tyr	Ser	Ser	Ala	Cys	Pro	Cys	Ser
			180					185					190		

Ala	Glu	Leu	Ala	Glu	His	Ala	Arg	Glu	Val	Arg	Gly	Leu	Tyr	Ser	Ile
		195					200					205			

Pro	His	Ser	Gln	Arg	Ser	Lys	Ala	Arg	Val	Phe	Val	Glu	Val	Gln	Pro
	210					215					220				

Gly Ala Glu Leu Thr Ile Glu Asp Val His Met His Cys Leu Asn Ala
225 230 235 240

Leu Gln Thr Glu Thr Gln Val Met Val Lys Arg Glu Asp Glu Gln Ala
245 250 255

Phe Ala Glu Met Asn Gly Ala Ala Ile Lys Phe Val Glu Asp Ala Ala
260 265 270

Arg Leu Ile Tyr Glu Gln Phe Asp Gln Asp Pro Arg Ile Lys Asp Phe
275 280 285

Glu Ile Ala Cys Ala His Leu Glu Ser Leu His Ser His Asp Ala Val
290 295 300

Ser Val Ile Ala Lys Gly Val Pro Gly Gly Phe Arg Ala Asp Phe Ser
305 310 315 320

Asp Phe Lys Ser Leu Ile Cys
325

<210> 45
<211> 1377
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 45
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acgcagggga agatcattga cggcagcaac ggcgatgtgg cctgcatca ctaccaccgc 180
tggcgcgagg acgtggccct catgagagac ttgggtatgc aggcataatcg cttctccatc 240
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tacaatcgcc tgggtggacgg gttgctggaa gctggcatca agccctttgc caccctctac 360
cactgggacc tgccgctggc gctacaggct gacggcggct ggccggagcg ctccacggcc 420
aaggcctttg tcgaatacgc cgacgtggtc agccgcgcgc tgggcatcg ggtgaagagc 480
tggatcacc ctaacgaacc gtggtgcatc agcatgctga gccatcaa at tggggagcat 540
gcgcccggct ggccgggactg gcaggctgcg ttggcggccg cgcaccacgt cctcctttcg 600
catggttggg ccgtgccgga actgcgtcgc aacagccgcg atgcagaaat cggcatcacg 660
ttgaacttta ccccggcgga gccagcttcg aacagcgcag ccgatttcaa ggcctatcgc 720

Val Ala Leu Met Arg Asp Leu Gly Met Gln Ala Tyr Arg Phe Ser Ile
65 70 75 80

Ser Trp Pro Arg Ile Leu Pro Thr Gly His Gly Gln Ile Asn Gln Ala
 85 90 95

Gly Leu Asp Phe Tyr Asn Arg Leu Val Asp Gly Leu Leu Glu Ala Gly
 100 105 110

Ile Lys Pro Phe Ala Thr Leu Tyr His Trp Asp Leu Pro Leu Ala Leu
 115 120 125

Gln Ala Asp Gly Gly Trp Pro Glu Arg Ser Thr Ala Lys Ala Phe Val
 130 135 140

Glu Tyr Ala Asp Val Val Ser Arg Ala Leu Gly Asp Arg Val Lys Ser
 145 150 155 160

Trp Ile Thr His Asn Glu Pro Trp Cys Ile Ser Met Leu Ser His Gln
 165 170 175

Ile Gly Glu His Ala Pro Gly Trp Arg Asp Trp Gln Ala Ala Leu Ala
 180 185 190

Ala Ala His His Val Leu Leu Ser His Gly Trp Ala Val Pro Glu Leu
 195 200 205

Arg Arg Asn Ser Arg Asp Ala Glu Ile Gly Ile Thr Leu Asn Phe Thr
 210 215 220

Pro Ala Glu Pro Ala Ser Asn Ser Ala Ala Asp Phe Lys Ala Tyr Arg
 225 230 235 240

Gln Phe Asp Gly Tyr Phe Asn Arg Trp Phe Leu Asp Pro Leu Tyr Gly
 245 250 255

Arg His Tyr Pro Ala Asp Met Val His Asp Tyr Ile Ala Gln Gly Tyr
 260 265 270

Leu Pro Ser Gln Gly Leu Thr Phe Val Glu Ala Gly Asp Leu Asp Ala
 275 280 285

Ile Ala Thr Arg Thr Asp Phe Leu Gly Val Asn Tyr Tyr Thr Arg Glu
 290 295 300

Val Val Arg Ser Gln Glu Ile Pro Glu Ser Glu Asn Ala Pro Arg Thr
 305 310 315 320

Val Leu Arg Ala Pro Gln Glu Glu Trp Thr Glu Met Gly Trp Glu Val
 325 330 335

Tyr Pro Glu Gly Leu Tyr Arg Leu Leu Asn Arg Leu His Phe Glu Tyr
 340 345 350

Gln Pro Arg Lys Leu Tyr Val Thr Glu Ser Gly Cys Ser Tyr Ser Asp
 355 360 365

Gly Pro Gly Pro Asn Gly Arg Ile Pro Asp Gln Arg Arg Ile Asn Tyr
 370 375 380

Leu Arg Asp His Phe Ala Ala Ala His Gln Ala Ile Gln Cys Gly Val
 385 390 395 400

Pro Leu Ala Gly Tyr Phe Val Trp Ser Phe Met Asp Asn Phe Glu Trp
 405 410 415

Ala Lys Gly Tyr Thr Gln Arg Phe Gly Ile Val Trp Val Asp Tyr Gln
 420 425 430

Ser Gln Arg Arg Ile Pro Lys Asp Ser Ala Tyr Trp Tyr Arg Asp Val
 435 440 445

Val Ala Ala Asn Ala Val Gln Val Pro Asp
 450 455

<210> 47
 <211> 1353
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 47
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 atcgaagggt ctccctctgc tgatggcaaa ggtgaatcga tatgggaccg tttttctcac 120
 acaccgggga acatttggaa cgctgaaacc ggggatatcg cctgcgatca ttaccggcgt 180
 tacgtggatg atgtaaagct gatttcacaa atcgggctta acgcgtaccg tttttcaatt 240
 tcctggccca gggatatttc agaggggaga ggaaaagcaa atgaaaaagg actcgatttt 300
 taccgcaggt tgattgaaca gctgcagcaa catcgaatca aaacggcagt gacactttac 360
 cactgggatc ttccacaagt tctgcaggat cgcggcgggt gggcaaaccg tgatacggcg 420
 aagtattttt ctgagtatgc cacctttctc tttgaaaaac tcgatctccc cgttgacatg 480

tggattactc ttaacgaacc atggggttatc gctattcttg ggcattgcttt tggatatccac 540
gctccaggga tgagtgaactt cagcacagcc ctccagggtct cgcataacct gcttctgggg 600
cacggggttg cggttaaagc atttcgggag tctaagaggg gtgatgaacc ggtaggtatt 660
acccttaacc ttgccccggt tgaaccgctg accgaaaagc ccgccgatct aaaggcagct 720
ttactttctg acggttttat gaaccgctgg taccttgatc ccctgttcaa aggtgggttac 780
cctgaagata tgatggatat ctattcccgg aactttgaac tgcccaaaat tgaaaagggg 840
gatgctcagg ttattgccga accgatcgac ttcctgggca taaataacta taccagggtt 900
ctcgtggaag ccagcgggtga tgaaaatgcc tttatgggca accctgtcaa ccccagggc 960
tctgaatata ctgaaatggg ttgggagggt tatccgcagg gtctctacga cctgctgacc 1020
agggttcacc gggattacgg gccaatgccg ctatatataa ctgaaaacgg ggcagccttt 1080
cccgatgaac ttgacagcaa tgggcagata gatgatccaa ggcggataaa ttacctggaa 1140
acttatcttc atcagtgctg gaaggcagtt caggacgggtg tgcctctaaa aggctatttt 1200
gtctggaccc tgatggataa cttcgagtgg gctttcgggt tcagcaagcg atttgggctc 1260
atatacgtag attaccagga tcagaaacgt tacttgaaaa acagcgccta ctggtatagc 1320
aaggttattg ggcgaaacgg cctcgagcta taa 1353

<210> 48
<211> 450
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (4)...(448)
<223> Glycosyl hydrolase family 1

<220>
<221> SITE
<222> (10)...(24)
<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>
<221> SITE
<222> (300)...(303)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (356)...(364)
<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 48
Met Lys Lys Tyr Leu Phe Pro Glu Asn Phe Leu Trp Gly Ala Ala Thr

1	5	10	15
Ala Ser Tyr Gln Ile Glu Gly Ser Pro Ser Ala Asp Gly Lys Gly Glu	20	25	30
Ser Ile Trp Asp Arg Phe Ser His Thr Pro Gly Asn Ile Trp Asn Ala	35	40	45
Glu Thr Gly Asp Ile Ala Cys Asp His Tyr Arg Arg Tyr Val Asp Asp	50	55	60
Val Lys Leu Ile Ser Gln Ile Gly Leu Asn Ala Tyr Arg Phe Ser Ile	65	70	75
Ser Trp Pro Arg Val Phe Pro Glu Gly Arg Gly Lys Ala Asn Glu Lys	85	90	95
Gly Leu Asp Phe Tyr Arg Arg Leu Ile Glu Gln Leu Gln Gln His Arg	100	105	110
Ile Lys Thr Ala Val Thr Leu Tyr His Trp Asp Leu Pro Gln Val Leu	115	120	125
Gln Asp Arg Gly Gly Trp Ala Asn Arg Asp Thr Ala Lys Tyr Phe Ser	130	135	140
Glu Tyr Ala Thr Phe Leu Phe Glu Lys Leu Asp Leu Pro Val Asp Met	145	150	155
Trp Ile Thr Leu Asn Glu Pro Trp Val Ile Ala Ile Leu Gly His Ala	165	170	175
Phe Gly Ile His Ala Pro Gly Met Ser Asp Phe Ser Thr Ala Leu Gln	180	185	190
Val Ser His Asn Leu Leu Leu Gly His Gly Leu Ala Val Lys Ala Phe	195	200	205
Arg Glu Ser Lys Arg Gly Asp Glu Pro Val Gly Ile Thr Leu Asn Leu	210	215	220
Ala Pro Val Glu Pro Leu Thr Glu Lys Pro Ala Asp Leu Lys Ala Ala	225	230	235
Leu Leu Ser Asp Gly Phe Met Asn Arg Trp Tyr Leu Asp Pro Leu Phe	245	250	255

Lys Gly Gly Tyr Pro Glu Asp Met Met Asp Ile Tyr Ser Arg Asn Phe
260 265 270

Glu Leu Pro Lys Ile Glu Lys Gly Asp Ala Gln Val Ile Ala Glu Pro
275 280 285

Ile Asp Phe Leu Gly Ile Asn Asn Tyr Thr Arg Val Leu Val Glu Ala
290 295 300

Ser Gly Asp Glu Asn Ala Phe Met Gly Asn Pro Val Asn Pro Gln Gly
305 310 315 320

Ser Glu Tyr Thr Glu Met Gly Trp Glu Val Tyr Pro Gln Gly Leu Tyr
325 330 335

Asp Leu Leu Thr Arg Val His Arg Asp Tyr Gly Pro Met Pro Leu Tyr
340 345 350

Ile Thr Glu Asn Gly Ala Ala Phe Pro Asp Glu Leu Asp Ser Asn Gly
355 360 365

Gln Ile Asp Asp Pro Arg Arg Ile Asn Tyr Leu Glu Thr Tyr Leu His
370 375 380

Gln Cys Trp Lys Ala Val Gln Asp Gly Val Pro Leu Lys Gly Tyr Phe
385 390 395 400

Val Trp Thr Leu Met Asp Asn Phe Glu Trp Ala Phe Gly Phe Ser Lys
405 410 415

Arg Phe Gly Leu Ile Tyr Val Asp Tyr Gln Asp Gln Lys Arg Tyr Leu
420 425 430

Lys Asn Ser Ala Tyr Trp Tyr Ser Lys Val Ile Gly Arg Asn Gly Leu
435 440 445

Glu Leu
450

<210> 49

<211> 591

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 49

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atggactttg agcggggcagt tgacaggaat atcattagat tacgctcttc gttaaaggaa      60
gaaatgaagg atctagttgc agttgaagct ccggtataca tattttttaa tggcagcgag      120
ctggtaaccc tgctctgcac cccggagaaa attgatcggt tggccctcgg tttccttcat      180
tcagaagggc tgcttaactc acttgatgat cttagtatga tcaggaccag ggagagcgaa      240
ggcctgggttg aaattgaact taaagaggcc tcgccggcac ttgataaatt atacgggaag      300
aggacaatta cttccgggtg cggtaaggga acaatttttt ttaatgttct cgattctctg      360
cgcagtaaac cactcgacgg aaagcttggt attacaaccg aagagattca taaattaatg      420
gatgacctgc agggggcgggc ggaactgttc aaggctaccg ggggtgttca cagcgctgcg      480
cttgccgaca gaaaggaaat actctttttc agtgaagata tcggccgcca taatgctatc      540
gataaaattg tgggagagtg tttgctggag ggggtatctc ctgaagataa g              591

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<210> 50

<211> 197

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (17)...(195)

<223> FdhD/NarQ family

<220>

<221> SITE

<222> (37)...(40)

<223> N-glycosylation site. Prosite id = PS00001

<400> 50

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Met Asp Phe Glu Arg Ala Val Asp Arg Asn Ile Ile Arg Leu Arg Ser
1              5              10              15

Ser Leu Lys Glu Glu Met Lys Asp Leu Val Ala Val Glu Ala Pro Val
                20              25              30

Thr Ile Phe Leu Asn Gly Ser Glu Leu Val Thr Leu Leu Cys Thr Pro
          35              40              45

Glu Lys Ile Asp Arg Leu Ala Leu Gly Phe Leu His Ser Glu Gly Leu
          50              55              60

Leu Asn Ser Leu Asp Asp Leu Ser Met Ile Arg Thr Arg Glu Ser Glu
65              70              75              80

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Gly Leu Val Glu Ile Glu Leu Lys Glu Ala Ser Pro Ala Leu Asp Lys
 85 90 95

Leu Tyr Gly Lys Arg Thr Ile Thr Ser Gly Cys Gly Lys Gly Thr Ile
 100 105 110

Phe Phe Asn Val Leu Asp Ser Leu Arg Ser Lys Pro Leu Asp Gly Lys
 115 120 125

Leu Val Ile Thr Thr Glu Glu Ile His Lys Leu Met Asp Asp Leu Gln
 130 135 140

Gly Arg Ala Glu Leu Phe Lys Ala Thr Gly Gly Val His Ser Ala Ala
 145 150 155 160

Leu Ala Asp Arg Lys Glu Ile Leu Phe Phe Ser Glu Asp Ile Gly Arg
 165 170 175

His Asn Ala Ile Asp Lys Ile Val Gly Glu Cys Leu Leu Glu Gly Val
 180 185 190

Ser Pro Glu Asp Lys
 195

<210> 51
 <211> 1014
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 51
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 caaccggccg ggctgccgcc gcgttcgccg gtgcagcgcg gcatcaacct gggcaatatg 120
 ctggaagcgc cggaggaggg ctggtggggg ctgcgcgctc agcgcgacta cctgacgacg 180
 atcgccgggg ccgggttcga tgcggtgcgc atcccgataa gctggtcaac ccatgctgcc 240
 agcgagccgc cctacaccat cgatccggct ttcttcgccc gcgttgatga agtcgtcggc 300
 tgggcgctgg cggacgggct gaaggccatc atcaacgtgc accactacga ggagatgatg 360
 agcgatccgg cggggcattt cccccggctg cgcgcgctgt gggcgcagat cgcggagcac 420
 tacgccgact acccgcccgc gctgatgttc gagctgctca acgaaccgtt cgaggcgctg 480
 acgccgctgc ggtggaacga gtacgccgcc gatctgatcg cgctgatccg ccagaccaac 540
 ccggggcgca ccctgatcgt cggcggggggc tgggtggaaca gtgtggaagg gctgatgcag 600

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ctccgcctgc cggatgatcc cgatctgctg gcgacgttcc attactacca cccgttcgag    660
ttcacgcatac agggggcgga gtggtcaccg gaagtgactg acctgagcgg gatcgcttgg    720
gggacggggcg aggaacgggt cgatctggag tccaatatcc gtattgcggc ggcctggggcg    780
gtgtacaacc ggcgcccgtt gctgttgggc gaattcggcg tctatggccg ggtggccgat    840
ctcgattcgc gcctgcgctg gacgacggcg gtgcgcgccg aggccgaggg gcagggcatc    900
ggctgggtgct actgggaatt cgccgccggc ttcggcattt acgaccggga aagccggacg    960
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<210> 52

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(20)

<220>

<221> DOMAIN

<222> (38)...(314)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (150)...(159)

<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<400> 52

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Met Ser Arg Gly Ile Leu Ile Leu Val Met Leu Ser Val Leu Ser Gly
1           5           10          15

```

```

Ala Ala Leu Ala Gln Pro Ala Gly Leu Pro Pro Arg Ser Pro Val Gln
          20          25          30

```

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Arg Cys Ile Asn Leu Gly Asn Met Leu Glu Ala Pro Glu Glu Gly Trp
          35          40          45

```

```

Trp Gly Leu Arg Val Glu Arg Asp Tyr Leu Thr Thr Ile Ala Gly Ala
          50          55          60

```

```

Gly Phe Asp Ala Val Arg Ile Pro Ile Ser Trp Ser Thr His Ala Ala
          65          70          75          80

```

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Ser Glu Pro Pro Tyr Thr Ile Asp Pro Ala Phe Phe Ala Arg Val Asp
          85          90          95

```

Glu Val Val Gly Trp Ala Leu Ala Asp Gly Leu Lys Ala Ile Ile Asn
 100 105 110

Val His His Tyr Glu Glu Met Met Ser Asp Pro Ala Gly His Phe Pro
 115 120 125

Arg Leu Arg Ala Leu Trp Ala Gln Ile Ala Glu His Tyr Ala Asp Tyr
 130 135 140

Pro Pro Ala Leu Met Phe Glu Leu Leu Asn Glu Pro Phe Glu Ala Leu
 145 150 155 160

Thr Pro Leu Arg Trp Asn Glu Tyr Ala Ala Asp Leu Ile Ala Leu Ile
 165 170 175

Arg Gln Thr Asn Pro Gly Arg Thr Leu Ile Val Gly Gly Gly Trp Trp
 180 185 190

Asn Ser Val Glu Gly Leu Met Gln Leu Arg Leu Pro Asp Asp Pro Asp
 195 200 205

Leu Leu Ala Thr Phe His Tyr Tyr His Pro Phe Glu Phe Thr His Gln
 210 215 220

Gly Ala Glu Trp Ser Pro Glu Val Thr Asp Leu Ser Gly Ile Ala Trp
 225 230 235 240

Gly Thr Gly Glu Glu Arg Leu Asp Leu Glu Ser Asn Ile Arg Ile Ala
 245 250 255

Ala Ala Trp Ala Val Tyr Asn Arg Arg Pro Leu Leu Leu Gly Glu Phe
 260 265 270

Gly Val Tyr Gly Arg Val Ala Asp Leu Asp Ser Arg Leu Arg Trp Thr
 275 280 285

Thr Ala Val Arg Ala Glu Ala Glu Ala Gln Gly Ile Gly Trp Cys Tyr
 290 295 300

Trp Glu Phe Ala Ala Gly Phe Gly Ile Tyr Asp Pro Glu Ser Arg Thr
 305 310 315 320

Phe Asn Pro Leu Tyr Arg Ala Leu Ile Pro Gln Ala Gly Pro Ala Arg
 325 330 335

Pro

<210> 53
<211> 1377
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 53
atgtggatgg ttcaagcgac atctttaatt caaaaataca atgtgcctgg cccacgctac 60
accagttatc caacgggttc ttattgggaa agtgagaatt tttcactaaa gcagtggcaa 120
caaacgctca aaaaatcctt tgatgagtcg aatcaaagtg aaggcatcag tctgtatatc 180
catttgccat ttgcgaaag tttatgcacc ttctgtgggt gccataaacg tgtgactaaa 240
aagcatgaga tggaaaagcc ttatatccaa gcggtattaa aagaatggga tttatatattgc 300
caacttttgg tggataaacc tgtcattaaa gaaattcatt tgggtggggg aactccgaca 360
tttttttagtc ctgaacattt aacgcagctg attaagggga tattggctaa agccgaagtt 420
gcagatgagc atgagtttag ttttgaagga catcccaaca atacgacacg tgaacatttg 480
caagcgctct atgatgttgg atttcgacgt gtcagttatg gcgtgcagga ctataacgaa 540
actgtgcaaa aagccattca ccgcattcag ccctatgaaa atgttaaaaa tgtcaccgag 600
tgggcgcgtg agattggcta tacctctatt tcgcatgatt tgggtctttgg cctgccgttt 660
caaagttagt acgatgtctt aaatacgatt gatcaaacca ataccttaat gccggatcgt 720
ttggctttgt atagctatgc ccatgtgcca tggattaaag gcaatgggtc acgcggtttt 780
aaagatgctg atgtcccgaa agacgagatt aaacgtcaat gttatgagga aggcaaaaaa 840
aaattattag aacatggcta tcatgaaatt ggtatggatc attttgctct agaacaagac 900
agtatgtatc agtcttttaa agcagggagc ttgcatcgta atttcatggg ttataccgca 960
tcgaaaacgc aagtgatgat tgggcttggg atttcatcaa ttagtgacag ttggtacagc 1020
tttgcgcaaa acgtgaaaac attagatgaa tattatacct tgctagaaaa aaatcagatt 1080
cccgtgttta aagggcatgt cttgaatcag gaagatttga tcatccgtaa acatatttta 1140
aatttgatgt gtggcttcca aacctcatgg gcaaattccc atatgcaatt tcctgaaatt 1200
cagtctgttt tggcacaatt agcagaaatg cagcaagatg gtttgattca aattgaagac 1260
gcatcgggtc cagttttaga agcgggcaag ccttttggtc gaaatatattg tatggccttt 1320
gatttaagac tcaagcgcaa caagcctgag aatcggattt ttctgatgac gatttaa 1377

<210> 54
<211> 458
<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (59)...(233)

<223> Radical SAM superfamily

<220>

<221> DOMAIN

<222> (316)...(431)

<223> HemN C-terminal region

<220>

<221> SITE

<222> (33)...(36)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (51)...(54)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (155)...(158)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (181)...(184)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (200)...(203)

<223> N-glycosylation site. Prosite id = PS00001

<400> 54

Met	Trp	Met	Val	Gln	Ala	Thr	Ser	Leu	Ile	Gln	Lys	Tyr	Asn	Val	Pro
1				5					10					15	

Gly	Pro	Arg	Tyr	Thr	Ser	Tyr	Pro	Thr	Val	Pro	Tyr	Trp	Glu	Ser	Glu
			20					25					30		

Asn	Phe	Ser	Leu	Lys	Gln	Trp	Gln	Gln	Thr	Leu	Lys	Lys	Ser	Phe	Asp
		35					40					45			

Glu	Ser	Asn	Gln	Ser	Glu	Gly	Ile	Ser	Leu	Tyr	Ile	His	Leu	Pro	Phe
	50					55					60				

Cys	Glu	Ser	Leu	Cys	Thr	Phe	Cys	Gly	Cys	His	Lys	Arg	Val	Thr	Lys
65					70					75					80

Lys His Glu Met Glu Lys Pro Tyr Ile Gln Ala Val Leu Lys Glu Trp
 85 90 95

Asp Leu Tyr Cys Gln Leu Leu Val Asp Lys Pro Val Ile Lys Glu Ile
 100 105 110

His Leu Gly Gly Gly Thr Pro Thr Phe Phe Ser Pro Glu His Leu Thr
 115 120 125

Gln Leu Ile Lys Gly Ile Leu Ala Lys Ala Glu Val Ala Asp Glu His
 130 135 140

Glu Phe Ser Phe Glu Gly His Pro Asn Asn Thr Thr Arg Glu His Leu
 145 150 155 160

Gln Ala Leu Tyr Asp Val Gly Phe Arg Arg Val Ser Tyr Gly Val Gln
 165 170 175

Asp Tyr Asn Glu Thr Val Gln Lys Ala Ile His Arg Ile Gln Pro Tyr
 180 185 190

Glu Asn Val Lys Asn Val Thr Glu Trp Ala Arg Glu Ile Gly Tyr Thr
 195 200 205

Ser Ile Ser His Asp Leu Val Phe Gly Leu Pro Phe Gln Ser Leu Asp
 210 215 220

Asp Val Leu Asn Thr Ile Asp Gln Thr Asn Thr Leu Met Pro Asp Arg
 225 230 235 240

Leu Ala Leu Tyr Ser Tyr Ala His Val Pro Trp Ile Lys Gly Asn Gly
 245 250 255

Gln Arg Gly Phe Lys Asp Ala Asp Val Pro Lys Asp Glu Ile Lys Arg
 260 265 270

Gln Cys Tyr Glu Glu Gly Lys Lys Lys Leu Leu Glu His Gly Tyr His
 275 280 285

Glu Ile Gly Met Asp His Phe Ala Leu Glu Gln Asp Ser Met Tyr Gln
 290 295 300

Ser Phe Lys Ala Gly Ser Leu His Arg Asn Phe Met Gly Tyr Thr Ala
 305 310 315 320

Ser Lys Thr Gln Val Met Ile Gly Leu Gly Ile Ser Ser Ile Ser Asp

325 330 335
 Ser Trp Tyr Ser Phe Ala Gln Asn Val Lys Thr Leu Asp Glu Tyr Tyr
 340 345 350
 Thr Leu Leu Glu Lys Asn Gln Ile Pro Val Phe Lys Gly His Val Leu
 355 360 365
 Asn Gln Glu Asp Leu Ile Ile Arg Lys His Ile Leu Asn Leu Met Cys
 370 375 380
 Gly Phe Gln Thr Ser Trp Ala Asn Pro Asp Met Gln Phe Pro Glu Ile
 385 390 395 400
 Gln Ser Val Leu Ala Gln Leu Ala Glu Met Gln Gln Asp Gly Leu Ile
 405 410 415
 Gln Ile Glu Asp Ala Ser Val Thr Val Leu Glu Ala Gly Lys Pro Phe
 420 425 430
 Val Arg Asn Ile Cys Met Ala Phe Asp Leu Arg Leu Lys Arg Asn Lys
 435 440 445
 Pro Glu Asn Arg Ile Phe Ser Met Thr Ile
 450 455

<210> 55
 <211> 1389
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 55
 atgagcgctt cgagtccttc ccgccccctg tccttcccag agcagttcgt ctgggggtgct 60
 gccgcggcct cctaccaagt cgagggcgcc gtccacgagg acgggaaggg cccctccgtc 120
 tgggacatgt tctgcgagaa gcccgagcgc gtcttccagg ggcacgacgg ggcggtggct 180
 tgcgaccact atcaccgcta ccgagaggac gtggcggttga tgcgacaggt gggcctgcac 240
 gcctaccgcc tgagcgtgtg ctggccccga gtgctcccgg agggcgtcgg gcagcccaac 300
 gagaagggcc tcgacttcta ctgcgcggtg gtggacgcgc tgctcgagge agggattacg 360
 ccctgggtaa cgctttttca ttgggactac cccttggctc tctatcaccc ggggggctgg 420
 ctcaaccggg atagcgcgga ttgggtttgcc gagtacgcgg gcctaatacg cgatcgctc 480
 tccgaccggg tgcagcattt cttcactcag aacgagcccc aggtctatat cggcttcgga 540

```

cacctcgagg gtaagcatgc tccaggagac accttgccca tgtcccaggt gctgcttgcg      600
gggcatcata gcctactggc gcacggcaag gccgtgcagg cgctccgcgc ccaggcgaag      660
cagcagctgc gcgtcggcta cgctcccgtc ggcatgcccc tccatccctt cacggactcg      720
gccgaggacg tggccgctgc gcggaaggcg accttttggg ttcgggagaa gaactcctgg      780
aacaacgcct ggtggatgga cccggtgttc ttgggtgagt acccggctca gggcctcgcc      840
ttcttcgggc gggacgtgcc gcaggtgcgc gagggagaca tgcagctcat cgcgagcccc      900
ttggacttct ttgggggtcaa catctaccag agcacccccg tgcgcgcgtc tagcgccgaa      960
agcggcttcg aggtcgtccc ccatccaacg ggctatccta tctactgcctt caactggccg     1020
atcacgcccc aggccctcta ctgggggtccg cgcttcttct acgagcgcta ccagaagccg     1080
atcgatcatca cggagaacgg actgtcctgt cgggacgtcg tcgctgtgga cgggaagggt     1140
cacgatccgg ctgcgcatga tttcaccacc cgctatctgc gcgagctcca ccgagccgtc     1200
gcggacggcg tcgcggtcga gggctacttc cactgggtcca tcatggacaa cttcgaatgg     1260
gctgccgggt accgcgagcg gttcgggctc attcacgtcg actacgagac cctggcgcgg     1320
acgcccaagg cgtccgctgc gtggtatcgc aaggtaatcg agagcaacgg agcgaccctt     1380
ttcggatga                                           1389

```

<210> 56

<211> 462

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (8)...(458)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (16)...(30)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (366)...(374)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 56

```

Met Ser Ala Ser Ser Pro Ser Arg Pro Leu Ser Phe Pro Glu Gln Phe
1           5           10           15

```

```

Val Trp Gly Ala Ala Ala Ala Ser Tyr Gln Val Glu Gly Ala Val His

```

20	25	30
Glu Asp Gly Lys Gly Pro Ser Val Trp Asp Met Phe Cys Glu Lys Pro 35 40 45		
Gly Ala Val Phe Gln Gly His Asp Gly Ala Val Ala Cys Asp His Tyr 50 55 60		
His Arg Tyr Arg Glu Asp Val Ala Leu Met Arg Gln Val Gly Leu His 65 70 75 80		
Ala Tyr Arg Leu Ser Val Cys Trp Pro Arg Val Leu Pro Glu Gly Val 85 90 95		
Gly Gln Pro Asn Glu Lys Gly Leu Asp Phe Tyr Ser Arg Leu Val Asp 100 105 110		
Ala Leu Leu Glu Ala Gly Ile Thr Pro Trp Val Thr Leu Phe His Trp 115 120 125		
Asp Tyr Pro Leu Ala Leu Tyr His Arg Gly Gly Trp Leu Asn Arg Asp 130 135 140		
Ser Ala Asp Trp Phe Ala Glu Tyr Ala Gly Leu Ile Ala Asp Arg Leu 145 150 155 160		
Ser Asp Arg Val Gln His Phe Phe Thr Gln Asn Glu Pro Gln Val Tyr 165 170 175		
Ile Gly Phe Gly His Leu Glu Gly Lys His Ala Pro Gly Asp Thr Leu 180 185 190		
Pro Met Ser Gln Val Leu Leu Ala Gly His His Ser Leu Leu Ala His 195 200 205		
Gly Lys Ala Val Gln Ala Leu Arg Ala Gln Ala Lys Gln Gln Leu Arg 210 215 220		
Val Gly Tyr Ala Pro Val Gly Met Pro Leu His Pro Phe Thr Asp Ser 225 230 235 240		
Ala Glu Asp Val Ala Ala Ala Arg Lys Ala Thr Phe Trp Val Arg Glu 245 250 255		
Lys Asn Ser Trp Asn Asn Ala Trp Trp Met Asp Pro Val Phe Leu Gly 260 265 270		

Glu Tyr Pro Ala Gln Gly Leu Ala Phe Phe Gly Arg Asp Val Pro Gln
 275 280 285

Val Arg Glu Gly Asp Met Gln Leu Ile Ala Gln Pro Leu Asp Phe Phe
 290 295 300

Gly Val Asn Ile Tyr Gln Ser Thr Pro Val Arg Ala Ser Ser Ala Glu
 305 310 315 320

Ser Gly Phe Glu Val Val Pro His Pro Thr Gly Tyr Pro Ile Thr Ala
 325 330 335

Phe Asn Trp Pro Ile Thr Pro Gln Ala Leu Tyr Trp Gly Pro Arg Phe
 340 345 350

Phe Tyr Glu Arg Tyr Gln Lys Pro Ile Val Ile Thr Glu Asn Gly Leu
 355 360 365

Ser Cys Arg Asp Val Val Ala Val Asp Gly Lys Val His Asp Pro Ala
 370 375 380

Arg Ile Asp Phe Thr Thr Arg Tyr Leu Arg Glu Leu His Arg Ala Val
 385 390 395 400

Ala Asp Gly Val Ala Val Glu Gly Tyr Phe His Trp Ser Ile Met Asp
 405 410 415

Asn Phe Glu Trp Ala Ala Gly Tyr Arg Glu Arg Phe Gly Leu Ile His
 420 425 430

Val Asp Tyr Glu Thr Leu Ala Arg Thr Pro Lys Ala Ser Ala Ala Trp
 435 440 445

Tyr Arg Lys Val Ile Glu Ser Asn Gly Ala Thr Leu Phe Gly
 450 455 460

<210> 57

<211> 414

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 57

atgattgctt catctatggt ctatggaacg gttcgtggaa tacaagagct aactcaaaac

60


```

gttattgcat tggataccgc aatgggtttcg cttaccagag ttgctgacgg aagtgatttt 120
gagtttgata gagttattga acgctcgatt gaaaacgtaa ccgaactatc aggtaagcta 180
actgattaca tggatttagt aacggagttt gctagaactg gtaaaacaat agatgaatct 240
tttaatttag ctaatacaac acaaagtgtt atgaatatct ctgaattaac agcagatgaa 300
tcagtaaata gtttaactgc cgcaatgatt gcttttaata ttaacgcaga tgatagtatt 360
agaattgctg ataagttgaa tgagggttaac aatatcagcc tccttttgtg gtaa 414

```

<210> 58

<211> 137

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SITE

<222> (52)...(55)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (86)...(89)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (93)...(96)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (133)...(136)

<223> N-glycosylation site. Prosite id = PS00001

<400> 58

```

Met Ile Ala Ser Ser Met Phe Tyr Gly Thr Val Arg Gly Ile Gln Glu
1           5           10          15

```

```

Leu Thr Gln Asn Val Ile Ala Leu Asp Thr Ala Met Val Ser Leu Thr
          20          25          30

```

```

Arg Val Ala Asp Gly Ser Asp Phe Glu Phe Asp Arg Val Ile Glu Arg
          35          40          45

```

```

Ser Ile Glu Asn Val Thr Glu Leu Ser Gly Lys Leu Thr Asp Tyr Met
          50          55          60

```

```

Asp Leu Val Thr Glu Phe Ala Arg Thr Gly Lys Thr Ile Asp Glu Ser
65          70          75          80

```

Phe Asn Leu Ala Asn Thr Thr Gln Met Leu Met Asn Ile Ser Glu Leu
 85 90 95

Thr Ala Asp Glu Ser Val Asn Ser Leu Thr Ala Ala Met Ile Ala Phe
 100 105 110

Asn Ile Asn Ala Asp Asp Ser Ile Arg Ile Ala Asp Lys Leu Asn Glu
 115 120 125

Val Asn Asn Ile Ser Leu Leu Leu Trp
 130 135

<210> 59
 <211> 1044
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 59
 atgagaat ttt ttgaaggatt tcagcgcgaggt gtaaacccttg gcggctggat ctcccagttc 60
 gacaagtacg accatgagca tttccgcagc tttattacgg aaaatgacat cgccgccatt 120
 gcagctcttg gttttgacca tgtccgcgtg ccggtggatt ataacgtgct ggaggatgag 180
 gagggcaacc gcatcgacag cggatttgtc tacctgagaa gctgctacga gtggtgccgc 240
 aaacacgacc tgaacatgct ggtggatctt caccgagtgt acggctactc ctccgatccg 300
 ctgaaaaaag atatggaccg caaacgcttc ttctatgccg aagctctgca ggagcgtttt 360
 ctgaagctct gggagcagat ctgtgaaacc tttaaagacg atcctgtgca cgtggcattc 420
 gagccgctga atgagatcgt tttaggagag gtcgcagacg cctggaacgt gatgatccgc 480
 aaatatatca agaccgtccg cgccatctgc ccggagcact atctggctcct tggaagcgtg 540
 cactacagcc acgttaccac catccctctt cttgaggcac cggcagatga caagatcgtc 600
 ttcaacttcc actgctacga gccgctggtc ttcacccacc agggcgcata ctggctggag 660
 gatatgattc cggatttccg catgacctat cctgccacca tggaagagtt ctacgaagca 720
 acaaagaaga tcctgcaaaa catgagtccg gatggattta aggatttcga tcaggagatg 780
 ggtccgggct tctttgagaa gatcttcaca ccggccctga aacgtgccga gcaggacaat 840
 gtagccctct actgcggcga gtacggcgctc attgatctgg cagataacca tgccaagatc 900
 cgctggctca aagacatcca caccaccttc tccaaatacg gcatcggaag tgccctctgg 960
 aactacaagg gcaaggattt cggctatgta gatgatcgct tcgccgagtg cagagaagca 1020
 ttatcagagt gcctgaaggc ctga 1044

<210> 60
 <211> 347
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (14)...(330)
 <223> Cellulase (glycosyl hydrolase family 5)

<400> 60
 Met Arg Ile Phe Glu Gly Phe Gln Arg Gly Val Asn Leu Gly Gly Trp
 1 5 10 15

Ile Ser Gln Phe Asp Lys Tyr Asp His Glu His Phe Arg Ser Phe Ile
 20 25 30

Thr Glu Asn Asp Ile Ala Ala Ile Ala Ala Leu Gly Phe Asp His Val
 35 40 45

Arg Val Pro Val Asp Tyr Asn Val Leu Glu Asp Glu Glu Gly Asn Arg
 50 55 60

Ile Asp Ser Gly Phe Val Tyr Leu Arg Ser Cys Tyr Glu Trp Cys Arg
 65 70 75 80

Lys His Asp Leu Asn Met Leu Val Asp Leu His Glu Cys Tyr Gly Tyr
 85 90 95

Ser Phe Asp Pro Leu Lys Lys Asp Met Asp Arg Lys Arg Phe Phe Tyr
 100 105 110

Ala Glu Ala Leu Gln Glu Arg Phe Leu Lys Leu Trp Glu Gln Ile Cys
 115 120 125

Glu Thr Phe Lys Asp Asp Pro Val His Val Ala Phe Glu Pro Leu Asn
 130 135 140

Glu Ile Val Leu Gly Glu Val Ala Asp Ala Trp Asn Val Met Ile Arg
 145 150 155 160

Lys Tyr Ile Lys Thr Val Arg Ala Ile Cys Pro Glu His Tyr Leu Val
 165 170 175

Leu Gly Ser Val His Tyr Ser His Val Thr Thr Ile Pro Leu Leu Glu
 180 185 190

Ala Pro Ala Asp Asp Lys Ile Val Phe Asn Phe His Cys Tyr Glu Pro
 195 200 205

Leu Val Phe Thr His Gln Gly Ala Tyr Trp Leu Glu Asp Met Ile Pro
 210 215 220

Asp Phe Arg Met Thr Tyr Pro Ala Thr Met Glu Glu Phe Tyr Glu Ala
 225 230 235 240

Thr Lys Lys Ile Leu Pro Asn Met Ser Pro Asp Gly Phe Lys Asp Phe
 245 250 255

Asp Gln Glu Met Gly Pro Gly Phe Phe Glu Lys Ile Phe Thr Pro Ala
 260 265 270

Leu Lys Arg Ala Glu Gln Asp Asn Val Ala Leu Tyr Cys Gly Glu Tyr
 275 280 285

Gly Val Ile Asp Leu Ala Asp Asn His Ala Lys Ile Arg Trp Leu Lys
 290 295 300

Asp Ile His Thr Thr Phe Ser Lys Tyr Gly Ile Gly Ser Ala Leu Trp
 305 310 315 320

Asn Tyr Lys Gly Lys Asp Phe Gly Tyr Val Asp Asp Arg Phe Ala Glu
 325 330 335

Cys Arg Glu Ala Phe Ile Glu Cys Leu Lys Ala
 340 345

<210> 61

<211> 1230

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 61

ttggtatgga caccagctcg atcaacgctt gctggatctt ctgaaatccc actaatgaca 60
 atgaatatat tcccgaatag aaaagactca cgaatgtccc tctggatcaa gcttggcata 120
 ctttgtatga tggctggaac ggtgatgggt cacggagcgc agactgggtca aggagaagca 180
 acaatgaatc aagcaaattgg cttcaaggta agcaacggga ccaatatcag ccattgggttg 240
 tcccagtgtt ttgaaacaat gccaccccg ggcggatttt tctccgaact ggatgttatc 300
 ttcacccgct cgctggggat ggatcatttc cgtcttcggg tggacgagaa ggaactttgg 360

```

acggaggatc ttgagaagat tcccgaagcg tgggattacc tcaggaatgc tctaagctgg      420
gctagaaagc atgagcttcg tgtgattgtg gatcttcacg tcgtgcgggc ccatcacttt      480
aatgcggcaa atgaaggggg aaccaacact ctgtgggatg atccggaggc gcaggaaagt      540
ttcctcaacc tttggaggca gctttcggca gagctcgctt acaccgatgt ggactgggtg      600
gcctatgaga tcatgaatga ggccgtcgcg gatgatccgg aggactggaa tcgtctcatc      660
gccaaagccc actccttgat ccgcgagcgt gagccaaggc gcacactcgt catcggatcc      720
aaccggtggc aaattccgtc aacgttcccg gatctgaaga ttccggacgg agatccgaac      780
atcctcctga gtttccattt ctacgcgctt ctgcttttca cccactatcg ggcaacctgg      840
gttgcctttt acgattatga tgggccgggtt tcctatcctg gcaggatcgt tgatgatgca      900
gctcttgaga aaaatgatta tactcctgca ttcaaagaca agattcgtgc gttgaatggg      960
gtgtatgaca tcgacgctct cgaaaaagaa atgcagccgg ctatcgaata cgcaaaacag     1020
aaagggttac cactgtattg cggagagtgg ggatgttttc atgctgtgga aagaaaacaa     1080
cgcttgcaat ggtacaaaga tatatccact attttgaaac gcaatgggat cgcccatgcc     1140
acatgggatt acaagggcga gttcggcatt gtggacactt ggacactagg tgttgattgg     1200
aatttggtag gagcaatcct gtcagagtag                                     1230

```

<210> 62

<211> 409

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (62)...(390)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (73)...(76)

<223> N-glycosylation site. Prosite id = PS00001

<400> 62

```

Met Val Trp Thr Pro Ala Arg Ser Thr Leu Ala Gly Ser Ser Glu Ile
1           5           10           15

```

```

Pro Leu Met Thr Met Asn Ile Phe Pro Asn Arg Lys Asp Ser Arg Met
          20           25           30

```

```

Ser Leu Trp Ile Lys Leu Gly Ile Leu Cys Met Met Ala Gly Thr Val
35           40           45

```


Met Val His Gly Ala Gln Thr Gly Gln Gly Glu Ala Thr Met Asn Gln
50 55 60

Ala Asn Gly Phe Lys Val Ser Asn Gly Thr Asn Ile Ser His Trp Leu
65 70 75 80

Ser Gln Cys Phe Glu Thr Met Pro Pro Arg Arg Gly Phe Phe Ser Glu
85 90 95

Leu Asp Val Ile Phe Ile Arg Ser Leu Gly Met Asp His Phe Arg Leu
100 105 110

Pro Val Asp Glu Lys Glu Leu Trp Thr Glu Asp Leu Glu Lys Ile Pro
115 120 125

Glu Ala Trp Asp Tyr Leu Arg Asn Ala Leu Ser Trp Ala Arg Lys His
130 135 140

Glu Leu Arg Val Ile Val Asp Leu His Val Val Arg Ser His His Phe
145 150 155 160

Asn Ala Ala Asn Glu Gly Gly Thr Asn Thr Leu Trp Asp Asp Pro Glu
165 170 175

Ala Gln Glu Ser Phe Leu Asn Leu Trp Arg Gln Leu Ser Ala Glu Leu
180 185 190

Ala Tyr Thr Asp Val Asp Trp Val Ala Tyr Glu Ile Met Asn Glu Ala
195 200 205

Val Ala Asp Asp Pro Glu Asp Trp Asn Arg Leu Ile Ala Lys Ala His
210 215 220

Ser Leu Ile Arg Glu Arg Glu Pro Arg Arg Thr Leu Val Ile Gly Ser
225 230 235 240

Asn Arg Trp Gln Ile Pro Ser Thr Phe Pro Asp Leu Lys Ile Pro Asp
245 250 255

Gly Asp Pro Asn Ile Leu Leu Ser Phe His Phe Tyr Ala Pro Leu Leu
260 265 270

Phe Thr His Tyr Arg Ala Thr Trp Val Ala Phe Tyr Asp Tyr Asp Gly
275 280 285

Pro Val Ser Tyr Pro Gly Arg Ile Val Asp Asp Ala Ala Leu Glu Lys
 290 295 300

Asn Asp Tyr Thr Pro Ala Phe Lys Asp Lys Ile Arg Ala Leu Asn Gly
 305 310 315 320

Val Tyr Asp Ile Asp Ala Leu Glu Lys Glu Met Gln Pro Ala Ile Glu
 325 330 335

Tyr Ala Lys Gln Lys Gly Leu Pro Leu Tyr Cys Gly Glu Trp Gly Cys
 340 345 350

Phe His Ala Val Glu Arg Lys Gln Arg Leu Gln Trp Tyr Lys Asp Ile
 355 360 365

Ser Thr Ile Leu Lys Arg Asn Gly Ile Ala His Ala Thr Trp Asp Tyr
 370 375 380

Lys Gly Glu Phe Gly Ile Val Asp Thr Trp Thr Leu Gly Val Asp Trp
 385 390 395 400

Asn Leu Val Gly Ala Ile Leu Ser Glu
 405

<210> 63
 <211> 1152
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 63
 atgaaacgga ggggaattcat gttgggggggt gcgggtggtg ctgcgttggc atcgactctt 60
 ggagtctccg ccggttccac ttccgggcag ggagtgaacg agaatgtgag ggtataccgg 120
 aatgcgattc cccgttggag ggggttcaac ctcatgccct ttttctcggc aatgagcacc 180
 aacccggaat acaatgggtct gacgggtgccg gaggatgacc taaactggat ccgcgactgg 240
 ggttttgact atgtccggct tccgattgat tactggattc tggttgattc cgattggcga 300
 gatgcaaagc gcatgcgggt agaggatggt cgcaaggccg accagaaggg atattcacgg 360
 ctggacgctg tgattgaagc ctgtatcgcg aagggtttgc acctcaacct gaatatgcat 420
 cgggtgtcccg ggtattgcat caatggctgg gaactggagc cctataacct cttcaaggat 480
 gagcaggcgg aggatgattt tgtctaccat tgggagttgc tcgcgagacg ctataaggga 540
 atcgatcctt cgctgctgag tttcaatctg ctgaatgagg ctcccaatcc tggagacaag 600

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atgtcgtcgg aggattatcg tcgggtgatg cttcgatccg ctgctgttat tcgggggata    660
agcccggacc gcatgattat tgtggacggg ctggaaatcg gtaaatacagt tgttccaggg    720
ctgatgcatg agccatttgc ccaagctggt catgcctacg agccccacga gttgagccat    780
tataatgcgc cttggacgtc ggtgtttatg ggtattcctg agccatcctg gccgacagtt    840
cgtttggatg gttctctgtt cgaccgcaag cgactggagt tgtatttcgc gccgtggggg    900
gagttggtcc gccaggggggt aggggtccac tgtggggaga ccggttgcta cattcatacg    960
ccccatcggg tgtttctgtc ctggttcgaa gatgttttgg atatacctgac cggatacga    1020
ataggggtggg ctctatggaa tttccgggga gatttcggaa tacttgattc caaacgcaag    1080
gatgtgcaat atgtcgattg gtatggacac cagctcgatc aacgcttgct ggatcttctg    1140
aatcccact aa                                                                1152

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<210> 64
 <211> 383
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SIGNAL
 <222> (1)...(24)

<220>
 <221> DOMAIN
 <222> (48)...(357)
 <223> Cellulase (glycosyl hydrolase family 5)

<400> 64
 Met Lys Arg Arg Glu Phe Met Leu Gly Gly Ala Gly Val Ala Ala Leu
 1 5 10 15

Ala Ser Thr Leu Gly Val Ser Ala Gly Ser Thr Ser Gly Gln Gly Val
 20 25 30

Asn Glu Asn Val Arg Val Tyr Arg Asn Ala Ile Pro Arg Trp Arg Gly
 35 40 45

Phe Asn Leu Met Pro Phe Phe Ser Ala Met Ser Thr Asn Pro Glu Tyr
 50 55 60

Asn Gly Leu Thr Val Pro Glu Asp Asp Leu Asn Trp Ile Arg Asp Trp
 65 70 75 80

Gly Phe Asp Tyr Val Arg Leu Pro Ile Asp Tyr Trp Ile Leu Val Asp
 85 90 95

Ser Asp Trp Arg Asp Ala Lys Arg Met Arg Val Glu Asp Val Arg Lys
 100 105 110

Ala Asp Gln Lys Gly Tyr Ser Arg Leu Asp Ala Val Ile Glu Ala Cys
 115 120 125

Ile Ala Lys Gly Leu His Leu Asn Leu Asn Met His Arg Cys Pro Gly
 130 135 140

Tyr Cys Ile Asn Gly Trp Glu Leu Glu Pro Tyr Asn Leu Phe Lys Asp
 145 150 155 160

Glu Gln Ala Glu Asp Asp Phe Val Tyr His Trp Glu Leu Leu Ala Arg
 165 170 175

Arg Tyr Lys Gly Ile Asp Pro Ser Leu Leu Ser Phe Asn Leu Leu Asn
 180 185 190

Glu Ala Pro Asn Pro Gly Asp Lys Met Ser Ser Glu Asp Tyr Arg Arg
 195 200 205

Val Met Leu Arg Ser Ala Ala Val Ile Arg Gly Ile Ser Pro Asp Arg
 210 215 220

Met Ile Ile Val Asp Gly Leu Glu Ile Gly Lys Ser Val Val Pro Gly
 225 230 235 240

Leu Met His Glu Pro Phe Ala Gln Ala Val His Ala Tyr Glu Pro His
 245 250 255

Glu Leu Ser His Tyr Asn Ala Pro Trp Thr Ser Val Phe Met Gly Ile
 260 265 270

Pro Glu Pro Ser Trp Pro Thr Val Arg Leu Asp Gly Ser Leu Phe Asp
 275 280 285

Arg Lys Arg Leu Glu Leu Tyr Phe Ala Pro Trp Gly Glu Leu Val Arg
 290 295 300

Gln Gly Val Gly Val His Cys Gly Glu Thr Gly Cys Tyr Ile His Thr
 305 310 315 320

Pro His Arg Val Phe Leu Ser Trp Phe Glu Asp Val Leu Asp Ile Leu
 325 330 335

Thr Gly Tyr Asp Ile Gly Trp Ala Leu Trp Asn Phe Arg Gly Asp Phe
 340 345 350

Gly Ile Leu Asp Ser Lys Arg Lys Asp Val Gln Tyr Val Asp Trp Tyr
 355 360 365

Gly His Gln Leu Asp Gln Arg Leu Leu Asp Leu Leu Lys Ser His
 370 375 380

<210> 65
 <211> 1131
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 65
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 gcggccgggg cgctggcggc cggatatggtc ctggcacccg tcagtgccgc caacgcggcc 120
 accaccctcg gtgcctcggc ggccggagaag ggccgggtact tcggtgcggc cgtcgggacg 180
 tacaagttca acgacagcac ctacatgtcg gtgctgaacc gcgagttcaa cagcctggtc 240
 gccgagaacg agatgaagtg ggacgcgacc gagccccagc gcggcgtggt caactacagc 300
 gccggggacc gcatcgtcaa ccacgcccga tcccagggca tgaaggtagc cggacacgcc 360
 ctgtttgtggc acgcccagca gccacgctgg acggagggcc tgtccggcgg cgacctgcgc 420
 aacgccgcga tcaaccatgt caccaggtg gccagccact tccgggggca gatctactcc 480
 tgggacgtgg tgaacgaggc ttctgccgac ggtggcagcg gtgcccggcg ggactcgaac 540
 ctccagcgca ccggcaacga ctggatcgag gcggcggttc gtgccgcccg ggcagccgat 600
 cccaacgcca agctctgcta caacgactac aacaccgacg ggatcaacgc gaagtccacc 660
 ggcgtctaca acatggtgcg tgacttcaag tcccgtgggg tgccgatcga ctgcgtgggc 720
 ttccagtcac acctgggcac caccctcccc ggtgactacc aggccaacct tcagcgcttc 780
 gccgacctgg gcgtcgacgt ggagatcacc gagctggaca tcacccaggg cggaaaccag 840
 gccaacatgt acggcgccgt caccgcgcgc tgccctggcg tctcgcgctg caccggcatc 900
 accgtgtggg gggtagggga ctgcgactcc tggcgtgggt gggacaacgc cctgctgttc 960
 gactgcgccg gcaacaagaa gcccgcgtag acggccgtcc tcgacgccct caacagcggc 1020
 tcgaaccgga accccaaccc caccggcaac cggctgcgca acgaggcctc cggtcgatgc 1080
 ctggacgtca acggcgcaag ctccgccaac gggtcacaaa tgatccaaag a 1131

<210> 66
 <211> 377

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(39)

<220>

<221> DOMAIN

<222> (42)...(337)

<223> Glycosyl hydrolase family 10

<220>

<221> SITE

<222> (99)...(102)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (268)...(278)

<223> Glycosyl hydrolases family 10 active site. Prosite id = PS00591

<220>

<221> SITE

<222> (375)...(378)

<223> N-glycosylation site. Prosite id = PS00001

<400> 66

Met	Asn	Thr	Leu	Leu	Pro	Arg	Arg	Arg	Leu	Trp	Ser	Ser	Thr	Ala	Ile
1				5					10					15	

Leu	Arg	Thr	Leu	Ala	Ala	Gly	Ala	Leu	Ala	Ala	Gly	Met	Val	Leu	Ala
			20					25					30		

Pro	Val	Ser	Ala	Ala	Asn	Ala	Ala	Thr	Thr	Leu	Gly	Ala	Ser	Ala	Ala
		35				40						45			

Glu	Lys	Gly	Arg	Tyr	Phe	Gly	Ala	Ala	Val	Gly	Thr	Tyr	Lys	Phe	Asn
	50					55					60				

Asp	Ser	Thr	Tyr	Met	Ser	Val	Leu	Asn	Arg	Glu	Phe	Asn	Ser	Leu	Val
65					70					75					80

Ala	Glu	Asn	Glu	Met	Lys	Trp	Asp	Ala	Thr	Glu	Pro	Gln	Arg	Gly	Val
				85					90					95	

Phe	Asn	Tyr	Ser	Ala	Gly	Asp	Arg	Ile	Val	Asn	His	Ala	Arg	Ser	Gln
			100					105						110	

Gly	Met	Lys	Val	Arg	Gly	His	Ala	Leu	Leu	Trp	His	Ala	Gln	Gln	Pro
		115					120					125			

Arg Trp Thr Glu Gly Leu Ser Gly Gly Asp Leu Arg Asn Ala Ala Ile
130 135 140

Asn His Val Thr Gln Val Ala Ser His Phe Arg Gly Gln Ile Tyr Ser
145 150 155 160

Trp Asp Val Val Asn Glu Ala Phe Ala Asp Gly Gly Ser Gly Ala Arg
165 170 175

Arg Asp Ser Asn Leu Gln Arg Thr Gly Asn Asp Trp Ile Glu Ala Ala
180 185 190

Phe Arg Ala Ala Arg Ala Ala Asp Pro Asn Ala Lys Leu Cys Tyr Asn
195 200 205

Asp Tyr Asn Thr Asp Gly Ile Asn Ala Lys Ser Thr Gly Val Tyr Asn
210 215 220

Met Val Arg Asp Phe Lys Ser Arg Gly Val Pro Ile Asp Cys Val Gly
225 230 235 240

Phe Gln Ser His Leu Gly Thr Thr Leu Pro Gly Asp Tyr Gln Ala Asn
245 250 255

Leu Gln Arg Phe Ala Asp Leu Gly Val Asp Val Glu Ile Thr Glu Leu
260 265 270

Asp Ile Thr Gln Gly Gly Asn Gln Ala Asn Met Tyr Gly Ala Val Thr
275 280 285

Arg Ala Cys Leu Ala Ile Ser Arg Cys Thr Gly Ile Thr Val Trp Gly
290 295 300

Val Arg Asp Cys Asp Ser Trp Arg Gly Gly Asp Asn Ala Leu Leu Phe
305 310 315 320

Asp Cys Ala Gly Asn Lys Lys Pro Ala Tyr Thr Ala Val Leu Asp Ala
325 330 335

Leu Asn Ser Gly Ser Asn Pro Asn Pro Asn Pro Thr Gly Asn Arg Leu
340 345 350

Arg Asn Glu Ala Ser Gly Arg Cys Leu Asp Val Asn Gly Ala Ser Ser
355 360 365

Ala Asn Gly Ser Gln Met Ile Gln Arg
370 375

<210> 67
<211> 1023
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 67
atgaaatata tatttttcgta tataataatg atgatttttaa tcggtttttat accggtctat 60
ggattcggcgc attcacctga ccaaacatac tctctcccct tcctcagcgt agaaggaaat 120
tcattcgtcg atgaaaacgg tgaggaggtt attttgcggg gtgtatcggt tcccgatccc 180
aatcgattgg atgatgctac tcaatggaac aaacgggtatt tccaggcagc aaaagattgg 240
aactgtaatg tcgtcagaat accggttcat ccgcaaagat ggcgggaaag gggaaaagaa 300
aattatctga aactttttaga taagggtatc gagtgggccc gtgaactcgg tatgtacgtg 360
atcattgact ggcacactat cggcaatccg attaccgaag tgttcttcgg cgagctctat 420
aatacgaccc agaccgaaac gttccgggttc tggagaacaa tagcggagcg atatgcaggt 480
aatcccgttg ttgcatttta tgaattgttt aatgaaccga ccgattataa cggtcggctc 540
gggaggatga cctgggatca atataaagaa ttcatcgaag agatcattta tataatttat 600
gcacacgacg aaaccgtgat accgcttgta ggcgggtttcg attggggata tgatctcagg 660
aatgttagag ataatccgat aaatgccccg ggtatcgcgt atgttactca cccgtatccg 720
caaaagcggg accaaccgtg ggaagaaaaa tgggaaaggg atttcggttt cgtagccgac 780
acctaccctg tgtttgctac cgagttcggg tttatgagtg aggatggttt ggggtgcacat 840
attcccgtta tcgggtgatga aacatacggg gaagcgatca tcagttactt caatgagaaa 900
ggtatatcgt ggacggcctg ggtgttcgat ccgctctggg cgccgcagct tattaagac 960
tggtatttta ccccgacccg gcagggacag ttttttaaag agaagctaag ggagttgaat 1020
taa 1023

<210> 68
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(23)

<220>

<221> DOMAIN

<222> (40)...(317)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (143)...(146)

<223> N-glycosylation site. Prosite id = PS00001

<400> 68

Met	Lys	Tyr	Ile	Phe	Ser	Tyr	Ile	Ile	Met	Met	Ile	Leu	Ile	Gly	Phe
1				5					10					15	

Ile	Pro	Val	Tyr	Gly	Phe	Gly	Asp	Ser	Pro	Asp	Gln	Thr	Tyr	Ser	Leu
		20						25					30		

Pro	Phe	Leu	Ser	Val	Glu	Gly	Asn	Ser	Phe	Val	Asp	Glu	Asn	Gly	Glu
		35					40					45			

Glu	Val	Ile	Leu	Arg	Gly	Val	Ser	Phe	Pro	Asp	Pro	Asn	Arg	Leu	Asp
	50					55					60				

Asp	Ala	Thr	Gln	Trp	Asn	Lys	Arg	Tyr	Phe	Gln	Ala	Ala	Lys	Asp	Trp
65					70					75					80

Asn	Cys	Asn	Val	Val	Arg	Ile	Pro	Val	His	Pro	Gln	Arg	Trp	Arg	Glu
			85						90					95	

Arg	Gly	Lys	Glu	Asn	Tyr	Leu	Lys	Leu	Leu	Asp	Lys	Gly	Ile	Glu	Trp
		100						105					110		

Ala	Gly	Glu	Leu	Gly	Met	Tyr	Val	Ile	Ile	Asp	Trp	His	Thr	Ile	Gly
		115					120					125			

Asn	Pro	Ile	Thr	Glu	Val	Phe	Phe	Gly	Glu	Leu	Tyr	Asn	Thr	Thr	Gln
	130					135					140				

Thr	Glu	Thr	Phe	Arg	Phe	Trp	Arg	Thr	Ile	Ala	Glu	Arg	Tyr	Ala	Gly
145					150					155					160

Asn	Pro	Val	Val	Ala	Phe	Tyr	Glu	Leu	Phe	Asn	Glu	Pro	Thr	Asp	Tyr
				165					170					175	

Asn	Gly	Arg	Leu	Gly	Arg	Met	Thr	Trp	Asp	Gln	Tyr	Lys	Glu	Phe	Ile
			180					185					190		

Glu	Glu	Ile	Ile	Tyr	Ile	Ile	Tyr	Ala	His	Asp	Glu	Thr	Val	Ile	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195	200	205
Leu Val Gly Gly Phe Asp Trp Gly Tyr Asp Leu Arg Asn Val Arg Asp 210 215 220		
Asn Pro Ile Asn Ala Pro Gly Ile Ala Tyr Val Thr His Pro Tyr Pro 225 230 235 240		
Gln Lys Arg Asp Gln Pro Trp Glu Glu Lys Trp Glu Arg Asp Phe Gly 245 250 255		
Phe Val Ala Asp Thr Tyr Pro Val Phe Ala Thr Glu Phe Gly Phe Met 260 265 270		
Ser Glu Asp Gly Leu Gly Ala His Ile Pro Val Ile Gly Asp Glu Thr 275 280 285		
Tyr Gly Glu Ala Ile Ile Ser Tyr Phe Asn Glu Lys Gly Ile Ser Trp 290 295 300		
Thr Ala Trp Val Phe Asp Pro Leu Trp Ser Pro Gln Leu Ile Lys Asp 305 310 315 320		
Trp Tyr Phe Thr Pro Thr Arg Gln Gly Gln Phe Phe Lys Glu Lys Leu 325 330 335		
Met Glu Leu Asn 340		

<210> 69
 <211> 1182
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 69
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 tgcgatatcg aagaaccgat cgccggagat tatcatacac ttgtggatca aaacgctata 120
 tcgcacaccc gcgcattatt caccaacctc gaacgtatcc gtcacgatca tatectcttc 180
 ggtcatcagg atgcgcttgc atacggtggt cactggcgca acgatgagcc gggtcgatcg 240
 gatgtattcg aagtaaccgg ttcgtatcct gcggtgtatg gctgggagat tggcgatatt 300
 gaacttgggtg caccggaaaa tctggataac gttaaacttcg atcaaataca gggctggatt 360
 cgccaagggt acgaacgcgg cggtataatt acgattagct ggcatatgaa caatccggca 420

tcggggtgggtg attcgtggga tgtgaatgga ggtcataaag cggtaactaa gatacttccc 480
ggcgggagaac ttcacgatac gtttaaagaa tggctggata cgtttgcaaa attcgcgaag 540
agccagattg cttttcccga aacaaataat gaacacctta tcccgggtcat attccggccg 600
tatcatgaaa acaccggaag ctggttcttg tggggcgccg accactgtac acctgaagaa 660
tataaaaagt tatggcgatt taccgtcgaa tacctgcgcg atgtaaaagg tgttcacaat 720
ctcctctggg cgtattcacc tgccggcaat gctgcggatt cagaggaagc atattttgct 780
cggtatcccg gcgacgacta tgttgatatt attggattcg acgattacgg cagtgtgcgg 840
aaaccgtatc aaatcgaacg ttttactaac cggattcgaa cgattgtaaa cttcgccgaa 900
gcacgaaata aaatcccggc aataacggaa accggctatg aaactatccc cgatccgcaa 960
tggtggacgg gtacattgct tagtgcactt gatcacgatt tgacaacccg gagaatagca 1020
tacgtacttg tgtggcgaaa ttcaaacaat gctaccgacc ggcagaatca ttattacgct 1080
ccgtatcccg gacatccaag tgctgacgat tttatcgcgt tcaggaatca cccgttgata 1140
gttttcgaag atgatctgcc gggatatgtat acactaccgt aa 1182

<210> 70

<211> 393

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(20)

<220>

<221> DOMAIN

<222> (35)...(351)

<223> Glycosyl hydrolase family 26

<220>

<221> SITE

<222> (355)...(358)

<223> N-glycosylation site. Prosite id = PS00001

<400> 70

Met Ser Phe Lys Asn His Ile Leu Leu Ser Leu Leu Ile Val Leu Leu
1 5 10 15

Phe Phe Ser Ala Cys Asp Ile Glu Glu Pro Ile Ala Gly Asp Tyr His
20 25 30

Thr Leu Val Asp Gln Asn Ala Ile Ser His Thr Arg Ala Leu Phe Thr
35 40 45

Asn Leu Glu Arg Ile Arg His Asp His Ile Leu Phe Gly His Gln Asp
 50 55 60

Ala Leu Ala Tyr Gly Val His Trp Arg Asn Asp Glu Pro Gly Arg Ser
 65 70 75 80

Asp Val Phe Glu Val Thr Gly Ser Tyr Pro Ala Val Tyr Gly Trp Glu
 85 90 95

Ile Gly Asp Ile Glu Leu Gly Ala Pro Glu Asn Leu Asp Asn Val Asn
 100 105 110

Phe Asp Gln Met Gln Gly Trp Ile Arg Glu Gly Tyr Glu Arg Gly Gly
 115 120 125

Ile Ile Thr Ile Ser Trp His Met Asn Asn Pro Ala Ser Gly Gly Asp
 130 135 140

Ser Trp Asp Val Asn Gly Gly His Lys Ala Val Thr Lys Ile Leu Pro
 145 150 155 160

Gly Gly Glu Leu His Asp Thr Phe Lys Glu Trp Leu Asp Thr Phe Ala
 165 170 175

Lys Phe Ala Lys Ser Gln Ile Ala Phe Pro Glu Thr Asn Asn Glu His
 180 185 190

Leu Ile Pro Val Ile Phe Arg Pro Tyr His Glu Asn Thr Gly Ser Trp
 195 200 205

Phe Trp Trp Gly Ala Asp His Cys Thr Pro Glu Glu Tyr Lys Lys Leu
 210 215 220

Trp Arg Phe Thr Val Glu Tyr Leu Arg Asp Val Lys Gly Val His Asn
 225 230 235 240

Leu Leu Trp Ala Tyr Ser Pro Ala Gly Asn Ala Ala Asp Ser Glu Glu
 245 250 255

Ala Tyr Phe Ala Arg Tyr Pro Gly Asp Asp Tyr Val Asp Ile Ile Gly
 260 265 270

Phe Asp Asp Tyr Gly Ser Val Arg Lys Pro Tyr Gln Ile Glu Arg Phe
 275 280 285

Thr Asn Arg Ile Arg Thr Ile Val Asn Phe Ala Glu Ala Arg Asn Lys
 290 295 300

Ile Pro Ala Ile Thr Glu Thr Gly Tyr Glu Thr Ile Pro Asp Pro Gln
 305 310 315 320

Trp Trp Thr Gly Thr Leu Leu Ser Ala Leu Asp His Asp Leu Thr Thr
 325 330 335

Arg Arg Ile Ala Tyr Val Leu Val Trp Arg Asn Ser Asn Asn Ala Thr
 340 345 350

Asp Arg Gln Asn His Tyr Tyr Ala Pro Tyr Pro Gly His Pro Ser Ala
 355 360 365

Asp Asp Phe Ile Ala Phe Arg Asn His Pro Leu Ile Val Phe Glu Asp
 370 375 380

Asp Leu Pro Gly Met Tyr Thr Leu Pro
 385 390

<210> 71

<211> 1089

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 71

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agaaggggag aagagcgaaa agagttcttt actaagaatg acgtagaatt tattgcaggc	180
atcggcttcg atcatattcg ttttctatt gacgaggagc aaatgtggga tgaaaaaggc	240
aacaaagagc ctgaagcgtt tcagttgctg cacaacgcga tagaatggag caggcaatcg	300
aacttaaaag ttattgtgga cctgcatatt ttgaggtcgc attatttcaa cgcggaagaa	360
aaaccgcttt ttacggaccc taaagctcag gaacgttttt accaatgttg ggcggatctg	420
tctggtgaat tgaaaaaata tccgaataca ctggtggctt atgaattaat gaacgaacct	480
gtagccgatg atccggaaga ctggaataga attgtaagag aatcagtaaa aaggctaagg	540
gtgcttgagc ccaatagggt tattgtaatc gggcttaacc gatggcagca ttatgacact	600
ctgaaggatt tatacgtgcc ggaaaacgac aaaaacatca ttttaagctt tcatttttat	660
aaccctatgt tgcttacgca ttacagggcc agctgggtaa atttcggcga ttaccagggt	720

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cccgттаact acccgggaca gttggtagac tcaaagcatt tgtcgggact gagcgaagat    780
ttaagaaaga aagtcgagca aaacaatggc gtttataata aggctcggat tgagaaaatg    840
atagccgaag ccgttgctgt agcaaaaaag cacaacctcc ctttgtattg tggatgaatgg    900
ggtgcctacg aaaaagcgcc aaggagagccc aggctacaat ggtacagaga catggtggat    960
gtgttgaaca aaaacaatat tgcctggact acctgggact ataaaggagg cttcggcata   1020
gttgacgcca aaggaaacaa agacgaacag ttgatcaatg tattaacagg aaaagagaaa   1080
aaaatgtaa                                     1089

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<210> 72
 <211> 362
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SIGNAL
 <222> (1)...(21)

<220>
 <221> DOMAIN
 <222> (22)...(340)
 <223> Cellulase (glycosyl hydrolase family 5)

<220>
 <221> SITE
 <222> (31)...(34)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (154)...(163)
 <223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<400> 72
 Met Lys Leu Leu Lys Leu Leu Ile Phe Leu Leu Ile Thr Val Ile Phe
 1 5 10 15

Ser Asp Val Ser Ala Gln Thr Phe Gln Ile Gln Lys Gly Lys Asn Ile
 20 25 30

Ser His Trp Leu Ser Gln Ser Lys Arg Arg Gly Glu Glu Arg Lys Glu
 35 40 45

Phe Phe Thr Lys Asn Asp Val Glu Phe Ile Ala Gly Ile Gly Phe Asp
 50 55 60

His Ile Arg Ile Pro Ile Asp Glu Glu Gln Met Trp Asp Glu Lys Gly
 65 70 75 80

Asn Lys Glu Pro Glu Ala Phe Gln Leu Leu His Asn Ala Ile Glu Trp
85 90 95

Ser Arg Gln Ser Asn Leu Lys Val Ile Val Asp Leu His Ile Leu Arg
100 105 110

Ser His Tyr Phe Asn Ala Glu Glu Lys Pro Leu Phe Thr Asp Pro Lys
115 120 125

Ala Gln Glu Arg Phe Tyr Gln Cys Trp Ala Asp Leu Ser Gly Glu Leu
130 135 140

Lys Lys Tyr Pro Asn Thr Leu Val Ala Tyr Glu Leu Met Asn Glu Pro
145 150 155 160

Val Ala Asp Asp Pro Glu Asp Trp Asn Arg Ile Val Arg Glu Ser Val
165 170 175

Lys Arg Leu Arg Val Leu Glu Pro Asn Arg Val Ile Val Ile Gly Ser
180 185 190

Asn Arg Trp Gln His Tyr Asp Thr Leu Lys Asp Leu Tyr Val Pro Glu
195 200 205

Asn Asp Lys Asn Ile Ile Leu Ser Phe His Phe Tyr Asn Pro Met Leu
210 215 220

Leu Thr His Tyr Arg Ala Ser Trp Val Asn Phe Gly Asp Tyr Gln Gly
225 230 235 240

Pro Val Asn Tyr Pro Gly Gln Leu Val Asp Ser Lys His Leu Ser Gly
245 250 255

Leu Ser Glu Asp Leu Arg Lys Lys Val Glu Gln Asn Asn Gly Val Tyr
260 265 270

Asn Lys Ala Arg Ile Glu Lys Met Ile Ala Glu Ala Val Ala Val Ala
275 280 285

Lys Lys His Asn Leu Pro Leu Tyr Cys Gly Glu Trp Gly Ala Tyr Glu
290 295 300

Lys Ala Pro Arg Glu Pro Arg Leu Gln Trp Tyr Arg Asp Met Val Asp
305 310 315 320

Gly Phe Gly Ile Val Asp Ala Lys Gly Asn Lys Asp Glu Gln Leu Ile
340 345 350

Asn Val Leu Thr Gly Lys Glu Lys Lys Met
355 360

<210>	73
<211>	1146
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from environmental sample

<400> 73						
gtggatatta	cgggacatcc	cgaccacatc	gccttcgcgc	gggaagttgc	cgagcaaagc	60
atggtctttgc	tgcaaaaccg	tgcgaacctc	gcccccttt	cggtatctga	ctattccacc	120
attgccgtga	tgggcccga	tgccaatgac	actttgctgg	gttcttacag	cggcggttccg	180
aaaacctact	acacggtact	cgacgggata	cggtcctatg	tcggtgaccg	ggcgaatgtg	240
gtttacgctc	agggggccga	gataaccaaa	cccggccatc	gggaggacaa	tgaagtattt	300
ccaccggatc	ctgaaaacga	ccggagacga	ctggccgaag	cgatagctgt	cgccgagAAC	360
gccgacctga	tcatacctgc	gatcggcggc	aatgaactga	cgggacgaga	ggcatgggcg	420
gcgcatacatc	cgggtgatcg	accggatctg	tcgttgctcg	gtttgcagga	ggatcttggt	480
gacgcagttg	gagcgatggg	ggttccatct	gtcgcattgg	ttttcgggtgc	acggccgctg	540
gacctcggca	atgtcgccga	aaaaattgat	gtggtcttcc	aaaactggta	cctggggccag	600
gaaaccggca	atgccgtcgc	caatgtgctg	tttggcgagg	tgtcaccgtc	cgccaaactc	660
cccatcagct	tcccgcggac	tgccggggcac	attcctgcct	actacaatta	caaaccatcg	720
gctcgacggg	tctacctttt	tgacgatgtc	actccgcggt	accatttcgg	gtacggcctc	780
agctatacga	cgtttgaata	cggggaaccg	cagctatcgg	atacactact	gtctggcgat	840
ggtgaaataa	ccctctacgt	tgaagttacc	aacaccggag	agcgaggcgg	ttcggaagtc	900
gtgcaactgt	acatcaacca	cgaatacaga	tccgtcacc	ggccggtaaa	ggagctcaag	960
ggattcgaaa	aggtgtatct	cgagccgaat	gaaactgccg	gtgtatcggt	caccatcact	1020
tcagatcagt	tgaggttctg	gaatatcgac	atggagttta	ccgctgaatc	cggtaaagtg	1080
aacctgatgg	tcggctcatc	cagccgtgac	gaagacctgc	agacgacggc	aatTTTTctt	1140
gaataa						1146

<210> 74
 <211> 381
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (21)...(264)
 <223> Glycosyl hydrolase family 3 C terminal domain

<220>
 <221> SITE
 <222> (49)...(52)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (335)...(338)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 74
 Met Asp Ile Thr Gly His Pro Asp His Ile Ala Phe Ala Arg Glu Val
 1 5 10 15

 Ala Glu Gln Ser Met Val Leu Leu Gln Asn Arg Ala Asn Leu Ala Pro
 20 25 30

 Leu Ser Val Ser Asp Tyr Ser Thr Ile Ala Val Ile Gly Pro Asn Ala
 35 40 45

 Asn Asp Thr Leu Leu Gly Ser Tyr Ser Gly Val Pro Lys Thr Tyr Tyr
 50 55 60

 Thr Val Leu Asp Gly Ile Arg Ser Tyr Val Gly Asp Arg Ala Asn Val
 65 70 75 80

 Val Tyr Ala Gln Gly Pro Lys Ile Thr Lys Pro Gly His Arg Glu Asp
 85 90 95

 Asn Glu Val Phe Pro Pro Asp Pro Glu Asn Asp Arg Arg Arg Leu Ala
 100 105 110

 Glu Ala Ile Ala Val Ala Glu Asn Ala Asp Leu Ile Ile Leu Ala Ile
 115 120 125

 Gly Gly Asn Glu Leu Thr Gly Arg Glu Ala Trp Ala Ala His His Pro
 130 135 140

 Gly Asp Arg Pro Asp Leu Ser Leu Leu Gly Leu Gln Glu Asp Leu Val

<211> 1014

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 75

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ctggggtacg acccaatctg gcacgacccg aagaaagggtc ggttcgaaga gcggcacttc      180
gccgagattc gcaagggcgagg cttcgacttc gttcgggtga acctccacgg gttcaaacaat      240
atgaacgccc cggacaaact cagtccggag ttcctgagcc gcgtggactg gatcgtgaag      300
cacgccagtg cggcggggcct gtcgggtcatc ctagacgagc atgaatatga ggaatgctcg      360
gacgacgtcg caatgtgccg gcggcggtttg gcggcattct ggacgcaggt cgcgccgcgc      420
tacaagggcg cgcccgatac ggttctgttc gagcttctca atgagccgca cgacaagttg      480
gatgccgaca cctggaacgc cttgtttccc gacatcctgg ccatcgtgag gcagtcgaac      540
ccgaagcgcc gcgtgggtgat cggcccgact cagtgggaaca acttcagcca gctggacacg      600
ctcaagctgc cggcagacga ccggaacatc gtcgtcacct tccattatta cgatccgttc      660
ccgtttaccc accagggcgcg gccgtggggt cgggacatgc tcaaggtgaa aggcacgag      720
tggaagcccc agcagagggc gaagatcgcc gaggacttcg gcaaggctcg ggaatggctg      780
cagaaaaccg gccgcgaaat cttgctcggc gagttcgggg cctacgatgt gagcgggtacg      840
ccaaccgcca tgcgttcagc ttatacggaa gcgggtggcg gcgagggcga acgccacggc      900
ttcgcttggg cctactggca gttcgacagc aatttcctgg cttgggacat gaagacaaac      960
ggctgggtcg agccgatcca caaggcactc atccccgagg cgaagcagcc ttag          1014
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<210> 76

<211> 337

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (37)...(316)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (150)...(159)

<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<400> 76

Met Leu Arg Lys Leu Ile Val Ser Val Phe Gly Phe Val Met Leu Thr

1	5	10	15
Ser	Ala	Ala	Ala
	20	25	30
Ala	Leu	Arg	Arg
	35	40	45
Asp	Pro	Lys	Lys
	50	55	60
Lys	Gly	Gly	Phe
65		70	
Met	Asn	Ala	Ala
	85	90	95
Trp	Ile	Val	Lys
	100	105	110
Glu	His	Glu	Tyr
	115	120	125
Arg	Leu	Ala	Ala
	130	135	140
Pro	Asp	Thr	Val
145		150	
Asp	Ala	Asp	Thr
	165	170	175
Arg	Gln	Ser	Asn
	180	185	190
Asn	Asn	Phe	Ser
	195	200	205
Asn	Ile	Val	Val
	210	215	220
Gln	Gly	Ala	Pro
225		230	
Trp	Lys	Pro	Glu
	245	250	255

Ala Glu Trp Ser Gln Lys Thr Gly Arg Glu Ile Leu Leu Gly Glu Phe
260 265 270

Gly Ala Tyr Asp Val Ser Gly Thr Pro Thr Ala Met Arg Ser Ala Tyr
275 280 285

Thr Glu Ala Val Ala Arg Glu Ala Glu Arg His Gly Phe Ala Trp Ala
290 295 300

Tyr Trp Gln Phe Asp Ser Asn Phe Leu Ala Trp Asp Met Lys Thr Asn
305 310 315 320

Gly Trp Val Glu Pro Ile His Lys Ala Leu Ile Pro Glu Ala Lys Gln
325 330 335

Pro

<210> 77
<211> 1125
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 77
atgaaaagga aacgggtttt tattcattct ctaatcgtat tttttttaat gattggttct 60
tttacttctt gtggatcagt cgccgatgat gccgaagaag ggtttgatat ttttagagga 120
accaatatcg ctcatgggtt atcacaaagt aatgcaaggg gcgaagagcg aaaaaatttc 180
tttaccgaaa atgatataaa atttattgct gatgctgggt ttgatcatat tcgtttgcca 240
attgacgagg ttcatcttct ggatgagaat atgaaccggc accaagatgc atttgatctt 300
atgcatgact gtattaagtg gtcagagaaa catggctctta gggttgtagt ggatttgcat 360
attattcggt cacattatct tgttggagat gataatacac tatgggatga aagacatgaa 420
caggaaaagt ttgttgatat ttggatggag ttatcatctg aactatctca atattcaaac 480
tcattagtag cttatgagtt aatgaatgaa cctgtagccc cttctcatga tgattggaat 540
agtttggttg cggaaactat agaggcaatt cgtaaagttg aacctgagag atatattgta 600
gttggatcaa atatgtggca aggtattgat acatttgagt atttggaagt tcccgaaaat 660
gatgatagaa taattcttag ttttcatttt tatgatccct ttattttgac tcattatact 720
gcatcttggg ggtatttaag agattactca gggcctgtta actatccggg atatcttggt 780

acaaatgacc agctgttgga tatgtcaaac gaaatgcaaa agttaattag ggagtttcag 840
acaaattttg atatttatac cattgaagaa ctgatatcta ttccatatag tattgcaaag 900
gaaaaagggg tgaaattata ttgtggagag tttgggtgcaa ttgatcaggc tccaagagat 960
gcgagattgg catggtacag agatgttggt caggtttttg agcgatatgg tatagctcat 1020
gccaactgga attacaaaga ttatggtacg tttggggataa agaactatag cgaggagata 1080
gatcaggaac tgtttgaaat cttaattgga acaaaacata aatag 1125

<210> 78

<211> 374

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(28)

<220>

<221> DOMAIN

<222> (25)...(353)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (165)...(174)

<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<220>

<221> SITE

<222> (360)...(363)

<223> N-glycosylation site. Prosite id = PS00001

<400> 78

Met Lys Arg Lys Arg Val Phe Ile His Ser Leu Ile Val Phe Phe Leu
1 5 10 15

Met Ile Gly Ser Phe Thr Ser Cys Gly Ser Val Ala Asp Asp Ala Glu
20 25 30

Glu Gly Phe Asp Ile Phe Arg Gly Thr Asn Ile Ala His Trp Leu Ser
35 40 45

Gln Ser Asn Ala Arg Gly Glu Glu Arg Lys Asn Phe Phe Thr Glu Asn
50 55 60

Asp Ile Lys Phe Ile Ala Asp Ala Gly Phe Asp His Ile Arg Leu Pro
65 70 75 80

Ile Asp Glu Val His Phe Trp Asp Glu Asn Met Asn Arg His Gln Asp

85

90

95

Ala Phe Asp Leu Met His Asp Cys Ile Lys Trp Ser Glu Lys His Gly
 100 105 110

Leu Arg Val Val Val Asp Leu His Ile Ile Arg Ser His Tyr Phe Val
 115 120 125

Gly Asp Asp Asn Thr Leu Trp Asp Glu Arg His Glu Gln Glu Lys Phe
 130 135 140

Val Asp Ile Trp Met Glu Leu Ser Ser Glu Leu Ser Gln Tyr Ser Asn
 145 150 155 160

Ser Leu Val Ala Tyr Glu Leu Met Asn Glu Pro Val Ala Pro Ser His
 165 170 175

Asp Asp Trp Asn Ser Leu Val Ala Glu Thr Ile Glu Ala Ile Arg Lys
 180 185 190

Val Glu Pro Glu Arg Tyr Ile Val Val Gly Ser Asn Met Trp Gln Gly
 195 200 205

Ile Asp Thr Phe Glu Tyr Leu Glu Val Pro Glu Asn Asp Asp Arg Ile
 210 215 220

Ile Leu Ser Phe His Phe Tyr Asp Pro Phe Ile Leu Thr His Tyr Thr
 225 230 235 240

Ala Ser Trp Gly Tyr Leu Arg Asp Tyr Ser Gly Pro Val Asn Tyr Pro
 245 250 255

Gly Tyr Leu Val Thr Asn Asp Gln Leu Leu Asp Met Ser Asn Glu Met
 260 265 270

Gln Lys Leu Ile Arg Glu Phe Gln Thr Asn Phe Asp Ile Tyr Thr Ile
 275 280 285

Glu Glu Leu Ile Ser Ile Pro Tyr Ser Ile Ala Lys Glu Lys Gly Leu
 290 295 300

Lys Leu Tyr Cys Gly Glu Phe Gly Ala Ile Asp Gln Ala Pro Arg Asp
 305 310 315 320

Ala Arg Leu Ala Trp Tyr Arg Asp Val Val Gln Val Phe Glu Arg Tyr
 325 330 335

Gly Ile Ala His Ala Asn Trp Asn Tyr Lys Asp Tyr Gly Thr Phe Gly
 340 345 350

Ile Lys Asn Tyr Ser Glu Glu Ile Asp Gln Glu Leu Phe Glu Ile Leu
 355 360 365

Ile Gly Thr Lys His Lys
 370

<210> 79
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 79
 atgaaatata aagctatttt tatatacctt attgttttga ttctatttta ctcaattaat 60
 atttatgcta atgcagaaaa caaccccctc cccttcctca gtgtcgaagg aaacaggttc 120
 gtcgatgaag atggaaatac ggtaatcctg cgaggtgtat cgttccccga tcccgaccgg 180
 ctggctgagg caactcaatg gaacaagcga tacttccagg cggcaaaaga ctggaactgt 240
 aatgtcgtcc ggattcctgt ccatccacag aaatggcggg aaagaggcga ggaaaattat 300
 ctgaaacttt tagataaggg aattcaatgg gcgggtgaac tcgggatgta tgtaatcatc 360
 gactggcata ccatcggtaa tccgataacc gaagtatttt tccgcgaact atacaatacg 420
 tcacgtgcgg agaccttcca gttctggaga acaatcgctg agcgctatgc cggtaaccgc 480
 gttgttgctt tctatgaact gttcaatgaa ccgaccgact acaacggccg tctcggaaga 540
 atgaactggg atcagtataa agagttttatc gaggagataa ttcacatcat ctattctcac 600
 gacgatacag ttatccctct cgttgccggt ttcgactggg cgtatgaact ccgccatata 660
 aaagataaac ctatagattt tcccggcata gcttatgtga ctcacccta tccccagaaa 720
 cgcgatccgc catgggaaga aaaatgggaa gaggatttcg ggtttgccgc cgatatgtat 780
 ccggtgtttg caaccgagtt cggtttcatg ggggaggatg aattaggtgc acacataccc 840
 gtcacggcg atgaaacata cggcgaagcc attatcgatt acttttataa aaaggggata 900
 tcgtggactg catgggtatt cgatccgctt tggtcgccgc agcttattag agactggtat 960
 tttaaccctg cccgacaggg gcagtttttt aaagagaagt tgatggagtt gaattag 1017

<210> 80
 <211> 338
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(25)

<220>

<221> DOMAIN

<222> (38)...(315)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (141)...(144)

<223> N-glycosylation site. Prosite id = PS00001

<400> 80

Met	Lys	Tyr	Lys	Ala	Ile	Phe	Ile	Tyr	Leu	Ile	Val	Leu	Ile	Leu	Phe
1				5					10					15	

Tyr	Ser	Ile	Asn	Ile	Tyr	Ala	Asn	Ala	Glu	Asn	Asn	Pro	Leu	Pro	Phe
			20					25					30		

Leu	Ser	Val	Glu	Gly	Asn	Arg	Phe	Val	Asp	Glu	Asp	Gly	Asn	Thr	Val
		35					40					45			

Ile	Leu	Arg	Gly	Val	Ser	Phe	Pro	Asp	Pro	Asp	Arg	Leu	Ala	Glu	Ala
	50					55					60				

Thr	Gln	Trp	Asn	Lys	Arg	Tyr	Phe	Gln	Ala	Ala	Lys	Asp	Trp	Asn	Cys
65					70					75					80

Asn	Val	Val	Arg	Ile	Pro	Val	His	Pro	Gln	Lys	Trp	Arg	Glu	Arg	Gly
				85					90					95	

Glu	Glu	Asn	Tyr	Leu	Lys	Leu	Leu	Asp	Lys	Gly	Ile	Gln	Trp	Ala	Gly
			100					105					110		

Glu	Leu	Gly	Met	Tyr	Val	Ile	Ile	Asp	Trp	His	Thr	Ile	Gly	Asn	Pro
		115					120					125			

Ile	Thr	Glu	Val	Phe	Phe	Arg	Glu	Leu	Tyr	Asn	Thr	Ser	Arg	Ala	Glu
	130					135					140				

Thr	Phe	Gln	Phe	Trp	Arg	Thr	Ile	Ala	Glu	Arg	Tyr	Ala	Gly	Asn	Pro
145					150					155					160

Val	Val	Ala	Phe	Tyr	Glu	Leu	Phe	Asn	Glu	Pro	Thr	Asp	Tyr	Asn	Gly
				165					170					175	

Arg Leu Gly Arg Met Asn Trp Asp Gln Tyr Lys Glu Phe Ile Glu Glu
180 185 190

Ile Ile His Ile Ile Tyr Ser His Asp Asp Thr Val Ile Pro Leu Val
195 200 205

Ala Gly Phe Asp Trp Ala Tyr Glu Leu Arg His Ile Lys Asp Lys Pro
210 215 220

Ile Asp Phe Pro Gly Ile Ala Tyr Val Thr His Pro Tyr Pro Gln Lys
225 230 235 240

Arg Asp Pro Pro Trp Glu Glu Lys Trp Glu Glu Asp Phe Gly Phe Ala
245 250 255

Ala Asp Met Tyr Pro Val Phe Ala Thr Glu Phe Gly Phe Met Gly Glu
260 265 270

Asp Glu Leu Gly Ala His Ile Pro Val Ile Gly Asp Glu Thr Tyr Gly
275 280 285

Glu Ala Ile Ile Asp Tyr Phe Tyr Lys Lys Gly Ile Ser Trp Thr Ala
290 295 300

Trp Val Phe Asp Pro Leu Trp Ser Pro Gln Leu Ile Arg Asp Trp Tyr
305 310 315 320

Phe Thr Pro Ser Arg Gln Gly Gln Phe Phe Lys Glu Lys Leu Met Glu
325 330 335

Leu Asn

<210> 81
<211> 1119
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 81
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ttcgtagtt ctgcagcgaa tcatcattat gaaaaaata cagtcaacga attttctgat 120
gatgtaaadc aaacaacatt agtccttcaa cccgggatat ccgaagccca gaataactcaa 180

aacctgccgc ggatttcggt tgaaggaaac caatttgtgg atgaatcggg aaacacagtc 240
acatttcagg gtgtcagtgt tgccgatccg cacaggctta ataatgccgg ccaatggaaa 300
cgggaactgt ttgaagaaat cgcaaactgg ggagcaaacg tcgttcgtct gccatacac 360
ccgctctggt ggcgggaacg gggagaggag caatacctcg aatggattga tgaagccgtg 420
gagtgggcca aagagctgga gatgtacctc atcatcgact ggcacagtat cgggaacctg 480
cggacagaac tcttttttcag ggatatctac aacaccaccc gccgtgaaac ttatgaattc 540
tggaggctga tttcggatcg ctatgctgat gaaaccacaa ttgcctttta cgaaatcttt 600
aatgaacca cacggcagca gggcaggctg ggaaccatga cctggaagca atggaaggaa 660
attctaaccg acattatcac aatcatttat gccacaatc ctgatgcgat tccgctggta 720
gcaggtttta actgggcgta tgaccttact ccggtccgcc actcaccctt cgattttgaa 780
ggtattgcct atgttaccca cccatatccg caaaaaagaa gcaggccctg ggttccaaaa 840
tgggaagaag atttcggttt tgtggctgac aaatatcctg tatttgccac tgaattcggc 900
tatatgaggg agtatgagcg gggcgctcat gtgcccgtaa tcggggacga agaatatggg 960
gaaatcctca tcaattatth ccgcgaaaaa gggatttcgt ggacagcctg ggtattcgat 1020
ccaagctggt cgccacagct cattcaggat tgggattata caccacacg ctcagggtgag 1080
tttttcagaa atgcgatgag aacgaaaaac aatgaataa 1119

<210> 82
<211> 372
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(25)

<220>
<221> DOMAIN
<222> (70)...(347)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (43)...(46)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (173)...(176)
<223> N-glycosylation site. Prosite id = PS00001

<400> 82
Met Asn Leu Leu Ala Gln Tyr Phe Ser Gly Leu Phe Leu Ile Phe Leu

1	5	10	15
Ile Ser Ile Phe Phe Val Ser Ser Ala Ala Asn His His Tyr Glu Lys	20	25	30
Asn Thr Val Asn Glu Phe Ser Asp Asp Val Asn Gln Thr Thr Leu Val	35	40	45
Leu Gln Pro Gly Ile Ser Glu Ala Gln Asn Thr Gln Asn Leu Pro Arg	50	55	60
Ile Ser Val Glu Gly Asn Gln Phe Val Asp Glu Ser Gly Asn Thr Val	65	70	75
Thr Phe Gln Gly Val Ser Val Ala Asp Pro His Arg Leu Asn Asn Ala	85	90	95
Gly Gln Trp Lys Arg Glu Leu Phe Glu Glu Ile Ala Asn Trp Gly Ala	100	105	110
Asn Val Val Arg Leu Pro Ile His Pro Leu Trp Trp Arg Glu Arg Gly	115	120	125
Glu Glu Gln Tyr Leu Glu Trp Ile Asp Glu Ala Val Glu Trp Ala Lys	130	135	140
Glu Leu Glu Met Tyr Leu Ile Ile Asp Trp His Ser Ile Gly Asn Leu	145	150	155
Arg Thr Glu Leu Phe Phe Arg Asp Ile Tyr Asn Thr Thr Arg Arg Glu	165	170	175
Thr Tyr Glu Phe Trp Arg Leu Ile Ser Asp Arg Tyr Ala Asp Glu Thr	180	185	190
Thr Ile Ala Phe Tyr Glu Ile Phe Asn Glu Pro Thr Arg Gln Gln Gly	195	200	205
Arg Leu Gly Thr Met Thr Trp Lys Gln Trp Lys Glu Ile Leu Thr Asp	210	215	220
Ile Ile Thr Ile Ile Tyr Ala His Asn Pro Asp Ala Ile Pro Leu Val	225	230	235
Ala Gly Phe Asn Trp Ala Tyr Asp Leu Thr Pro Val Arg His Ser Pro	245	250	255

Leu Asp Phe Glu Gly Ile Ala Tyr Val Thr His Pro Tyr Pro Gln Lys
260 265 270

Arg Ser Arg Pro Trp Val Pro Lys Trp Glu Glu Asp Phe Gly Phe Val
275 280 285

Ala Asp Lys Tyr Pro Val Phe Ala Thr Glu Phe Gly Tyr Met Arg Glu
290 295 300

Tyr Glu Arg Gly Ala His Val Pro Val Ile Gly Asp Glu Glu Tyr Gly
305 310 315 320

Glu Ile Leu Ile Asn Tyr Phe Arg Glu Lys Gly Ile Ser Trp Thr Ala
325 330 335

Trp Val Phe Asp Pro Ser Trp Ser Pro Gln Leu Ile Gln Asp Trp Asp
340 345 350

Tyr Thr Pro Thr Arg Ser Gly Glu Phe Phe Arg Asn Ala Met Arg Thr
355 360 365

Lys Asn Asn Glu
370

<210> 83
<211> 1089
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 83
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ggcgtgccga tcgttctgcg cgagggcgac gtgcaggcgc tgggtgctggc ggtcgagcca 120
gtaaccgagg cgcggctggg tgggctgcbc gggctggggc cagggctggg gcttgcaatc 180
acgcagcgcc gcgccacgac actgaaggcg cgcgcctatg atgaggatct tgcgcgagtg 240
gtgggtgccc agggggtagg ctgcgactgg ctgcgggcgg tggcggaccc ctccgacgat 300
ctgcgctttc cgatgaaggg cccgctgatg accgctcgcg agggcacggc cgcgctgcat 360
cgcgctgcac ttcaactggg gaaatccgcg cagcttcttc cggccgcact tgttcagccg 420
cttgcggtac ccgagggcgt gcccgtcacg gggctgacag tgctcgatat cgccgatgtc 480
agccgtgaat tggcgcgcga gacagtgttg tatccagtgg tgcattgcgcg cttgccgatg 540

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ctggcgggcgc aagcggggccg cgtgcatatc ttccgacccc gcgacggcgg cgttgagcat      600
tacgccatcg agatcggcca gcccgaccgt gccgcgcccg tgctcacgcg gctgcattcg      660
gcctgtttca caggcgatgt gctggggtcg ctcaaagtgc attgcggccc gcaactgcag      720
gcagcactcg cgcagatggg cgaggaaggc gcgggggtgc tgctctatct caatcaggag      780
ggtcgcggca tcgggcttgc caacaagatg cgcgcctatt cgctgcagga tcagggcttt      840
gacacggtcg aggccaatca ccgtctgggg ttcgaggatg acgagcggga tttccgcatc      900
ggggccgcgc ttctgcggcg gatgggggttc tctcgggcgc ggctgctgac caacaaccct      960
cggaaggatga acatgctgaa tgcgcatcgg gtcgaagtgg tggaacgggt gccgcttcgg     1020
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<210> 84
 <211> 362
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (168)...(339)
 <223> GTP cyclohydrolase II

<400> 84
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Asp Leu Arg Leu Gly Val Pro Ile Val Leu Arg Glu Gly Asp Val Gln
 20 25 30

Ala Leu Val Leu Ala Val Glu Pro Val Thr Glu Ala Arg Leu Gly Gly
 35 40 45

Leu Arg Gly Leu Gly Pro Gly Leu Val Leu Ala Ile Thr Gln Arg Arg
 50 55 60

Ala Thr Thr Leu Lys Ala Arg Ala Tyr Asp Glu Asp Leu Ala Arg Val
 65 70 75 80

Val Val Pro Glu Gly Val Gly Cys Asp Trp Leu Arg Ala Val Ala Asp
 85 90 95

Pro Ser Asp Asp Leu Arg Phe Pro Met Lys Gly Pro Leu Met Thr Ala
 100 105 110

Arg Glu Gly Thr Ala Ala Leu His Arg Ala Ala Leu Gln Leu Val Lys
 115 120 125

Ser Ala Gln Leu Leu Pro Ala Ala Leu Val Gln Pro Leu Ala Asp Pro
 130 135 140

Glu Ala Leu Pro Val Thr Gly Leu Thr Val Leu Asp Ile Ala Asp Val
 145 150 155 160

Ser Arg Glu Leu Ala Arg Glu Thr Val Leu Tyr Pro Val Val His Ala
 165 170 175

Arg Leu Pro Met Leu Ala Ala Gln Ala Gly Arg Val His Ile Phe Arg
 180 185 190

Pro Arg Asp Gly Gly Val Glu His Tyr Ala Ile Glu Ile Gly Gln Pro
 195 200 205

Asp Arg Ala Ala Pro Val Leu Thr Arg Leu His Ser Ala Cys Phe Thr
 210 215 220

Gly Asp Val Leu Gly Ser Leu Lys Cys Asp Cys Gly Pro Gln Leu Gln
 225 230 235 240

Ala Ala Leu Ala Gln Met Gly Glu Glu Gly Ala Gly Val Leu Leu Tyr
 245 250 255

Leu Asn Gln Glu Gly Arg Gly Ile Gly Leu Ala Asn Lys Met Arg Ala
 260 265 270

Tyr Ser Leu Gln Asp Gln Gly Phe Asp Thr Val Glu Ala Asn His Arg
 275 280 285

Leu Gly Phe Glu Asp Asp Glu Arg Asp Phe Arg Ile Gly Ala Ala Leu
 290 295 300

Leu Arg Arg Met Gly Phe Ser Arg Ala Arg Leu Leu Thr Asn Asn Pro
 305 310 315 320

Arg Lys Val Asn Met Leu Asn Ala His Arg Val Glu Val Val Glu Arg
 325 330 335

Val Pro Leu Arg Val Gly Glu Thr Val Glu Asn Arg Ala Tyr Leu Ala
 340 345 350

Thr Lys Ala Ala Lys Ser Gly His Leu Leu
 355 360

<210> 85
 <211> 1284
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 85
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 gacacgaatg ccgtggagcc gtcgggcctc gcctgcgacc actttcggcg ctttgccgac 180
 gacttccgcc tcttacgcca actcggacag ccagcgcacc gcctgtcgct ggaatggagc 240
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 ctgggtactt tgcgagacct cggaaatcgag ccatgggtca ccatccacca cttcacttgc 360
 cctcgctggt tcgtggaaca gggaggggtt acacgcgatg attcagcgcg ctctctcggt 420
 cgccataccg aacgcgtggc gagggagttc tccgacctag tcacaaactg gtgcaccata 480
 aatgagccaa acgtcgtggc agaactcggc tatcgcttcg gatactttcc gccgcgggtg 540
 caggacgatg agctggcagc ggaagtgtc accaacttct ttcgcttaca cgctgaaatg 600
 gcagaagttt tgcgcgctca cgcgcagaga tcggcgcaaa tcggtatcac ccttgcgatg 660
 caagcacacg agccgctgcg catcgaaagc gaagcggacc gcgcactggc ggcgcgggcg 720
 gacgccgaga ccaacggcgt catgctcaac gccttgcgaa ccggtgtatt cgccatcccg 780
 ggacgggagc cgggtggaaat ccctggactg aaaacgtcat cgaccttcgt ggggggtccag 840
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 cgcgcagcag aaactggact cgaagtgatc gtcacagaga acgggatggc gcacgacgat 1020
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 cgcgggtgtgc gcatcggagg gtacttttac tggtcgacca tggacaactt cgaatggaac 1140
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 ctgggtcgagc actggactcg ctga 1284

<210> 86
 <211> 427
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (5)...(417)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (334)...(342)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<400> 86

Met	Asn	Thr	Ala	His	Arg	Ile	Glu	Phe	Pro	Arg	Gln	Phe	Ile	Phe	Gly
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			20					25					30		

Trp	Trp	Ala	His	Glu	His	Ala	Thr	Asp	Thr	Asn	Ala	Val	Glu	Pro	Ser
		35					40					45			

Gly	Leu	Ala	Cys	Asp	His	Phe	Arg	Arg	Phe	Ala	Asp	Asp	Phe	Arg	Leu
	50					55					60				

Leu	Arg	Gln	Leu	Gly	Gln	Pro	Ala	His	Arg	Leu	Ser	Leu	Glu	Trp	Ser
65					70					75					80

Arg	Ile	Glu	Pro	Ala	Pro	Gly	Glu	Ile	Asp	Arg	Ser	Ala	Leu	Ser	His
				85					90					95	

Tyr	Arg	Arg	Val	Leu	Gly	Thr	Leu	Arg	Asp	Leu	Gly	Ile	Glu	Pro	Trp
			100					105					110		

Val	Thr	Ile	His	His	Phe	Thr	Cys	Pro	Arg	Trp	Phe	Val	Glu	Gln	Gly
		115					120					125			

Gly	Phe	Thr	Arg	Met	Asp	Ser	Ala	Arg	Ser	Leu	Val	Arg	His	Thr	Glu
	130					135					140				

Arg	Val	Ala	Arg	Glu	Phe	Ser	Asp	Leu	Val	Thr	Asn	Trp	Cys	Thr	Ile
145					150					155					160

Asn	Glu	Pro	Asn	Val	Val	Ala	Glu	Leu	Gly	Tyr	Arg	Phe	Gly	Tyr	Phe
			165						170					175	

Pro	Pro	Arg	Leu	Gln	Asp	Asp	Glu	Leu	Ala	Ala	Glu	Val	Leu	Thr	Asn
			180					185						190	

Phe Phe Arg Leu His Ala Glu Met Ala Glu Val Leu Arg Ala His Ala
 195 200 205

Gln Arg Ser Ala Gln Ile Gly Ile Thr Leu Ala Met Gln Ala His Glu
 210 215 220

Pro Leu Arg Ile Glu Ser Glu Ala Asp Arg Ala Leu Ala Ala Arg Arg
 225 230 235 240

Asp Ala Glu Thr Asn Gly Val Met Leu Asn Ala Leu Arg Thr Gly Val
 245 250 255

Phe Ala Tyr Pro Gly Arg Glu Pro Val Glu Ile Pro Gly Leu Lys Thr
 260 265 270

Ser Ser Thr Phe Val Gly Val Gln Tyr Tyr Ser Arg Val Arg Tyr Asp
 275 280 285

Ala Glu Ser Gln Gly Pro Ala Met Pro Asp Phe Glu Arg Thr Leu Ser
 290 295 300

Gln Met Gly Trp Glu Val Tyr Pro Glu Gly Phe Gly Pro Leu Leu Glu
 305 310 315 320

Arg Ala Ala Glu Thr Gly Leu Glu Val Ile Val Thr Glu Asn Gly Met
 325 330 335

Ala His Asp Asp Asp Arg Val Arg Val Arg Phe Ile Ala Asp His Leu
 340 345 350

Arg Val Val His Arg Leu Leu Glu Arg Gly Val Arg Ile Gly Gly Tyr
 355 360 365

Phe Tyr Trp Ser Thr Met Asp Asn Phe Glu Trp Asn Phe Gly Tyr Gly
 370 375 380

Pro Lys Phe Gly Leu Ile Glu Val Asp Arg Ser Thr Leu Glu Arg Arg
 385 390 395 400

Pro Arg Arg Ser Ala Tyr Phe Phe Arg Asp Met Ile Gln Gln Arg Val
 405 410 415

Leu Asp Asp Asp Leu Val Glu His Trp Thr Arg
 420 425

<210> 87
<211> 1167
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 87
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atcaagcgcg gcacgaacat cagccactgg ctgtcgcagt cggagcagcg cggtgaggct 180
cgcagactgc atatccagga ggacgacttc gcccgctctgg aagagctggg cttcgacttc 240
gtgcgcaccc ccatcgacga ggtgcagttc tgggacgagc agggcaacaa gctgcccag 300
gcgtgggacg tgctgaacaa cgccctcgac tggagcaaga agcacaacct gcgtgccatc 360
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ccggtagccc ctgagcacga gatgtggaac cagctggtag ccaaggtaca caaggccctg 600
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atgtcaggaa agaaactggg agaatag 1167

<210> 88
<211> 388
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(23)

<220>
<221> DOMAIN
<222> (48)...(365)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (23)...(26)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (46)...(49)
<223> N-glycosylation site. Prosite id = PS00001

<400> 88
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1 5 10 15

Ala Phe Thr Ser Cys Gln Asn Lys Ser Gln Asn Glu Ala Gln Asp Gln
20 25 30

Ala Gly Gln Val Asn Asn Phe Arg Ile Lys Arg Gly Thr Asn Ile Ser
35 40 45

His Trp Leu Ser Gln Ser Glu Gln Arg Gly Glu Ala Arg Arg Leu His
50 55 60

Ile Gln Glu Asp Asp Phe Ala Arg Leu Glu Glu Leu Gly Phe Asp Phe
65 70 75 80

Val Arg Ile Pro Ile Asp Glu Val Gln Phe Trp Asp Glu Gln Gly Asn
85 90 95

Lys Leu Pro Glu Ala Trp Asp Leu Leu Asn Asn Ala Leu Asp Trp Ser
100 105 110

Lys Lys His Asn Leu Arg Ala Ile Val Asp Leu His Ile Ile Arg Ala
115 120 125

His Tyr Phe Asn Ala Val Asn Glu Ala Asp Gln Ala Ala Asn Thr Leu
130 135 140

Phe Thr Ser Glu Glu Ala Gln Glu Gly Leu Leu Asn Leu Trp Arg Gln
145 150 155 160

Leu Ser Glu Phe Leu Lys Asp Arg Ser Asn Asp Trp Val Ala Tyr Glu
165 170 175

Phe Met Asn Glu Pro Val Ala Pro Glu His Glu Met Trp Asn Gln Leu
180 185 190

Val Ala Lys Val His Lys Ala Leu Arg Glu Leu Glu Pro Gln Arg Thr
195 200 205

Leu Val Val Gly Ser Asn Met Trp Gln Gly His Glu Thr Met Lys Tyr
210 215 220

Leu Lys Val Pro Glu Gly Asp Lys Asn Ile Ile Leu Ser Phe His Tyr
225 230 235 240

Tyr Asn Pro Met Leu Leu Thr His Tyr Gly Ala Trp Trp Ser Pro Leu
245 250 255

Cys Ala Ala Tyr Lys Gly Lys Val Asn Tyr Pro Gly Val Leu Val Ser
260 265 270

Lys Glu Asp Tyr Asp Ala Ala Pro Ala Ala Ile Lys Asp Gln Leu Lys
275 280 285

Pro Phe Thr Glu Glu Val Trp Asn Ile Asp Lys Ile Arg Glu Gln Phe
290 295 300

Lys Asp Ala Ile Glu Ala Ala Lys Lys Tyr Asp Leu Gln Leu Phe Cys
305 310 315 320

Gly Glu Trp Gly Val Tyr Glu Pro Val Asp Arg Glu Leu Ala Tyr Lys
325 330 335

Trp Tyr Arg Asp Val Leu Thr Val Phe Asp Glu Phe Asn Ile Ala Trp
340 345 350

Thr Thr Trp Cys Tyr Asp Ala Asp Phe Gly Phe Trp Asp Gln Gln Arg
355 360 365

His Cys Tyr Lys Asp Tyr Pro Leu Val Glu Leu Leu Met Ser Gly Lys
370 375 380

Lys Leu Gly Glu
385

<210> 89

<211> 1500

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 89

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cagcttagca	ttaaaggtag	tcagctagtc	aatcaaaacg	gaaaaccggt	gcagctgaag	180
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tggctaagag	acgattgggg	aattaccgtc	ttccgggcgg	caatgtacac	ggctgacggc	300
ggttatatcg	agaatccgtc	tgtgaaaaat	aaagtcaaag	aagctgttga	agcggcaaaa	360
gagctcggga	tatatgtcat	cattgactgg	catattttta	atgacggcaa	tccaaatcaa	420
aataaagaga	aggcgaagga	attctttaag	gaaatgtcaa	gcctttacgg	aagctcacca	480
aacgttatat	atgaaattgc	taatgaaccg	aacgggtgat	taaattggaa	gcgcgatatc	540
aaaccgtatg	cggaagaagt	gatttctgtt	atccgtaaaa	atgaccggga	taacatcatt	600
attaccggaa	caggcacttg	gagccaggat	gtcaacgatg	ctgcgggatg	tcagcttaag	660
gatgcaaacg	tcatgtacgc	gcttcatttt	tatgccggta	cacacggcca	gtttttaagg	720
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ctcgacagca	agaaaatcag	ctgggtaaac	tggaaacctt	ctgataagca	ggaatcatcc	900
tcagctttta	agccgggggc	atctaaaaca	ggcggctggc	cgttatcaga	tttatccgct	960
tcagggacat	ttgtaagaga	aaacattcgc	ggctcccaaa	attcgagtga	agacagatct	1020
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ggccaaaact	tcgactgtga	ttacgcgaag	atcggatgca	gcaatgtgac	gcacaagttt	1260
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gggacgctgt	caccgggagc	aagcaccgga	gaaattcaaa	ttcgtcttca	caatgaggac	1380
tggagcaatt	attcacaagc	cggggattat	tcttttttcc	agtcgaatac	gtttaaagat	1440
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<210> 90

<211> 499

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(29)

<220>
<221> DOMAIN
<222> (47)...(301)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> DOMAIN
<222> (356)...(437)
<223> Cellulose binding domain

<220>
<221> SITE
<222> (164)...(173)
<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<220>
<221> SITE
<222> (296)...(299)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (339)...(342)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (383)...(386)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (393)...(396)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (421)...(424)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (446)...(449)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (470)...(473)
<223> N-glycosylation site. Prosite id = PS00001

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1 5 10 15

Leu Thr Ile Ser Gly Val Ala Ala Pro Glu Ala Ser Ala Ala Gly Ala

20					25					30					
Lys	Thr	Pro	Val	Ala	Leu	Asn	Gly	Gln	Leu	Ser	Ile	Lys	Gly	Thr	Gln
		35					40					45			
Leu	Val	Asn	Gln	Asn	Gly	Lys	Pro	Val	Gln	Leu	Lys	Gly	Ile	Ser	Ser
	50					55					60				
His	Gly	Leu	Gln	Trp	Phe	Gly	Asp	Tyr	Val	Asn	Lys	Asp	Thr	Leu	Lys
65					70					75					80
Trp	Leu	Arg	Asp	Asp	Trp	Gly	Ile	Thr	Val	Phe	Arg	Ala	Ala	Met	Tyr
				85					90					95	
Thr	Ala	Asp	Gly	Gly	Tyr	Ile	Glu	Asn	Pro	Ser	Val	Lys	Asn	Lys	Val
			100					105					110		
Lys	Glu	Ala	Val	Glu	Ala	Ala	Lys	Glu	Leu	Gly	Ile	Tyr	Val	Ile	Ile
		115					120					125			
Asp	Trp	His	Ile	Leu	Asn	Asp	Gly	Asn	Pro	Asn	Gln	Asn	Lys	Glu	Lys
	130					135					140				
Ala	Lys	Glu	Phe	Phe	Lys	Glu	Met	Ser	Ser	Leu	Tyr	Gly	Ser	Ser	Pro
145					150					155					160
Asn	Val	Ile	Tyr	Glu	Ile	Ala	Asn	Glu	Pro	Asn	Gly	Asp	Val	Asn	Trp
				165					170					175	
Lys	Arg	Asp	Ile	Lys	Pro	Tyr	Ala	Glu	Glu	Val	Ile	Ser	Val	Ile	Arg
			180					185					190		
Lys	Asn	Asp	Pro	Asp	Asn	Ile	Ile	Ile	Thr	Gly	Thr	Gly	Thr	Trp	Ser
		195					200					205			
Gln	Asp	Val	Asn	Asp	Ala	Ala	Asp	Asp	Gln	Leu	Lys	Asp	Ala	Asn	Val
	210					215					220				
Met	Tyr	Ala	Leu	His	Phe	Tyr	Ala	Gly	Thr	His	Gly	Gln	Phe	Leu	Arg
225					230					235					240
Asp	Lys	Ala	Asp	Tyr	Ala	Leu	Ser	Lys	Gly	Ala	Pro	Ile	Phe	Val	Thr
				245					250					255	
Glu	Trp	Gly	Thr	Ser	Asp	Ala	Ser	Gly	Asn	Gly	Gly	Val	Tyr	Leu	Asp
			260					265					270		

Gln Ser Arg Glu Trp Leu Asn Tyr Leu Asp Ser Lys Lys Ile Ser Trp
 275 280 285

Val Asn Trp Asn Leu Ser Asp Lys Gln Glu Ser Ser Ser Ala Leu Lys
 290 295 300

Pro Gly Ala Ser Lys Thr Gly Gly Trp Pro Leu Ser Asp Leu Ser Ala
 305 310 315 320

Ser Gly Thr Phe Val Arg Glu Asn Ile Arg Gly Ser Gln Asn Ser Ser
 325 330 335

Glu Asp Arg Ser Glu Thr Pro Lys Gln Glu Lys Pro Ala Gln Glu Asn
 340 345 350

Ser Ile Ser Val Gln Tyr Arg Thr Gly Asp Gly Ser Val Asn Ser Asn
 355 360 365

Gln Ile Arg Pro Gln Ile Asn Val Lys Asn Asn Ser Lys Thr Thr Val
 370 375 380

Asn Leu Lys Asn Val Thr Val Arg Tyr Trp Tyr Asn Thr Lys Asn Lys
 385 390 395 400

Gly Gln Asn Phe Asp Cys Asp Tyr Ala Lys Ile Gly Cys Ser Asn Val
 405 410 415

Thr His Lys Phe Val Thr Leu His Lys Pro Val Lys Gly Ala Asp Ala
 420 425 430

Tyr Leu Glu Leu Gly Phe Arg Asn Gly Thr Leu Ser Pro Gly Ala Ser
 435 440 445

Thr Gly Glu Ile Gln Ile Arg Leu His Asn Glu Asp Trp Ser Asn Tyr
 450 455 460

Ser Gln Ala Gly Asp Tyr Ser Phe Phe Gln Ser Asn Thr Phe Lys Asp
 465 470 475 480

Thr Lys Lys Ile Thr Leu Tyr Asn Asn Gly Lys Leu Ile Trp Gly Thr
 485 490 495

Glu Pro Lys

<210> 91
<211> 1725
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

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aaagaaatga agtgggtgga gaaaacactt caatccatgt ccttacatga aaaagtaggg 120
caattatttt gtcccattgg cggttcagat aataaacaag aattagaagc ctttattaag 180
gaatatcatc ctggcggcat catgtaccgt cctaatacag gagcaaaaat acaggaaaca 240
catcggttgt tacaagagct atccccggta cctttattaa tttctgctaa ccttagaggcc 300
ggtggtaatg ggattgctac ggatgggtact tacttcggaa agcaaatgca ggtggctgca 360
acagataatg aagaaatggc ctataaatta ggattagttg ctggccgtga aggccgtgtg 420
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tgggatcaaa cctttgggat ggtttatcaa gaaatgatag acagtggggc aaaatcgatt 720
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aaccgtaaca taaaagaaga ttatgagttc atgctgaatg gaattgaaac tggaattcta 1020
accttggaag gagtagatga agctgttact agagtacttg ctcttaaagc atctctaggt 1080
ctgaatgtac aaaaggaatt gggaatatta gtacctgaag aagcgggaatt gtcggtatta 1140
caatctgaag aacatttgga ttgggcaaga gaatgtgcag accaatcggg tacattagta 1200
aaggatacac aaaaactgct gcctattagt gctgatcagt ataaacgggt tcgactttat 1260
gtattgggtg atcaagaagg agggctaaag gaaggcggct ccgtcactca accgtttatc 1320
gattctctta aaaatgctgg ctttgaagta gatttatata atgacaagca agttaatttc 1380
caagaactgt ttatgagtgt aaacgagttt aaaaagaact atgatctgat catttatgtc 1440
gccaaccttg aaaccgctag taaccaaacg acagtcagaa ttaattggca gcagccgcta 1500
aatgccaacg ctccatgggt tgttaaagat ataccgacat tattttatttc ggttgctaac 1560

ccataccatc tacaggacgt accaatgggtt aagacctata taaatgctta ttcattctaat 1620
 gaatatgtgg tagaagcaat tgtagataaa atcttaggaa aatcagagtt taaaggggaag 1680
 aatccccgtcg atccgttttg tgggaaatgg gataccagac tttaa 1725

<210> 92
 <211> 574
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (87)...(320)
 <223> Glycosyl hydrolase family 3 N terminal domain

<220>
 <221> SITE
 <222> (7)...(10)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (495)...(498)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 92
 Met Leu Lys Leu Ser Asp Asn Leu Thr Phe Leu Lys Ser Lys Pro Phe
 1 5 10 15

Phe Leu Asn Glu Lys Glu Met Lys Trp Val Glu Lys Thr Leu Gln Ser
 20 25 30

Met Ser Leu His Glu Lys Val Gly Gln Leu Phe Cys Pro Ile Gly Gly
 35 40 45

Ser Asp Asn Lys Gln Glu Leu Glu Ala Phe Ile Lys Glu Tyr His Pro
 50 55 60

Gly Gly Ile Met Tyr Arg Pro Asn Thr Gly Ala Lys Ile Gln Glu Thr
 65 70 75 80

His Arg Leu Leu Gln Glu Leu Ser Pro Val Pro Leu Leu Ile Ser Ala
 85 90 95

Asn Leu Glu Ala Gly Gly Asn Gly Ile Ala Thr Asp Gly Thr Tyr Phe
 100 105 110

Gly Lys Gln Met Gln Val Ala Ala Thr Asp Asn Glu Glu Met Ala Tyr
 115 120 125

Lys Leu Gly Leu Val Ala Gly Arg Glu Gly Arg Val Ala Gly Cys Asn
130 135 140

Trp Ala Phe Ala Pro Ile Val Asp Ile Asp Met Asn Tyr Arg Asn Pro
145 150 155 160

Ile Thr Asn Val Arg Thr Tyr Gly Ser Asp Pro Ile Arg Val Ala Gln
165 170 175

Met Ser Lys Ala Phe Met Lys Gly Ile His Glu Ser Gly Leu Ala Ala
180 185 190

Ala Val Lys His Phe Pro Gly Asp Gly Val Asp Asp Arg Asp Gln His
195 200 205

Leu Leu Ser Ser Val Asn Thr Leu Ser Thr Glu Glu Trp Asp Gln Thr
210 215 220

Phe Gly Met Val Tyr Gln Glu Met Ile Asp Ser Gly Ala Lys Ser Ile
225 230 235 240

Met Ala Gly His Ile Met Leu Pro Glu Tyr Ser Arg Glu Leu Leu Pro
245 250 255

Gly Ile Glu Asp Glu Gln Ile Met Pro Ala Thr Leu Ala Pro Glu Leu
260 265 270

Leu Asn Gly Leu Leu Arg Glu Lys Leu Gly Phe Asn Gly Leu Ile Val
275 280 285

Thr Asp Ala Ser Pro Met Leu Gly Phe Thr Thr Ser Glu Arg Arg Glu
290 295 300

Ile Ala Val Pro Lys Ala Ile Ala Ser Gly Cys Asp Met Phe Leu Phe
305 310 315 320

Asn Arg Asn Ile Lys Glu Asp Tyr Glu Phe Met Leu Asn Gly Ile Glu
325 330 335

Thr Gly Ile Leu Thr Leu Glu Arg Val Asp Glu Ala Val Thr Arg Val
340 345 350

Leu Ala Leu Lys Ala Ser Leu Gly Leu Asn Val Gln Lys Glu Leu Gly
355 360 365

Ile Leu Val Pro Glu Glu Ala Glu Leu Ser Val Leu Gln Ser Glu Glu
370 375 380

His Leu Asp Trp Ala Arg Glu Cys Ala Asp Gln Ser Val Thr Leu Val
385 390 395 400

Lys Asp Thr Gln Lys Leu Leu Pro Ile Ser Ala Asp Gln Tyr Lys Arg
405 410 415

Val Arg Leu Tyr Val Leu Gly Asp Gln Glu Gly Gly Leu Lys Glu Gly
420 425 430

Gly Ser Val Thr Gln Pro Phe Ile Asp Ser Leu Lys Asn Ala Gly Phe
435 440 445

Glu Val Asp Leu Tyr Asn Asp Lys Gln Val Asn Phe Gln Glu Leu Phe
450 455 460

Met Ser Val Asn Glu Phe Lys Lys Asn Tyr Asp Leu Ile Ile Tyr Val
465 470 475 480

Ala Asn Leu Glu Thr Ala Ser Asn Gln Thr Thr Val Arg Ile Asn Trp
485 490 495

Gln Gln Pro Leu Asn Ala Asn Ala Pro Trp Phe Val Lys Asp Ile Pro
500 505 510

Thr Leu Phe Ile Ser Val Ala Asn Pro Tyr His Leu Gln Asp Val Pro
515 520 525

Met Val Lys Thr Tyr Ile Asn Ala Tyr Ser Ser Asn Glu Tyr Val Val
530 535 540

Glu Ala Ile Val Asp Lys Ile Leu Gly Lys Ser Glu Phe Lys Gly Lys
545 550 555 560

Asn Pro Val Asp Pro Phe Cys Gly Lys Trp Asp Thr Arg Leu
565 570

<210> 93

<211> 546

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 93
 atgagaataa aaaattttaa aacgaaccgt atcacaacc cgctgggatt tgatatagga 60
 aaaccacgta tatcttttgt cacttatgac actacggcta aaaagcaaag agcagcgcaa 120
 atacaggttg cgctagatca agagtttacg aacctaacat ttgacagtgg gaaaagcacg 180
 gagatagata gtctagcata cgaactgcc a tttcaattag agtcttacac tcgctactac 240
 tggcgtgtga ccgtttgggc ggataatggg gatgtggcca caagtgaaat tgcttggttt 300
 gaaacagcca aactaggcga ttcttgggag gccaaagtga ttacccccga ttttgataag 360
 gaaatccatc ccgtactatc aagggaattt gatattgtcaa aagaagtcgt ttctgcccgt 420
 gcctatgttt gcggtttggg attatatgaa atggagatta atgggtctaaa ggctggggat 480
 gaatatctga cccctaattt caacgcctat gataaatggc tgcagtacca gacctatgat 540
 attacca 546

<210> 94
 <211> 182
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SITE
 <222> (51)...(54)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 94
 Met Arg Ile Lys Asn Leu Lys Thr Asn Arg Ile Thr Asn Pro Leu Gly
 1 5 10 15
 Phe Asp Ile Gly Lys Pro Arg Ile Ser Phe Val Thr Tyr Asp Thr Thr
 20 25 30
 Ala Lys Lys Gln Thr Ala Ala Gln Ile Gln Val Ala Leu Asp Gln Glu
 35 40 45
 Phe Thr Asn Leu Thr Phe Asp Ser Gly Lys Ser Thr Glu Ile Asp Ser
 50 55 60
 Leu Ala Tyr Glu Leu Pro Phe Gln Leu Glu Ser Tyr Thr Arg Tyr Tyr
 65 70 75 80
 Trp Arg Val Thr Val Trp Ala Asp Asn Gly Asp Val Ala Thr Ser Glu
 85 90 95
 Ile Ala Trp Phe Glu Thr Ala Lys Leu Gly Asp Ser Trp Glu Ala Lys
 100 105 110

Trp Ile Thr Pro Asp Phe Asp Lys Glu Ile His Pro Val Leu Ser Arg
115 120 125

Glu Phe Asp Leu Ser Lys Glu Val Val Ser Ala Arg Ala Tyr Val Cys
130 135 140

Gly Leu Gly Leu Tyr Glu Met Glu Ile Asn Gly Leu Lys Ala Gly Asp
145 150 155 160

Glu Tyr Leu Thr Pro Asn Phe Asn Ala Tyr Asp Lys Trp Leu Gln Tyr
165 170 175

Gln Thr Tyr Asp Ile Thr
180

<210> 95
<211> 2298
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 95
atgatcaatc aagatataaa acaattaatc tcacaaatga ccttggaaga aaaagctggt 60
ctttgttctg gattagattt ttggaattta aaaggatatc aaagactggg aataccctcg 120
ataatggtaa ccgatgggtcc gcatggactc cgtaaacaaa aaatgggagc agatcattta 180
gggctgtttg acagtattcc tgcgacatgt ttcccatctg cagccggttt agctagtact 240
tggaataaag agttaatata tgaagttggg gttgcattag gaaaggaatg ccaggcagag 300
gatgtggcaa tacttcttgg ccttggagca aacattaagc gctcaccctt ttgtggcaga 360
aactttgaat atttttcggg agatccattc ctttcatcag aaatggctgc gtcccatatc 420
aaggggtgttc aaagtgaggg ggttgggaca tcacttaagc acttcgctgc aaataatcaa 480
gaacaccgaa gaatgtcgac agatgctatt gtggatgaaa ggacgttgcg agaaatatat 540
ttggccagct ttgaaaacgc tgtaaagaaa gcgcagccat ggactgtgat gtgcgcctac 600
aacaagggtca atggagactt tgcacagaa aataaaacat tgttaactga catcctgcga 660
gatgagtggg gctttgaagg aattgttggt tctgactggg gggcgggtta tgaacctgtt 720
gacggattaa atgccgggtt agacctggaa atgccttcaa gtagtgggat tggtgaaaag 780
aaaatcatca atgctgtaag aaatgggtcag cttttagaag ataaactaga tcaggcagtt 840
gaaagaattc tacgtattat cttaatggca gtagaaaaca agaaagaaac cgctgactat 900

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gataaagaac aacatcataa gcttgcaaga aaagcagcaa gtgaaagtat ggttttatta 960
aagaatgaag ataatatcct gccgttaaag aaagaaggaa ccatttcgat tattggttca 1020
tttgccaaaa aaccaaggta tcaaggcggg ggaagctcac acattaaccc gacaaagctt 1080
gaaaatatct atgaagaaat agagaaaaca gcggggccaaa atgtgaacgt tttatacgcg 1140
gaaggatatc atcttgaaaa ggatttaatc gatgatcaat taattgaaga ggcaaaaaaa 1200
acggcagcaa aatccgatgt aaccgtattg tttgtaggtc ttcctgaccg atatgaatct 1260
gaaggatatg atagagagca cctgaatata ccggagaatc accgtctttt agtcgaagcg 1320
gttgcggaag taaaaaagaa tatagttggt gtactaagta atggggcacc gcttgttatg 1380
ccatggcttg ataaggtgaa ggggctgctg gaaagttacc tgggaggtca ggcactagga 1440
ggtgcgattg cagacatcct attcggagaa gttaatccaa gtggaaagct tgccgaaact 1500
tttcccgtaa aattaggtga caatccttct tatctcaact ttccaggaga gagggataaa 1560
gttgagtata aagaaggcat ctttgttggt tatcgttatt acgatacaaa acagattgag 1620
ccgctgtttc catttgata tggtttaagc tatacaaact ttgaatataa aaaccttgta 1680
attgataaaa aagaaataaa agatacagaa attgtcacag ttaccgtgaa tgtgaaaaat 1740
acaggaaaag tgccctgggaa agaaatcatc cagttatatg taaaagatat aaaaagcagt 1800
gtagttcgtc ctgaaaaaga gttaaaaggc tttggaaagg tttccttaca gcctggggaa 1860
gacaaaacta tttcctttta attggataaa cgcgcatttg catattacaa cacggaattg 1920
aaggattggt atgtagaatc aggagaattt gaaattttgg tggggaaatc gtccagagaa 1980
attgaactaa cagaaaaaat tatggttcac tctacttccc cagttttctt ggagggtcac 2040
cgaaattcca cggtcggaga tcttttaact gatccaattc taggtgaaaa agctaattgct 2100
ctaattagag agctaacaaa aggaagtcca ttatttgatg ctgggtcaga tcacggagag 2160
ggtgcagaaa tgatggaagc gatgttaaaa tacatgcctt tgcgtgctct tatgaatttt 2220
agtgggtggag acattaccga agagaaacta actgaattta ttaaggaact taattcaact 2280
aattttgtaa gcctttta 2298

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<210> 96

<211> 765

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (30)...(252)

<223> Glycosyl hydrolase family 3 N terminal domain

<220>
 <221> DOMAIN
 <222> (317)...(531)
 <223> Glycosyl hydrolase family 3 C terminal domain

<220>
 <221> SITE
 <222> (214)...(217)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (221)...(238)
 <223> Glycosyl hydrolases family 3 active site. Prosite id = PS00775

<220>
 <221> SITE
 <222> (692)...(695)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (750)...(753)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (769)...(772)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 96
 Met Ile Asn Gln Asp Ile Lys Gln Leu Ile Ser Gln Met Thr Leu Glu
 1 5 10 15

 Glu Lys Ala Gly Leu Cys Ser Gly Leu Asp Phe Trp Asn Leu Lys Gly
 20 25 30

 Ile Glu Arg Leu Gly Ile Pro Ser Ile Met Val Thr Asp Gly Pro His
 35 40 45

 Gly Leu Arg Lys Gln Lys Met Gly Ala Asp His Leu Gly Leu Phe Asp
 50 55 60

 Ser Ile Pro Ala Thr Cys Phe Pro Ser Ala Ala Gly Leu Ala Ser Thr
 65 70 75 80

 Trp Asn Lys Glu Leu Ile Tyr Glu Val Gly Val Ala Leu Gly Lys Glu
 85 90 95

 Cys Gln Ala Glu Asp Val Ala Ile Leu Leu Gly Pro Gly Ala Asn Ile
 100 105 110

 Lys Arg Ser Pro Leu Cys Gly Arg Asn Phe Glu Tyr Phe Ser Glu Asp
 115 120 125

Pro Phe Leu Ser Ser Glu Met Ala Ala Ser His Ile Lys Gly Val Gln
 130 135 140

Ser Glu Gly Val Gly Thr Ser Leu Lys His Phe Ala Ala Asn Asn Gln
 145 150 155 160

Glu His Arg Arg Met Ser Thr Asp Ala Ile Val Asp Glu Arg Thr Leu
 165 170 175

Arg Glu Ile Tyr Leu Ala Ser Phe Glu Asn Ala Val Lys Lys Ala Gln
 180 185 190

Pro Trp Thr Val Met Cys Ala Tyr Asn Lys Val Asn Gly Asp Phe Ala
 195 200 205

Ser Glu Asn Lys Thr Leu Leu Thr Asp Ile Leu Arg Asp Glu Trp Gly
 210 215 220

Phe Glu Gly Ile Val Val Ser Asp Trp Gly Ala Val Asn Glu Pro Val
 225 230 235 240

Asp Gly Leu Asn Ala Gly Leu Asp Leu Glu Met Pro Ser Ser Ser Gly
 245 250 255

Ile Gly Glu Lys Lys Ile Ile Asn Ala Val Arg Asn Gly Gln Leu Leu
 260 265 270

Glu Asp Lys Leu Asp Gln Ala Val Glu Arg Ile Leu Arg Ile Ile Leu
 275 280 285

Met Ala Val Glu Asn Lys Lys Glu Thr Ala Asp Tyr Asp Lys Glu Gln
 290 295 300

His His Lys Leu Ala Arg Lys Ala Ala Ser Glu Ser Met Val Leu Leu
 305 310 315 320

Lys Asn Glu Asp Asn Ile Leu Pro Leu Lys Lys Glu Gly Thr Ile Ser
 325 330 335

Ile Ile Gly Ser Phe Ala Lys Lys Pro Arg Tyr Gln Gly Gly Gly Ser
 340 345 350

Ser His Ile Asn Pro Thr Lys Leu Glu Asn Ile Tyr Glu Glu Ile Glu
 355 360 365

Lys Thr Ala Gly Gln Asn Val Asn Val Leu Tyr Ala Glu Gly Tyr His
 370 375 380

Leu Glu Lys Asp Leu Ile Asp Asp Gln Leu Ile Glu Glu Ala Lys Lys
 385 390 395 400

Thr Ala Ala Lys Ser Asp Val Thr Val Leu Phe Val Gly Leu Pro Asp
 405 410 415

Arg Tyr Glu Ser Glu Gly Tyr Asp Arg Glu His Leu Asn Ile Pro Glu
 420 425 430

Asn His Arg Leu Leu Val Glu Ala Val Ala Glu Val Gln Lys Asn Ile
 435 440 445

Val Val Val Leu Ser Asn Gly Ala Pro Leu Val Met Pro Trp Leu Asp
 450 455 460

Lys Val Lys Gly Leu Leu Glu Ser Tyr Leu Gly Gly Gln Ala Leu Gly
 465 470 475 480

Gly Ala Ile Ala Asp Ile Leu Phe Gly Glu Val Asn Pro Ser Gly Lys
 485 490 495

Leu Ala Glu Thr Phe Pro Val Lys Leu Gly Asp Asn Pro Ser Tyr Leu
 500 505 510

Asn Phe Pro Gly Glu Arg Asp Lys Val Glu Tyr Lys Glu Gly Ile Phe
 515 520 525

Val Gly Tyr Arg Tyr Tyr Asp Thr Lys Gln Ile Glu Pro Leu Phe Pro
 530 535 540

Phe Gly Tyr Gly Leu Ser Tyr Thr Asn Phe Glu Tyr Lys Asn Leu Val
 545 550 555 560

Ile Asp Lys Lys Glu Ile Lys Asp Thr Glu Ile Val Thr Val Thr Val
 565 570 575

Asn Val Lys Asn Thr Gly Lys Val Pro Gly Lys Glu Ile Ile Gln Leu
 580 585 590

Tyr Val Lys Asp Ile Lys Ser Ser Val Val Arg Pro Glu Lys Glu Leu
 595 600 605

Lys Gly Phe Gly Lys Val Ser Leu Gln Pro Gly Glu Asp Lys Thr Ile
610 615 620

Ser Phe Lys Leu Asp Lys Arg Ala Phe Ala Tyr Tyr Asn Thr Glu Leu
625 630 635 640

Lys Asp Trp Tyr Val Glu Ser Gly Glu Phe Glu Ile Leu Val Gly Lys
645 650 655

Ser Ser Arg Glu Ile Glu Leu Thr Glu Lys Ile Met Val His Ser Thr
660 665 670

Ser Pro Val Phe Leu Glu Val His Arg Asn Ser Thr Val Gly Asp Leu
675 680 685

Leu Thr Asp Pro Ile Leu Gly Glu Lys Ala Asn Ala Leu Ile Arg Glu
690 695 700

Leu Thr Lys Gly Ser Pro Leu Phe Asp Ala Gly Ser Asp His Gly Glu
705 710 715 720

Gly Ala Glu Met Met Glu Ala Met Leu Lys Tyr Met Pro Leu Arg Ala
725 730 735

Leu Met Asn Phe Ser Gly Gly Asp Ile Thr Glu Glu Lys Leu Thr Glu
740 745 750

Phe Ile Lys Glu Leu Asn Ser Thr Asn Phe Val Ser Leu
755 760 765

<210> 97
<211> 615
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 97
atgttataacc caattataac tgaaactcgc agtatcatcg atttaaattgg tatctggaaa 60
tttaaatttag ataattggtga aggactgcag gaaaaatggt atgaaaacgg attaacagac 120
acgatcagta tggctgtacc atcttccttt aatgatattg gagtaaattgc cagtatacgc 180
gatcatgttg gctgggtatg gtatgagcgg gaatttttctg tccccgccat ccttcaatct 240
gagcgtgtgg ttttgcgatt cggttccgca acacatctag ctaagggtttt cgtaaattggt 300
gaacttggtg ttgaacataa gggcgggtttt ttaccggttg aagcagaaat aaataagttt 360

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ttacaaaaag ggaaaaatcg aataacgggt gctgtcaaca atattcttga ttactcaact    420
ttacccggttg gcacagtaat agaaaaggat attcctggag ttggcaaagt aatacgcaat    480
cagccaaatt ttgacttctt caactacgct ggcttgcacc gtccagtga aatatatact    540
acaccgacta cttatgtgaa ggatgtaacc attgtaacgg aaatagatgg acagggtcac    600
tattcaattg attaa                                                    615

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<210> 98
<211> 204
<212> PRT
<213> Unknown

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<220>
<223> Obtained from environmental sample

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<220>
<221> DOMAIN
<222> (9)...(182)
<223> Glycosyl hydrolases family 2, sugar binding domain

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<220>
<221> SITE
<222> (56)...(59)
<223> N-glycosylation site. Prosite id = PS00001

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```

<400> 98
Met Leu Tyr Pro Ile Ile Thr Glu Thr Arg Ser Ile Ile Asp Leu Asn
1              5              10              15

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Gly Ile Trp Lys Phe Lys Leu Asp Asn Gly Glu Gly Leu Gln Glu Lys
          20              25              30

```

```

Trp Tyr Glu Asn Gly Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser
          35              40              45

```

```

Ser Phe Asn Asp Ile Gly Val Asn Ala Ser Ile Arg Asp His Val Gly
          50              55              60

```

```

Trp Val Trp Tyr Glu Arg Glu Phe Ser Val Pro Ala Ile Leu Gln Ser
65              70              75              80

```

```

Glu Arg Val Val Leu Arg Phe Gly Ser Ala Thr His Leu Ala Lys Val
          85              90              95

```

```

Phe Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
          100              105              110

```

```

Phe Glu Ala Glu Ile Asn Lys Phe Leu Gln Lys Gly Lys Asn Arg Ile
          115              120              125

```

Thr Val Ala Val Asn Asn Ile Leu Asp Tyr Ser Thr Leu Pro Val Gly
 130 135 140

Thr Val Ile Glu Lys Asp Ile Pro Gly Val Gly Lys Val Ile Arg Asn
 145 150 155 160

Gln Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val
 165 170 175

Lys Ile Tyr Thr Thr Pro Thr Thr Tyr Val Lys Asp Val Thr Ile Val
 180 185 190

Thr Glu Ile Asp Gly Gln Val His Tyr Ser Ile Asp
 195 200

<210> 99
 <211> 1404
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 99
 atgaatcatt ccctttcatt tccgccatcc tttgtatggg ggcgcggcaac cgcaagctac 60
 caactggaag gatcaaccca aggcgtggac ggctgcgccg agtccgtctg ggatatgcac 120
 tgccgaagat ccggcgcgat caaggacggc tcgaacggat tcgtcgcttg cgatcactac 180
 catcgctatc gcgaggatgt ggcgctcatg aacgagcttg gcttgaatgc ctatcgattc 240
 tcaatcatgt ggccccgcgt catgccccgaa ggcaccggcg cggatgaacga gaagggcatg 300
 gatttctacg atcggttggg tgatgaactg ctgcgccg gcatcacacc ttgggttact 360
 ttgttccact gggactttcc cctagccttg ttccaacgcg gtggctggct gaatgcggat 420
 tccccgcaat ggtttgagga ttacactcgg gaagtgggta aacgcttgtc ggatcgtgtg 480
 catcactggc taacgctcaa cgaaccggcg tgcttcattg agtttggcca ccgtaccggc 540
 atgcatgcac ccggcttgca actggcggac aaggaagcct gccgggtctg gcaccatgcc 600
 atgctggccc acggtcgcgc cgttcgcgct attcgccagg aatccgtgca tccatcaccc 660
 caggtcggct acgcgccggt cttccgcact accatcccgg aactgaaga tcctgccgac 720
 atcgaagcgg cccggacctc gatgtttgct catcaggccg gcaacctgtt cgatacgcgg 780
 tggaacctcg acccctgctt tcgggggcgcg tatccggaga tcatgatgca gtattggggc 840
 gatgccgcgc cgcgcatcca ggacggcgac atggagttga tccgtcagga actcgatttt 900
 ctcggcctga atatttacca gtccgagcgc attcggggccg gtgcgggatgg cgcacccgag 960

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gtggtgccat accctgcgga ttatccgcgc aaccagctcg gttggcccat cacgccggag 1020
gccctgcgct gggcgaccct ctttctcttt gaggagtacg ggaaaccct gatcatcaca 1080
gaaaacggaa tcaccctcga cgacaagccc aatgcagacg gcgaggtgaa tgatgtccag 1140
cggatcgctt ttctgaatga ctatcttagc ggtctccagc gcagcgtgga cgacggcatc 1200
cctgtactgg gctattttcca ctggtcgctg tgcgacaact ttgagtgggc agaaggctat 1260
gtccctcgct tcggcctgat ccatgtggac tatgccagtc aacgcagaac catcaaggcc 1320
tcaggacggt ttaccgcga catcattcgg ggccagacag ccacgccctg catcgcccaa 1380
tccagtcagc cggaacaac ctaa 1404

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<210> 100
 <211> 467
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (3)...(454)
 <223> Glycosyl hydrolase family 1

<220>
 <221> SITE
 <222> (2)...(5)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (11)...(25)
 <223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<400> 100
 Met Asn His Ser Leu Ser Phe Pro Pro Ser Phe Val Trp Gly Ala Ala
 1 5 10 15

Thr Ala Ser Tyr Gln Leu Glu Gly Ser Thr Gln Gly Val Asp Gly Cys
 20 25 30

Ala Glu Ser Val Trp Asp Met His Cys Arg Arg Ser Gly Ala Ile Lys
 35 40 45

Asp Gly Ser Asn Gly Phe Val Ala Cys Asp His Tyr His Arg Tyr Arg
 50 55 60

Glu Asp Val Ala Leu Met Asn Glu Leu Gly Leu Asn Ala Tyr Arg Phe
 65 70 75 80

Glu Lys Gly Met Asp Phe Tyr Asp Arg Leu Val Asp Glu Leu Leu Ala
100 105 110

Ala Gly Ile Thr Pro Trp Val Thr Leu Phe His Trp Asp Phe Pro Leu
115 120 125

Ala Leu Phe Gln Arg Gly Gly Trp Leu Asn Ala Asp Ser Pro Gln Trp
130 135 140

Phe Glu Asp Tyr Thr Arg Glu Val Val Lys Arg Leu Ser Asp Arg Val
145 150 155 160

His His Trp Leu Thr Leu Asn Glu Pro Ala Cys Phe Ile Glu Phe Gly
165 170 175

His Arg Thr Gly Met His Ala Pro Gly Leu Gln Leu Ala Asp Lys Glu
180 185 190

Ala Cys Arg Val Trp His His Ala Met Leu Ala His Gly Arg Ala Val
195 200 205

Arg Ala Ile Arg Gln Glu Ser Val His Pro Ser Pro Gln Val Gly Tyr
210 215 220

Ala Pro Val Phe Arg Thr Thr Ile Pro Asp Thr Glu Asp Pro Ala Asp
225 230 235 240

Ile Glu Ala Ala Arg Thr Ser Met Phe Ala His Gln Ala Gly Asn Leu
245 250 255

Phe Asp Thr Arg Trp Asn Leu Asp Pro Cys Phe Arg Gly Ala Tyr Pro
260 265 270

Glu Ile Met Met Gln Tyr Trp Gly Asp Ala Ala Pro Arg Ile Gln Asp
275 280 285

Gly Asp Met Glu Leu Ile Arg Gln Glu Leu Asp Phe Leu Gly Leu Asn
290 295 300

Ile Tyr Gln Ser Glu Arg Ile Arg Ala Gly Ala Asp Gly Ala Pro Glu
305 310 315 320

Val Val Pro Tyr Pro Ala Asp Tyr Pro Arg Asn Gln Leu Gly Trp Pro

325

330

335

Ile Thr Pro Glu Ala Leu Arg Trp Ala Thr Leu Phe Leu Phe Glu Glu
 340 345 350

Tyr Gly Lys Pro Leu Ile Ile Thr Glu Asn Gly Ile Thr Leu Asp Asp
 355 360 365

Lys Pro Asn Ala Asp Gly Glu Val Asn Asp Val Gln Arg Ile Ala Phe
 370 375 380

Leu Asn Asp Tyr Leu Ser Gly Leu Gln Arg Ser Val Asp Asp Gly Ile
 385 390 395 400

Pro Val Leu Gly Tyr Phe His Trp Ser Leu Cys Asp Asn Phe Glu Trp
 405 410 415

Ala Glu Gly Tyr Val Pro Arg Phe Gly Leu Ile His Val Asp Tyr Ala
 420 425 430

Ser Gln Arg Arg Thr Ile Lys Ala Ser Gly Arg Phe Tyr Arg Asp Ile
 435 440 445

Ile Arg Gly Gln Thr Ala Thr Pro Cys Ile Ala Gln Ser Ser Gln Pro
 450 455 460

Glu Thr Thr
 465

<210> 101

<211> 1101

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 101

atgagaaatc atctgaatgt accctttttac tttatcttct tttttttaat agcgtcaata 60

tttacagtct gttcatcatc aactgcttct gataacaatg agcatccacc gccagtggaa 120

gtcgcggatc aggacgcttt tcgtgatgct tttgaagtga atgaattact tggacgcggt 180

attaatctgg gtaatgccct tgaagcgccc aatgaaggcg aatggggaat ggtaatccag 240

gaagagtttc ttgatctgat acttgcagca ggttttgagt ctgtacgaat tccgattcgc 300

tggaatgccc atgccagtga aagtcaccct ttcaccattc aacgatcggt ttttgatcgg 360

gttgatgaag tcatccaatg gtcgctggat cgtggccttt ctgtaatgat caatattcat 420

cactacaatg aactgatgca aaacccgcag cagcaccggc agcgggtttt gcgactctgg 480
aaccagattg ctacacacta taaagattat ccggataatc tggtttttga aatccttaat 540
gaacctcatg ataatctgac tccttctatc tggaatagtt atttgaggga tgctattggc 600
atgattcgcc agacaaaccc acgcagggtt atcgctatcg gaacagcaaa ctgggggtggt 660
ttcggagcat tatcacaact tgaaatcccc tcaaacgacg gccagatcat tgcaactggt 720
cattattatg aacccttcag gttcacccat cagggggctg aatgggcagg accggaaaca 780
aacgattggc tggggacacg atgggatgga tcggatgagg aaaaatttga tattgaaagt 840
ggttttgatg ccgtacagtc ctgggcagtg acaaataacc ggctgttca tctcggagaa 900
ttcggtgctt acagtactgc cgataatgaa tcacgcgaac gctggacaac ctttgttcgg 960
gaatccgctg agcaacgcaa tttcagctgg gcatactggg aatttgcagc cggttttggg 1020
atctatgacc gtaatcagtg gcaatggagg gattatctgt tgagggcttt gataccggat 1080
agcccggtcc tgttggagta a 1101

<210> 102
<211> 366
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(29)

<220>
<221> DOMAIN
<222> (64)...(342)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (176)...(185)
<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<220>
<221> SITE
<222> (313)...(316)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (332)...(335)
<223> N-glycosylation site. Prosite id = PS00001

<400> 102
Met Arg Asn His Leu Asn Val Pro Phe Tyr Phe Ile Phe Phe Leu
1 5 10 15

Ile Ala Ser Ile Phe Thr Val Cys Ser Ser Ser Thr Ala Ser Asp Asn
20 25 30

Asn Glu His Pro Pro Pro Val Glu Val Ala Asp Gln Asp Ala Phe Arg
35 40 45

Asp Ala Phe Glu Val Asn Glu Leu Leu Gly Arg Gly Ile Asn Leu Gly
50 55 60

Asn Ala Leu Glu Ala Pro Asn Glu Gly Glu Trp Gly Met Val Ile Gln
65 70 75 80

Glu Glu Phe Leu Asp Leu Ile Leu Ala Ala Gly Phe Glu Ser Val Arg
85 90 95

Ile Pro Ile Arg Trp Asn Ala His Ala Ser Glu Ser His Pro Phe Thr
100 105 110

Ile Gln Arg Ser Phe Phe Asp Arg Val Asp Glu Val Ile Gln Trp Ser
115 120 125

Leu Asp Arg Gly Leu Ser Val Met Ile Asn Ile His His Tyr Asn Glu
130 135 140

Leu Met Gln Asn Pro Gln Gln His Arg Gln Arg Phe Leu Arg Leu Trp
145 150 155 160

Asn Gln Ile Ala Thr His Tyr Lys Asp Tyr Pro Asp Asn Leu Val Phe
165 170 175

Glu Ile Leu Asn Glu Pro His Asp Asn Leu Thr Pro Ser Ile Trp Asn
180 185 190

Ser Tyr Leu Arg Asp Ala Ile Gly Met Ile Arg Gln Thr Asn Pro Arg
195 200 205

Arg Val Ile Ala Ile Gly Thr Ala Asn Trp Gly Gly Phe Gly Ala Leu
210 215 220

Ser Gln Leu Glu Ile Pro Ser Asn Asp Arg Gln Ile Ile Ala Thr Val
225 230 235 240

His Tyr Tyr Glu Pro Phe Arg Phe Thr His Gln Gly Ala Glu Trp Ala
245 250 255

Gly Pro Glu Thr Asn Asp Trp Leu Gly Thr Arg Trp Asp Gly Ser Asp
260 265 270

Glu Glu Lys Phe Asp Ile Glu Ser Gly Phe Asp Ala Val Gln Ser Trp
275 280 285

Ala Val Thr Asn Asn Arg Pro Val His Leu Gly Glu Phe Gly Ala Tyr
290 295 300

Ser Thr Ala Asp Asn Glu Ser Arg Glu Arg Trp Thr Thr Phe Val Arg
305 310 315 320

Glu Ser Ala Glu Gln Arg Asn Phe Ser Trp Ala Tyr Trp Glu Phe Ala
325 330 335

Ala Gly Phe Gly Ile Tyr Asp Arg Asn Gln Trp Gln Trp Arg Asp Tyr
340 345 350

Leu Leu Arg Ala Leu Ile Pro Asp Ser Pro Val Leu Leu Glu
355 360 365

<210> 103

<211> 1101

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 103

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atcagccact ggttgctcga gagtgggaagg cgtgggtgctg atcgggaggc gttctttacc 180
agggcggatg tggaggccat cgccggcttc ggttatgata acattcgttt gccattgat 240
gaggagcaga tgtgggatga gtcgggcaac aaggaaccac gtgcctttga attgctgcat 300
gaagccattg gctgggcttt ggacaatgag ctcagggtca ttgtcgacct gcacatcatc 360
aggtcgact attttaatgc gcctgagaac ccgctttgga ccgatcgtgc tgaacagttg 420
aaatttgctg agatgtggcg acagttgtct gatgagctgc agggctatcc gctcgatagg 480
gtggcctatg aattgatgaa tgaggccgtg gctgatgata cggacgattg gaaccggctt 540
gtggctgaga cgatggaggc gctacggatg ctggaaccgg agcgcaagat tgtcattggc 600
tccaaccgct ggcagtctgt gcatacatct cctgacctgg tgatcccggg taatgaccgg 660
catatcatat tgagttttca cttctacgaa ccattttctg tgacgcacca caaggcctcc 720

tggacacaca tccgtgatta caccggtccg gtgaactatc cgggtttgac tgtagaccgc 780
accacactgg aggggttgtc tgaagaactg gtgaccgcga ttggccatca caatgggggtg 840
tatacaaaag aaacgatgga ggagatgatc atgatccac tgcaatatgc caaagaccgc 900
gggctcccc tttattgtgg agagtgggga tgtttccga ccatgcccc ggagatgcgc 960
ctgcaatggc acgccgatgt gcgtgcgatc ctggaaaagc atgagattgc ctgggcaaac 1020
tgggattaca aggggtggtt cgggtgtggt gaccgcaacg gcgaaccccc ccatgattta 1080
ttggaagtgc tcttaaaata a 1101

<210> 104

<211> 366

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> SIGNAL

<222> (1)...(20)

<220>

<221> DOMAIN

<222> (42)...(349)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (40)...(43)

<223> N-glycosylation site. Prosite id = PS00001

<400> 104

Met Leu Ile Ile Gly Gly Leu Leu Val Leu Leu Gly Phe Ser Ser Cys
1 5 10 15

Gly Arg Gln Ala Glu Pro Ala Ala Asp Ser Phe Arg Gly Phe His Asp
20 25 30

Phe Asp Ile Arg Arg Gly Val Asn Ile Ser His Trp Leu Ser Gln Ser
35 40 45

Gly Arg Arg Gly Ala Asp Arg Glu Ala Phe Phe Thr Arg Ala Asp Val
50 55 60

Glu Ala Ile Ala Gly Phe Gly Tyr Asp His Ile Arg Leu Pro Ile Asp
65 70 75 80

Glu Glu Gln Met Trp Asp Glu Ser Gly Asn Lys Glu Pro Arg Ala Phe
85 90 95

Glu Leu Leu His Glu Ala Ile Gly Trp Ala Leu Asp Asn Glu Leu Arg
100 105 110

Val Ile Val Asp Leu His Ile Ile Arg Ser His Tyr Phe Asn Ala Pro
115 120 125

Glu Asn Pro Leu Trp Thr Asp Arg Ala Glu Gln Leu Lys Phe Val Glu
130 135 140

Met Trp Arg Gln Leu Ser Asp Glu Leu Gln Gly Tyr Pro Leu Asp Arg
145 150 155 160

Val Ala Tyr Glu Leu Met Asn Glu Ala Val Ala Asp Asp Pro Asp Asp
165 170 175

Trp Asn Arg Leu Val Ala Glu Thr Met Glu Ala Leu Arg Met Leu Glu
180 185 190

Pro Glu Arg Lys Ile Val Ile Gly Ser Asn Arg Trp Gln Ser Val His
195 200 205

Thr Phe Pro Asp Leu Val Ile Pro Asp Asn Asp Pro His Ile Ile Leu
210 215 220

Ser Phe His Phe Tyr Glu Pro Phe Leu Leu Thr His His Lys Ala Ser
225 230 235 240

Trp Thr His Ile Arg Asp Tyr Thr Gly Pro Val Asn Tyr Pro Gly Leu
245 250 255

Thr Val Asp Pro Thr His Leu Glu Gly Leu Ser Glu Glu Leu Val Thr
260 265 270

Arg Ile Gly His His Asn Gly Val Tyr Thr Lys Glu Thr Met Glu Glu
275 280 285

Met Ile Met Ile Pro Leu Gln Tyr Ala Lys Asp Arg Gly Leu Pro Leu
290 295 300

Tyr Cys Gly Glu Trp Gly Cys Phe Pro Thr Met Pro Gln Glu Met Arg
305 310 315 320

Leu Gln Trp Tyr Ala Asp Val Arg Ala Ile Leu Glu Lys His Glu Ile
325 330 335

Ala Trp Ala Asn Trp Asp Tyr Lys Gly Gly Phe Gly Val Val Asp Arg

340

345

350

Asn Gly Glu Pro His His Asp Leu Leu Glu Val Leu Leu Lys
 355 360 365

<210> 105

<211> 1047

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 105

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atgcaacact tcatcaacgg cgtcaacctg ggaggctggc tctcccaata ccagaaatac      60
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ggcttcgacc acatccgcct gccggtcgat tatccggttc tcgaatcgga cgacgcgccc      180
ggtatctatc atgaagatgg ctttgcctat cttgactctt gcctggaatg gtgccaggcc      240
gctgggctgg cagtcgtctt cgacctgcat catgcccccg gctacagttt cacgaacacg      300
ctcaagcctg aaaccctgca cctgaacgta ctcttcgagc aggaaatcgc ccaaaatcga      360
tttatcgccc tctgggaaac cattgttcgg cgctaccagg ccgccggctt gcctatcatc      420
tttgaactac tgaatgaaat ggtgctgcca gacagcggcc cctggaacgc cctggcccac      480
aaaaccgtcg ccgccctgcg acagatttcg cccgattgca aaatcatgat tggcggcaat      540
aactacaacg ccgcatccga actcaaaaac ataaccctgc acaacgaccc caacatccta      600
tacaccttcc atttctacga accggccctg ttcacccacc agaaagcccc ctgggtgcag      660
attgctgtcg aatacaacca ggaactcgaa taccctggct cgtacaccaa cctggccgcc      720
tttctccggc gcaatcccca ctatcaagaa tcctatggat ggcagggtcaa ccgccgtatc      780
gaccgcgacc tcctgctcga attcacccaa cccgccctgg actttgtcca gcagaccggg      840
cgcgacctgt actgcggtga attcggcgtc attgaatacg tcgagcctgc cagccgccaa      900
aactggcacg ccgacctgct ggacatcctg cgccagcaga agattggccg cgccgtctgg      960
acttataaac aaatggatth tggcctgggt gacgcggacg gcaagggtgt cgaccccaaa     1020
cttctcgaaa tcttgtgtca atcctga                                     1047

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<210> 106

<211> 348

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (2)...(330)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (192)...(195)

<223> N-glycosylation site. Prosite id = PS00001

<400> 106

Met	Gln	His	Phe	Ile	Asn	Gly	Val	Asn	Leu	Gly	Gly	Trp	Leu	Ser	Gln
1				5					10					15	

Tyr	Gln	Lys	Tyr	Asp	His	Glu	His	Phe	Arg	Thr	Phe	Ile	Thr	Arg	Arg
			20					25					30		

Asp	Ile	Glu	Gln	Ile	Ala	Ser	Trp	Gly	Phe	Asp	His	Ile	Arg	Leu	Pro
		35					40					45			

Val	Asp	Tyr	Pro	Val	Leu	Glu	Ser	Asp	Asp	Ala	Pro	Gly	Ile	Tyr	His
	50					55					60				

Glu	Asp	Gly	Phe	Ala	Tyr	Leu	Asp	Ser	Cys	Leu	Glu	Trp	Cys	Gln	Ala
65					70					75					80

Ala	Gly	Leu	Ala	Val	Val	Phe	Asp	Leu	His	His	Ala	Pro	Gly	Tyr	Ser
				85					90					95	

Phe	Thr	Asn	Thr	Leu	Lys	Pro	Glu	Thr	Leu	His	Leu	Asn	Val	Leu	Phe
			100					105					110		

Glu	Gln	Glu	Ile	Ala	Gln	Asn	Arg	Phe	Ile	Ala	Leu	Trp	Glu	Thr	Ile
		115					120					125			

Val	Arg	Arg	Tyr	Gln	Ala	Ala	Gly	Leu	Pro	Ile	Ile	Phe	Glu	Leu	Leu
	130					135					140				

Asn	Glu	Met	Val	Leu	Pro	Asp	Ser	Gly	Pro	Trp	Asn	Ala	Leu	Ala	His
145					150					155					160

Lys	Thr	Val	Ala	Ala	Leu	Arg	Gln	Ile	Ser	Pro	Asp	Cys	Lys	Ile	Met
			165						170					175	

Ile	Gly	Gly	Asn	Asn	Tyr	Asn	Ala	Ala	Ser	Glu	Leu	Lys	Asn	Ile	Thr
			180					185					190		

Leu	His	Asn	Asp	Pro	Asn	Ile	Leu	Tyr	Thr	Phe	His	Phe	Tyr	Glu	Pro
		195					200					205			

Ala Leu Phe Thr His Gln Lys Ala Pro Trp Val Gln Ile Ala Val Glu
210 215 220

Tyr Asn Gln Glu Leu Glu Tyr Pro Gly Ser Tyr Thr Asn Leu Ala Ala
225 230 235 240

Phe Leu Arg Arg Asn Pro His Tyr Gln Glu Ser Tyr Gly Trp Gln Val
245 250 255

Asn Arg Arg Ile Asp Arg Asp Leu Leu Leu Glu Phe Thr Gln Pro Ala
260 265 270

Leu Asp Phe Val Gln Gln Thr Gly Arg Asp Leu Tyr Cys Gly Glu Phe
275 280 285

Gly Val Ile Glu Tyr Val Glu Pro Ala Ser Arg Gln Asn Trp His Ala
290 295 300

Asp Leu Leu Asp Ile Leu Arg Gln Gln Lys Ile Gly Arg Ala Val Trp
305 310 315 320

Thr Tyr Lys Gln Met Asp Phe Gly Leu Val Asp Ala Asp Gly Lys Val
325 330 335

Val Asp Pro Lys Leu Leu Glu Ile Leu Cys Gln Ser
340 345

<210> 107
<211> 1137
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 107
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gggtttcacg actttgacat caggcgcggg gtgaacatca gccattgggt gtcgcagagt 180
ggaaggcgtg gtgctgatcg ggaggcgttc tttaccaggg cggatgtgga ggccatcgcc 240
ggcttcgggt atgatcacat tcgtttgccc atcgatgaag agcagatgtg ggatgagtcg 300
ggcaacaagg agccacgtgc ctttgaattg ctgcatgagg ccattggctg ggctttggac 360
aatgagctca gggtcattgt tgacctgcac atcatcaggt cgcactatct taatgcgcct 420
gagaacccgc tttggaccga tcgtgctgaa cagttgaaat ttgttgagat gtggcgacag 480

ttgtctgatg agctgcaggg ctatccgctc gataggggtgg cctatgaatt gatgaatgag 540
gccgtggctg atgatccgga cgattggaac cggcttgtgg ctgagacgat ggaggcgcta 600
cggatgctgg aaccggagcg caagattgtc attggctcca accgctggca gtctgtgcat 660
acatttcctg acctggtgat cccggataat gacccgcata tcatattgag ttttcacttc 720
tacgaaccat ttctgctgac gcaccacaag gcctcctgga cacacatccg tgattacacc 780
gggccgggtga actatccggg tttagactgta gacccgaccc acctggagggg gttgtctgaa 840
gaactgggtga cccggattgg ccatcacaat ggggtgtata caaaagaaac gatggaggag 900
atgatcatga tcccactgca atatgccaaa gaacggggggc tccccctgta ttgcgggggag 960
tggggatgtt tcccgaccat gccccaggag atgcgcctgc aatggtagcg cgatgtgcgt 1020
gcgacccctgg aaaagcatga gattgcctgg gcaaactggg attacaaggg tggtttcggt 1080
gtggttgacc gcaacggcga accccacccat gatttattgg aagtcttact aaaataa 1137

<210> 108
<211> 378
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(32)

<220>
<221> DOMAIN
<222> (54)...(361)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (52)...(55)
<223> N-glycosylation site. Prosite id = PS00001

<400> 108
Met Glu Lys Gln Ile Cys Ser Asn Val Phe Ser Thr Met Leu Ile Ile
1 5 10 15

Gly Gly Leu Leu Val Leu Leu Gly Phe Ser Ser Cys Gly Arg Gln Ala
20 25 30

Glu Pro Ala Ala Asp Ser Phe Arg Gly Phe His Asp Phe Asp Ile Arg
35 40 45

Arg Gly Val Asn Ile Ser His Trp Leu Ser Gln Ser Gly Arg Arg Gly
50 55 60

Ala	Asp	Arg	Glu	Ala	Phe	Phe	Thr	Arg	Ala	Asp	Val	Glu	Ala	Ile	Ala	
65					70					75					80	
Gly	Phe	Gly	Tyr	Asp	His	Ile	Arg	Leu	Pro	Ile	Asp	Glu	Glu	Gln	Met	
				85					90					95		
Trp	Asp	Glu	Ser	Gly	Asn	Lys	Glu	Pro	Arg	Ala	Phe	Glu	Leu	Leu	His	
			100					105					110			
Glu	Ala	Ile	Gly	Trp	Ala	Leu	Asp	Asn	Glu	Leu	Arg	Val	Ile	Val	Asp	
		115					120					125				
Leu	His	Ile	Ile	Arg	Ser	His	Tyr	Phe	Asn	Ala	Pro	Glu	Asn	Pro	Leu	
	130					135					140					
Trp	Thr	Asp	Arg	Ala	Glu	Gln	Leu	Lys	Phe	Val	Glu	Met	Trp	Arg	Gln	
145					150					155					160	
Leu	Ser	Asp	Glu	Leu	Gln	Gly	Tyr	Pro	Leu	Asp	Arg	Val	Ala	Tyr	Glu	
				165					170					175		
Leu	Met	Asn	Glu	Ala	Val	Ala	Asp	Asp	Pro	Asp	Asp	Trp	Asn	Arg	Leu	
			180				185						190			
Val	Ala	Glu	Thr	Met	Glu	Ala	Leu	Arg	Met	Leu	Glu	Pro	Glu	Arg	Lys	
		195					200					205				
Ile	Val	Ile	Gly	Ser	Asn	Arg	Trp	Gln	Ser	Val	His	Thr	Phe	Pro	Asp	
	210					215					220					
Leu	Val	Ile	Pro	Asp	Asn	Asp	Pro	His	Ile	Ile	Leu	Ser	Phe	His	Phe	
225					230					235					240	
Tyr	Glu	Pro	Phe	Leu	Leu	Thr	His	His	Lys	Ala	Ser	Trp	Thr	His	Ile	
				245					250					255		
Arg	Asp	Tyr	Thr	Gly	Pro	Val	Asn	Tyr	Pro	Gly	Leu	Thr	Val	Asp	Pro	
			260					265					270			
Thr	His	Leu	Glu	Gly	Leu	Ser	Glu	Glu	Leu	Val	Thr	Arg	Ile	Gly	His	
		275					280					285				
His	Asn	Gly	Val	Tyr	Thr	Lys	Glu	Thr	Met	Glu	Glu	Met	Ile	Met	Ile	
	290					295					300					

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Pro Leu Gln Tyr Ala Lys Glu Arg Gly Leu Pro Leu Tyr Cys Gly Glu
305 310 315 320

Trp Gly Cys Phe Pro Thr Met Pro Gln Glu Met Arg Leu Gln Trp Tyr
325 330 335

Ala Asp Val Arg Ala Ile Leu Glu Lys His Glu Ile Ala Trp Ala Asn
340 345 350

Trp Asp Tyr Lys Gly Gly Phe Gly Val Val Asp Arg Asn Gly Glu Pro
355 360 365

His His Asp Leu Leu Glu Val Leu Leu Lys
370 375

<210> 109

<211> 1248

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 109

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gaccatttcc ttatgggtgt agccatcaac cgcctgattg caatgggcca tacgaatgtc      180
cgggcccaga acgccagccg gaccccggaa cagctcaagg gggacattgc cctgggtcaag      240
gcgcagttca acctgatcgt caatgagaac gatctgaaac cgattctcat tcacccgagg      300
ccaggaccgg acgggtacga cttcgcccca gcggatgcct tcgtgaagtt cggcatggac      360
aacaatatgt atatcgtggg ccacaccctc ctctggcaca gccagggtgcc caactgggtc      420
ttccaagggt ctgctccggc gactccggaa acgccacctg ctgccacgga cgcggcggtc      480
gcaccccgcg gcggacgagg aggtcgcggc gggattaccg gcccctggc gaccgcgag      540
gagttgatcg aacgcatgcg cgagcacatt cacaccgtcg tcggccgcta taagggaag      600
atcaaggtct gggacgtcgt caacgaagcc ctgcgccgac gcggcaccga gaccctgcga      660
agcacgtact ggaccctaat catcggggcg gaattcatcg ccatggcctt tcgattcgcc      720
cacgaagccg atccggatgc gatccttcgt tacaacgatt atggcctgga gaaccctgcc      780
aagcgtgaga aactcaagaa gctgatcgcg tcgctccagg agcagaacgt tccggttcat      840
gccatcggca cgcaaaccga tatcagcgtc tccacgacgt tcgaaagaat ggatgagacc      900
ttgagggacc tggcatccat cgggcttccc gtccacatca ccgaactgga tgtcaacgcc      960

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gccgcggggg gccagagggg caccaatgcg gacattgccg gcactgccga gcgtacggcg 1020
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gcgatcatga agcacaagga ctcggtgaag atggtcacgt tctggggcgt caatgacgcg 1140
gtttcgtggc tcgcacgcgg caccctcgtg ctgttcgacg gcaacaatca gcccaagccg 1200
gctttcgatg cggtcattcg cgtcgccacg gaggcggcac agaactga 1248

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<210> 110
 <211> 415
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SIGNAL
 <222> (1)...(28)

<220>
 <221> DOMAIN
 <222> (34)...(409)
 <223> Glycosyl hydrolase family 10

<220>
 <221> SITE
 <222> (312)...(322)
 <223> Glycosyl hydrolases family 10 active site. Prosite id = PS00591

<400> 110
 Met Lys Thr His Ser Phe Asn Leu Arg Ser Arg Ile Thr Leu Leu Thr
 1 5 10 15

Ala Ala Leu Leu Phe Ile Gly Ala Thr Ala Gly Ala Ala Thr Thr Pro
 20 25 30

Ile Thr Leu Lys Asp Ala Tyr Lys Asp His Phe Leu Met Gly Val Ala
 35 40 45

Ile Asn Arg Leu Ile Ala Met Gly Asp Thr Asn Val Arg Ala Asp Asn
 50 55 60

Ala Ser Arg Thr Pro Glu Gln Leu Lys Gly Asp Ile Ala Leu Val Lys
 65 70 75 80

Ala Gln Phe Asn Leu Ile Val Asn Glu Asn Asp Leu Lys Pro Ile Leu
 85 90 95

Ile His Pro Arg Pro Gly Pro Asp Gly Tyr Asp Phe Ala Pro Ala Asp
 100 105 110

Ala Phe Val Lys Phe Gly Met Asp Asn Asn Met Tyr Ile Val Gly His
 115 120 125

Thr Leu Leu Trp His Ser Gln Val Pro Asn Trp Phe Phe Gln Gly Ser
 130 135 140

Ala Pro Ala Thr Pro Glu Thr Pro Pro Ala Ala Thr Asp Ala Ala Val
 145 150 155 160

Ala Pro Arg Gly Gly Arg Gly Gly Arg Gly Gly Ile Thr Gly Pro Leu
 165 170 175

Ala Thr Arg Glu Glu Leu Ile Glu Arg Met Arg Glu His Ile His Thr
 180 185 190

Val Val Gly Arg Tyr Lys Gly Lys Ile Lys Val Trp Asp Val Val Asn
 195 200 205

Glu Ala Leu Ala Asp Gly Gly Thr Glu Thr Leu Arg Ser Thr Tyr Trp
 210 215 220

Thr Gln Ile Ile Gly Pro Glu Phe Ile Ala Met Ala Phe Arg Phe Ala
 225 230 235 240

His Glu Ala Asp Pro Asp Ala Ile Leu Arg Tyr Asn Asp Tyr Gly Leu
 245 250 255

Glu Asn Pro Ala Lys Arg Glu Lys Leu Lys Lys Leu Ile Ala Ser Leu
 260 265 270

Gln Glu Gln Asn Val Pro Val His Ala Ile Gly Thr Gln Thr His Ile
 275 280 285

Ser Val Ser Thr Thr Phe Glu Arg Met Asp Glu Thr Leu Arg Asp Leu
 290 295 300

Ala Ser Ile Gly Leu Pro Val His Ile Thr Glu Leu Asp Val Asn Ala
 305 310 315 320

Ala Ala Gly Gly Gln Arg Gly Thr Asn Ala Asp Ile Ala Gly Thr Ala
 325 330 335

Glu Arg Thr Ala Gly Gly Val Val Ser Glu Ala Asp Lys Arg Leu Ala
 340 345 350

Asp Ala Tyr Ala Asn Leu Phe Arg Ala Ile Met Lys His Lys Asp Ser

355

360

365

Val Lys Met Val Thr Phe Trp Gly Val Asn Asp Ala Val Ser Trp Leu
 370 375 380

Ala Arg Gly Thr Pro Leu Leu Phe Asp Gly Asn Asn Gln Pro Lys Pro
 385 390 395 400

Ala Phe Asp Ala Val Ile Arg Val Ala Thr Glu Ala Ala Gln Asn
 405 410 415

<210> 111
 <211> 1131
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 111
 atgcgaagac tgatcaccat catccttgcg acggctgtcg caatcttata gaccacatca 60
 tgctccaaga ccgctgaacg agagggcttc ttgatcaagc gaggaaccaa cctcagccat 120
 tggctctccc agagcaagga aaggggagag gctcgcaggc tccatatcca ggaggatgac 180
 ttgctcgcc tcgacagcct cggtttcgac catgtgcgca tccctgtcga cgaggaacaa 240
 ctctgggacg aggatggcaa caagctcaca gaagcatggg aactgctcga tttcgccctc 300
 gacatggcgc gcaagtacaa cctgcgcgct atcgtggacc ttcacatcat ccgcgccccat 360
 tacttcaacg ccgtcaacga aggcgcgctg aatactctct tcaccagcga ggaggcgcag 420
 cagggcctga tcaacctttg gtaccagctt tccgacttcc tcaaggaccg cagcgtcgac 480
 tgggttgctt acgagttcat gaacgagcca gtcgctcctg agcatgagca atggaacgcc 540
 ctgctcgcaa aggtgcacaa ggcgcttcgt gagcgtgaac cggagcgtac cctcgtgatc 600
 gggttctaacc tgtggcaggg tcaccagacc ttcaagtacc tccgcgtacc tgagaatgac 660
 ccgaacatca tcctgagctt ccactactac aacccttcga tcctcaccca caacatggct 720
 ccgtggactc cgggtgggcaa atataccggt tccatcaatt atccgggcgt catcgtctct 780
 gctgaggatt acgctgcgca gagccctgag gtgcaggccg aggtgaagca gtatacggag 840
 atggtctgga accgcgacac gatctacagc cagatgaagg atgcgatcga ggtggctgcc 900
 agctatggac tgcagctctt ctgcggcgaa tggggcgtgt atgaacctgt cgaccgtgag 960
 cttgcatacg catggaccaa ggatatgctg tcggtgttcg acgagttcga catcgcattg 1020
 acgacctggg gttacgatgc cgacttcggc ttctgggacc aggcgaaaca tgatttcaag 1080
 gacaagcctc ttgtcgatct cctgatgggt tccaagggtc ttgaacaata g 1131

<210> 112
 <211> 376
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SIGNAL
 <222> (1)...(22)

<220>
 <221> DOMAIN
 <222> (39)...(353)
 <223> Cellulase (glycosyl hydrolase family 5)

<220>
 <221> SITE
 <222> (37)...(40)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 112
 Met Arg Arg Leu Ile Thr Ile Ile Leu Ala Thr Ala Val Ala Ile Leu
 1 5 10 15

Ser Thr Thr Ser Cys Ser Lys Thr Ala Glu Arg Glu Gly Phe Leu Ile
 20 25 30

Lys Arg Gly Thr Asn Leu Ser His Trp Leu Ser Gln Ser Lys Glu Arg
 35 40 45

Gly Glu Ala Arg Arg Leu His Ile Gln Glu Asp Asp Phe Ala Arg Leu
 50 55 60

Asp Ser Leu Gly Phe Asp His Val Arg Ile Pro Val Asp Glu Glu Gln
 65 70 75 80

Leu Trp Asp Glu Asp Gly Asn Lys Leu Thr Glu Ala Trp Glu Leu Leu
 85 90 95

Asp Phe Ala Leu Asp Met Ala Arg Lys Tyr Asn Leu Arg Ala Ile Val
 100 105 110

Asp Leu His Ile Ile Arg Ala His Tyr Phe Asn Ala Val Asn Glu Gly
 115 120 125

Ala Ser Asn Thr Leu Phe Thr Ser Glu Glu Ala Gln Gln Gly Leu Ile
 130 135 140

Asn Leu Trp Tyr Gln Leu Ser Asp Phe Leu Lys Asp Arg Ser Val Asp

$\langle 210 \rangle$	113
$\langle 211 \rangle$	1095

<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 113
atgaaggtga cccgaacagc tgtcgcgggc attgtcgccg cagcggtcct catcacgata 60
ggcacgtcga ccgcgtcggc tgaggatgaa ccaaccagcg agaacacgtc gacggatcag 120
ccgttgcgcg tcctggcagc caaagccggg atcgcgttcg gcacggccgt cgacatgaac 180
gcgtacaaca acgacgcgac ctaccgtgag ctcgtcggcc aggagttctc gagcgtcacg 240
gccgagaacg tcatgaagtg gcagctcctc gagccgcagc gaggggtcta caactgggggt 300
ccggccgata agctcgtgcg cgtagccaac gagaacggcc agaaggtgcg cgggcacacg 360
ctcatctggc acaaccagct gccacactgg cttaccagcg gagtgcctc cggtgagata 420
acaccggacg agctccggca gctcctgagg aaccacatct tcacggtgat gcgccacttc 480
aagggcgaga tccaccagtg ggatgtcgcc aacgagggtca tcgacgacag cggcaacctg 540
cgcaacacga tctggctgca gaacctgggt ccgagctaca tcgcggacgc gttccggtgg 600
gctcgcaagg ccgaccggga cgccgccctc tatctgaacg actacaacgt cgagggccccg 660
aacgccaagg ccgatgcgta ctacgccctg gtcaagcagc tcctcgccga cgacgtgccg 720
gtggacggct tcggaataca ggggcacctc ggtgtgcagt tcggcttctg gcccgcgagt 780
gcggtggccg acaacatggg gcgcttcgag gactcggcc tgcagacggc ggtcacccgag 840
gcggatgtcc ggatgatcat gccgcccgcg gaggacaagc tggccgcaca ggcacgtggc 900
tacagcacgt tgggtccagg ctgcctgatg gccaaagcgt gcaggtcgtt caccgtctgg 960
ggcttcaccg acaagtactc ctgggttccg ggcaccttcc ccggccaggg cgcggcgaac 1020
ctcctggccg aggacttcca gcccaagccg gcttactacg ccgtccagga tgacctcgcg 1080
cgcgccggac ggtag 1095

<210> 114
<211> 364
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(27)

<220>
<221> DOMAIN
<222> (41)...(359)
<223> Glycosyl hydrolase family 10

<220>

<221> SITE

<222> (35)...(38)

<223> N-glycosylation site. Prosite id = PS00001

<400> 114

Met Lys Val Thr Arg Thr Ala Val Ala Gly Ile Val Ala Ala Ala Val
 1 5 10 15

Leu Ile Thr Ile Gly Thr Ser Thr Ala Ser Ala Glu Asp Glu Pro Thr
 20 25 30

Ser Glu Asn Thr Ser Thr Asp Gln Pro Leu Arg Val Leu Ala Ala Lys
 35 40 45

Ala Gly Ile Ala Phe Gly Thr Ala Val Asp Met Asn Ala Tyr Asn Asn
 50 55 60

Asp Ala Thr Tyr Arg Glu Leu Val Gly Gln Glu Phe Ser Ser Val Thr
 65 70 75 80

Ala Glu Asn Val Met Lys Trp Gln Leu Leu Glu Pro Gln Arg Gly Val
 85 90 95

Tyr Asn Trp Gly Pro Ala Asp Gln Leu Val Arg Val Ala Asn Glu Asn
 100 105 110

Gly Gln Lys Val Arg Gly His Thr Leu Ile Trp His Asn Gln Leu Pro
 115 120 125

Thr Trp Leu Thr Ser Gly Val Ala Ser Gly Glu Ile Thr Pro Asp Glu
 130 135 140

Leu Arg Gln Leu Leu Arg Asn His Ile Phe Thr Val Met Arg His Phe
 145 150 155 160

Lys Gly Glu Ile His Gln Trp Asp Val Ala Asn Glu Val Ile Asp Asp
 165 170 175

Ser Gly Asn Leu Arg Asn Thr Ile Trp Leu Gln Asn Leu Gly Pro Ser
 180 185 190

Tyr Ile Ala Asp Ala Phe Arg Trp Ala Arg Lys Ala Asp Pro Asp Ala
 195 200 205

Ala Leu Tyr Leu Asn Asp Tyr Asn Val Glu Gly Pro Asn Ala Lys Ala
 210 215 220

Asp Ala Tyr Tyr Ala Leu Val Lys Gln Leu Leu Ala Asp Asp Val Pro
225 230 235 240

Val Asp Gly Phe Gly Ile Gln Gly His Leu Gly Val Gln Phe Gly Phe
245 250 255

Trp Pro Ala Ser Ala Val Ala Asp Asn Met Gly Arg Phe Glu Ala Leu
260 265 270

Gly Leu Gln Thr Ala Val Thr Glu Ala Asp Val Arg Met Ile Met Pro
275 280 285

Pro Asp Glu Asp Lys Leu Ala Ala Gln Ala Arg Gly Tyr Ser Thr Leu
290 295 300

Val Gln Gly Cys Leu Met Ala Lys Arg Cys Arg Ser Phe Thr Val Trp
305 310 315 320

Gly Phe Thr Asp Lys Tyr Ser Trp Val Pro Gly Thr Phe Pro Gly Gln
325 330 335

Gly Ala Ala Asn Leu Leu Ala Glu Asp Phe Gln Pro Lys Pro Ala Tyr
340 345 350

Tyr Ala Val Gln Asp Asp Leu Ala Arg Ala Gly Arg
355 360

<210> 115

<211> 774

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 115

atggacttgc agctaggcgg aaagcgcgtg ctgatcacgg gtgcgtccaa aggcacgcgc 60

ctggcctgcg ccgtcgcctt tgcgcgcgag ggtgccgacc cgattctggt ggcgcgcgat 120

gatgcggcgt tgcacacgc cacgtccgcc atccgcgaac aaagcggccg cgcggcacat 180

gccatcacgc tggacctggc cctgcctggc gcggcggaaa agctggccaa ggaaaccggc 240

cccatcgaca tactggtcaa caacgcgggc gcggtgcccg gcggcgcgct ggaccagggtg 300

caagacgaac gctggcgcgc gggctgggaa ttgaaagtgc acggctacat cagcctggcg 360

cgctgctact acccgcacat gcgcgaagcg gcgcggggcg tcacgcgcaa catcatcggc 420

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atggcgggcg cggcgccccg cgccgactac atctgcggcg cggcggccaa tgcctcactg 480
attgccttta cccgcgcgct ggggtggcgaa gcgccccgcc acggcgtgcg cgtctttggc 540
gtcaaccctt cgcgcacgcg gaccgaccgc gtgctgaccc tggccccggca acgcgcgcag 600
gcgcgctggg gcgacgaaac ccgttggcag gaaacgctgt cggacctgcc cttcaaccgg 660
ctgatggaac ccgccgaagt ggccgacatg attgtgttcg gcgcctcgcc gcgcgcgggt 720
tacctgagcg gcacgggtcat cgacctggac ggcggcgaac agtacgcgaa atag 774

<210> 116

<211> 257

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (8)...(172)

<223> short chain dehydrogenase

<220>

<221> SITE

<222> (159)...(162)

<223> N-glycosylation site. Prosite id = PS00001

<400> 116

Met Asp Leu Gln Leu Gly Gly Lys Arg Val Leu Ile Thr Gly Ala Ser
1 5 10 15

Lys Gly Ile Gly Leu Ala Cys Ala Val Ala Phe Ala Arg Glu Gly Ala
20 25 30

Asp Pro Ile Leu Val Ala Arg Asp Asp Ala Ala Leu His His Ala Thr
35 40 45

Ser Ala Ile Arg Glu Gln Ser Gly Arg Ala Ala His Ala Ile Thr Leu
50 55 60

Asp Leu Ala Leu Pro Gly Ala Ala Glu Lys Leu Ala Lys Glu Thr Gly
65 70 75 80

Pro Ile Asp Ile Leu Val Asn Asn Ala Gly Ala Val Pro Gly Gly Ala
85 90 95

Leu Asp Gln Val Gln Asp Glu Arg Trp Arg Ala Gly Trp Glu Leu Lys
100 105 110

Val His Gly Tyr Ile Ser Leu Ala Arg Cys Tyr Tyr Pro His Met Arg
115 120 125

Glu Ala Gly Ala Gly Val Ile Ala Asn Ile Ile Gly Met Ala Gly Ala
 130 135 140
 Ala Pro Arg Ala Asp Tyr Ile Cys Gly Ala Ala Ala Asn Ala Ser Leu
 145 150 155 160
 Ile Ala Phe Thr Arg Ala Leu Gly Gly Glu Ala Pro Arg His Gly Val
 165 170 175
 Arg Val Phe Gly Val Asn Pro Ser Arg Thr Arg Thr Asp Arg Val Leu
 180 185 190
 Thr Leu Ala Arg Gln Arg Ala Gln Ala Arg Trp Gly Asp Glu Thr Arg
 195 200 205
 Trp Gln Glu Thr Leu Ser Asp Leu Pro Phe Asn Arg Leu Met Glu Pro
 210 215 220
 Ala Glu Val Ala Asp Met Ile Val Phe Gly Ala Ser Pro Arg Ala Gly
 225 230 235 240
 Tyr Leu Ser Gly Thr Val Ile Asp Leu Asp Gly Gly Glu Gln Tyr Ala
 245 250 255

Lys

<210> 117
 <211> 747
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 117
 atgcccaaag tcatgctcgt taccggcggc agccgtggca tcggcgccgc cgtcgccaag 60
 ctggcgccgc gccgcggcta cgcggtcggc atcaactacc gcacccattc cgacgccgcc 120
 gacgccgtcg tggccgagat ccagcaggcg ggcggcaccg cgctggccat ccaggccgac 180
 gtgtcgcaag aagatgacgt gctgcacatg ttccgcacgc tggacgagcg cctgggcccgc 240
 atcgacgcgc tgggtcaataa cgccggcatc ctggaaacgc agatgcgcct ggaccagatg 300
 gaagcggacc gcctgctgcg cgtgctgtcc accaacgtca tcggcgcttt cctgtgtgcg 360
 cgccaagcgg tgcgcaggat gtcgacgcgc catggcgggc tgggcggcgc catcgtcaac 420

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gtgtcttcgg cggcggcgcg cctgggctcg cccaatgaat acgtggatta cgcggcctcc 480
aagggcgcg c tggacacgat gaccatcggc ctgtccaaag aggtagcgcc cgaaggtatc 540
cgcgtgaatg gcgtgcgccc cggcaccatc tacaccgaca tgcacgcaag cggcggcgag 600
ccgggccggg tggatcgctt gaaaagcgtg atcccgtgc gccgcggcgg ctcggtggaa 660
gaagtggcgg gcgccgtcat gtggctgttt tccgaagaag ccggctatac cagcggctcg 720
ttcatcgacg tgtccggcgg tagttga 747

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<210> 118
 <211> 248
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (3)...(176)
 <223> short chain dehydrogenase

<220>
 <221> SITE
 <222> (142)...(145)
 <223> N-glycosylation site. Prosite id = PS00001

<220>
 <221> SITE
 <222> (146)...(174)
 <223> Short-chain dehydrogenases/reductases family signature. Prosite id = PS00061

<400> 118
 Met Pro Lys Val Met Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Ala
 1 5 10 15

Ala Val Ala Lys Leu Ala Ala Arg Arg Gly Tyr Ala Val Gly Ile Asn
 20 25 30

Tyr Arg Thr His Ser Asp Ala Ala Asp Ala Val Val Ala Glu Ile Gln
 35 40 45

Gln Ala Gly Gly Thr Ala Leu Ala Ile Gln Ala Asp Val Ser Gln Glu
 50 55 60

Asp Asp Val Leu His Met Phe Arg Thr Leu Asp Glu Arg Leu Gly Arg
 65 70 75 80

Ile Asp Ala Leu Val Asn Asn Ala Gly Ile Leu Glu Thr Gln Met Arg
 85 90 95

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Leu Asp Gln Met Glu Ala Asp Arg Leu Leu Arg Val Leu Ser Thr Asn
 100 105 110

Val Ile Gly Ala Phe Leu Cys Ala Arg Glu Ala Val Arg Arg Met Ser
 115 120 125

Thr Arg His Gly Gly Val Gly Gly Ala Ile Val Asn Val Ser Ser Ala
 130 135 140

Ala Ala Arg Leu Gly Ser Pro Asn Glu Tyr Val Asp Tyr Ala Ala Ser
 145 150 155 160

Lys Gly Ala Leu Asp Thr Met Thr Ile Gly Leu Ser Lys Glu Val Ala
 165 170 175

Pro Glu Gly Ile Arg Val Asn Gly Val Arg Pro Gly Thr Ile Tyr Thr
 180 185 190

Asp Met His Ala Ser Gly Gly Glu Pro Gly Arg Val Asp Arg Leu Lys
 195 200 205

Ser Val Ile Pro Leu Arg Arg Gly Gly Ser Val Glu Glu Val Ala Gly
 210 215 220

Ala Val Met Trp Leu Phe Ser Glu Glu Ala Gly Tyr Thr Ser Gly Ser
 225 230 235 240

Phe Ile Asp Val Ser Gly Gly Ser
 245

<210> 119
 <211> 1611
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 119
 atgcaaaagc ggtatgacgt cattgtcgtg ggcagcggga tcgccggcct cagttttgcg 60
 ctaaaagtcg ccaaggcggg gcatcgcgta gggattttga ccaaaaaaga ccgtgctgaa 120
 agcaacacca attatgcca aggcggcac gcggcagtca cttcgcagac agatgatttc 180
 gagctgcatg tgcaggacac attgaccgcg ggagatggac tctgcgacga ggcagtcgtc 240
 cgcacgatta tcggcgaggc tcccgcccga atccaggagc tgatcgattt gggggtggcc 300
 ttctcacatt tggaagatgg acgggtttcc ctccatcgcg aagggggtca ctcgaaaagg 360

cgcattcttc acgttcagga tgtcaccggc aaagcgattg aagaagccct cctccatgcc 420
atcgaacagt cgccgctgat cgacctgaat gagcacgtct ttgccatcga cttactgact 480
gaacgcaagc tggcgctggc gggctttgag gtggaagggtg ctaaaaaccg ggtggtcgga 540
ctctatgcgc tcgatgaagc cactcaggag gttcacgtat ttgaggctcc agtcgtcatg 600
ctggcaacgg gaggcgtcgg gcagggtctac ctctacagca ccaacccaag gatcgcgacc 660
ggtgatggat tggccatggc ttaccgggct ggcgccgaaa tccgcaacct cgagtgtatc 720
caatttcate ctacagcgct atacaccacc accaatgacc gctttctgat cagcgaagcc 780
gtccgggggtg aagggggccat cctccgcaat caggagggag aggctttcat ggctcgctac 840
gatgaccgca aggacctcgc cccccgggat attgtggcca gagcaattga cagtgaaatg 900
aagcagtccg gctcatccca tgtctggctc gacatcactc atcgggatga aaccgatctg 960
cgggagcgtt tccccaacat tttcgaggcc tgccctgaagg tcggagtcaa catggcgcaa 1020
tcctccatcc cggtgggttc ggcgatgcac tacctctgcg gaggcgtagc caccgacctc 1080
aatgcggcca ccgacatcac tggactgttt gcctgtgggg aagttgcctg cacgggattg 1140
catggtgcca accgtctcgc cagcaacagc ctgctggagg cagtggatcat ggcgcaccgg 1200
gcctccgctc cagtggatgc atacctcaac agcaaacctc accgctatgc acaattgccg 1260
gaatggacgg atggcaacgt gcaggacagc gacgagcgtg tcgtgatcag ccacaactgg 1320
gatgaactca aacgcacgat gtgggactac gtgggcatcg tccgcaccac caagcggctt 1380
cagcgcgcgc aacgacgcat tcgtcacctc cagcaggaaa tcgaagagta ttactggaat 1440
ttcaagggtg agtcctccct tctggagtta cggaatctgg ttgtgggtggc ggatctgggtt 1500
atccactgtg ccctccaacg ccatgagagc cgtggcctgc attgcacccg ggattatccc 1560
ggcaagttgc ccaccccgat caataccgcc gttcgcagaa gaaccggtta a 1611

<210> 120
<211> 536
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (6)...(260)
<223> FAD dependent oxidoreductase

<220>
<221> DOMAIN
<222> (6)...(380)
<223> Pyridine nucleotide-disulphide oxidoreductase

<220>

<221> DOMAIN

<222> (6)...(391)

<223> FAD binding domain

<220>

<221> DOMAIN

<222> (440)...(534)

<223> Fumarate reductase/succinate dehydrogenase flavoprotein C-terminal domain

<400> 120

Met Gln Lys Arg Tyr Asp Val Ile Val Val Gly Ser Gly Ile Ala Gly
 1 5 10 15

Leu Ser Phe Ala Leu Lys Val Ala Lys Ala Gly His Arg Val Gly Ile
 20 25 30

Leu Thr Lys Lys Asp Arg Ala Glu Ser Asn Thr Asn Tyr Ala Gln Gly
 35 40 45

Gly Ile Ala Ala Val Thr Ser Gln Thr Asp Asp Phe Glu Leu His Val
 50 55 60

Gln Asp Thr Leu Thr Ala Gly Asp Gly Leu Cys Asp Glu Ala Val Val
 65 70 75 80

Arg Thr Ile Ile Gly Glu Ala Pro Ala Arg Ile Gln Glu Leu Ile Asp
 85 90 95

Leu Gly Val Ala Phe Ser His Leu Glu Asp Gly Arg Val Ser Leu His
 100 105 110

Arg Glu Gly Gly His Ser Lys Arg Arg Ile Leu His Val Gln Asp Val
 115 120 125

Thr Gly Lys Ala Ile Glu Glu Ala Leu Leu His Ala Ile Glu Gln Ser
 130 135 140

Pro Leu Ile Asp Leu Asn Glu His Val Phe Ala Ile Asp Leu Leu Thr
 145 150 155 160

Glu Arg Lys Leu Ala Leu Ala Gly Phe Glu Val Glu Gly Ala Lys Asn
 165 170 175

Arg Val Val Gly Leu Tyr Ala Leu Asp Glu Ala Thr Gln Glu Val His
 180 185 190

Val Phe Glu Ala Pro Val Val Met Leu Ala Thr Gly Gly Val Gly Gln
 195 200 205

Val Tyr Leu Tyr Ser Thr Asn Pro Arg Ile Ala Thr Gly Asp Gly Leu
210 215 220

Ala Met Ala Tyr Arg Ala Gly Ala Glu Ile Arg Asn Leu Glu Cys Ile
225 230 235 240

Gln Phe His Pro Thr Ala Leu Tyr Thr Thr Thr Asn Asp Arg Phe Leu
245 250 255

Ile Ser Glu Ala Val Arg Gly Glu Gly Ala Ile Leu Arg Asn Gln Glu
260 265 270

Gly Glu Ala Phe Met Ala Arg Tyr Asp Asp Arg Lys Asp Leu Ala Pro
275 280 285

Arg Asp Ile Val Ala Arg Ala Ile Asp Ser Glu Met Lys Gln Ser Gly
290 295 300

Ser Ser His Val Trp Leu Asp Ile Thr His Arg Asp Glu Thr Asp Leu
305 310 315 320

Arg Glu Arg Phe Pro Asn Ile Phe Glu Ala Cys Leu Lys Val Gly Val
325 330 335

Asn Met Ala Gln Ser Ser Ile Pro Val Val Pro Ala Met His Tyr Leu
340 345 350

Cys Gly Gly Val Ala Thr Asp Leu Asn Ala Ala Thr Asp Ile Thr Gly
355 360 365

Leu Phe Ala Cys Gly Glu Val Ala Cys Thr Gly Leu His Gly Ala Asn
370 375 380

Arg Leu Ala Ser Asn Ser Leu Leu Glu Ala Val Val Met Ala His Arg
385 390 395 400

Ala Ser Val Ala Val Asp Ala Tyr Leu Asn Ser Lys Pro His Arg Tyr
405 410 415

Ala Gln Leu Pro Glu Trp Thr Asp Gly Asn Val Gln Asp Ser Asp Glu
420 425 430

Arg Val Val Ile Ser His Asn Trp Asp Glu Leu Lys Arg Thr Met Trp
435 440 445

Asp Tyr Val Gly Ile Val Arg Thr Thr Lys Arg Leu Gln Arg Ala Gln
 450 455 460

Arg Arg Ile Arg His Leu Gln Gln Glu Ile Glu Glu Tyr Tyr Trp Asn
 465 470 475 480

Phe Lys Val Glu Ser Ser Leu Leu Glu Leu Arg Asn Leu Val Val Val
 485 490 495

Ala Asp Leu Val Ile His Cys Ala Leu Gln Arg His Glu Ser Arg Gly
 500 505 510

Leu His Cys Thr Arg Asp Tyr Pro Gly Lys Leu Pro Thr Pro Ile Asn
 515 520 525

Thr Ala Val Arg Arg Arg Thr Gly
 530 535

<210> 121
 <211> 990
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 121
 atgccttttg atgccattgg agaaagcttc cgtgccagcc agcaactccc gctgatcaag 60
 gtcgacggca accgtttcgt gattgaggag accggtgagc cgatcgtctt ccggggcgtc 120
 tccgcctccg acccggctgc gctactggaa cgcgggtcaat ggggtcgccg ttactttgaa 180
 gagatggcca agtggaatgc caacgttgtg cgcattcctg ttcacccggc agactggcgt 240
 aatctcggcg aagacatcta tctcgcccta ctcgaccagg cgattgaatg gtcggctgaa 300
 ctcggcatgc acgtcatcat cgactggcac actatcggca atattctgac cggtatattat 360
 caccgcgaca tttatgaaac caccctgat gagacttacc gtttttggtta caccatcgcc 420
 attcgttatc agggtaacc gacagtggcc ttttatgaac tctacaatga gccaccaaac 480
 cgaggcggtc gcatgggccc ccttccttgg gaagaatatg ccagttcat cgaagggtg 540
 atttccatgc tctacgcat cgacgacacc gttattccac tggtcgctgg cttcgactgg 600
 ggatatgatt tgagctatgt tgcggaacgc ccgatccgtt ttccaggagt cgcctatgtc 660
 acccaccctt acccgcagaa gcgccccgag ccttgggaac cgatctggca ggaggaatgg 720
 ggttttgctg ccgacaccta tcccatgatc gccactgagt ttggcttcat gagtgaggac 780
 ggtcccggag ccacaaccc ggttatcggg gatgaacact atggcgaatc ggtcatccgc 840

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tttttcgagg aacgcggcat ttcctggacg gcctgggtgt ttgatacctct ctggtcaccc      900
cagcttttcg aagactggga aacctatacc cccacccggc aaggccgatt ctttaaagag      960
aaaatgatgg aactgaatcc cccgcgttga                                          990

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<210> 122
 <211> 329
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (25)...(302)
 <223> Cellulase (glycosyl hydrolase family 5)

<400> 122
 Met Pro Phe Asp Ala Ile Gly Glu Ser Phe Arg Ala Ser Gln Gln Leu
 1 5 10 15

Pro Leu Ile Lys Val Asp Gly Asn Arg Phe Val Ile Ala Glu Thr Gly
 20 25 30

Glu Pro Ile Val Phe Arg Gly Val Ser Ala Ser Asp Pro Ala Ala Leu
 35 40 45

Leu Glu Arg Gly Gln Trp Gly Arg Arg Tyr Phe Glu Glu Met Ala Lys
 50 55 60

Trp Asn Ala Asn Val Val Arg Ile Pro Val His Pro Ala Asp Trp Arg
 65 70 75 80

Asn Leu Gly Glu Asp Ile Tyr Leu Ala Leu Leu Asp Gln Ala Ile Glu
 85 90 95

Trp Ser Ala Glu Leu Gly Met His Val Ile Ile Asp Trp His Thr Ile
 100 105 110

Gly Asn Ile Leu Thr Gly Ile Tyr His Arg Asp Ile Tyr Glu Thr Thr
 115 120 125

Arg Asp Glu Thr Tyr Arg Phe Trp Tyr Thr Ile Ala Ile Arg Tyr Gln
 130 135 140

Gly Asn Pro Thr Val Ala Phe Tyr Glu Leu Tyr Asn Glu Pro Thr Asn
 145 150 155 160

185/248

Arg Gly Gly Arg Met Gly Pro Leu Pro Trp Glu Glu Tyr Ala Gln Phe
 165 170 175

Ile Glu Gly Leu Ile Ser Met Leu Tyr Ala Ile Asp Asp Thr Val Ile
 180 185 190

Pro Leu Val Ala Gly Phe Asp Trp Gly Tyr Asp Leu Ser Tyr Val Ala
 195 200 205

Glu Arg Pro Ile Arg Phe Pro Gly Val Ala Tyr Val Thr His Pro Tyr
 210 215 220

Pro Gln Lys Arg Pro Glu Pro Trp Glu Pro Ile Trp Gln Glu Glu Trp
 225 230 235 240

Gly Phe Val Ala Asp Thr Tyr Pro Met Ile Ala Thr Glu Phe Gly Phe
 245 250 255

Met Ser Glu Asp Gly Pro Gly Ala His Asn Pro Val Ile Gly Asp Glu
 260 265 270

His Tyr Gly Glu Ser Val Ile Arg Phe Phe Glu Glu Arg Gly Ile Ser
 275 280 285

Trp Thr Ala Trp Val Phe Asp Pro Leu Trp Ser Pro Gln Leu Phe Glu
 290 295 300

Asp Trp Glu Thr Tyr Thr Pro Thr Arg Gln Gly Arg Phe Phe Lys Gln
 305 310 315 320

Lys Met Met Glu Leu Asn Pro Pro Arg
 325

<210> 123
 <211> 1398
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 123
 atgccgatga gcacagaaac gactttttcct tctgattttca cctgggggcgc agcaacagcc 60
 gcctaccaga tcgaagggggg cgatcgcgct ggcggggcgcg gccgttccgt gtgggacatg 120
 ttttgcgaga aacgaggagc tattttgggag gggcatacgg ggcagcgagc gagtctgcat 180
 cttcagcgct ggcgtgagga cgtaatgttg atgcaacagc tcggactgcg gggctatcgt 240

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tttagcgtca gctggccgcg cgtcttcccg acaggagtcg gcaaagtcaa ccgtgaaggg 300
ttggcctttt acgatcagct cgtagacgcc ttgctcgagg ccggcatcac cccctttata 360
acgctatttc attgggactt cccgctcgat ttgtaccacc gaggcggctg gttgaatcgc 420
gacagcgccg actggtttgc ctccacgcc gagtgcctcg gcaaggcact gggcgacagg 480
gtcaagcact gggtgaccct caacgagccg caggttttca taggcctcgg tcattacgaa 540
gggcgtcatg ccccgggggt gaagctctcc atcgcgga aa tgctgcgctg cgggcaccac 600
gccttgctcg cgcacgggaa ggccgtgcaa gccctgcgcg ctcccgtcga cggccccctgc 660
aagattggat ttgctccggt ggggattccc aagcttccgg cgagtgcgag ctccagaggat 720
atcgccgcgg cacgaaaggc ccagttcgcg gcgggagcgc cgccgtattg gacgctgagc 780
tggtgggcgg atccggtggt tcaggggaca tatcccgctg atgcctgcca ggctctcgga 840
gcggacgcgc cgcaggtggc cgatcacgac atgagcatca tcagcgagcc gactgatttc 900
ctgggcctca acctttatca aggggtggtg gtgcgtgccg atcacacggg tcaaccagaa 960
acggtgccgt ttccgcgggg attccccgtg actgcgctca actgggcccgt aaccccagag 1020
gcgctgtatt ggggcccgcg ctttgccctc gaacgctaca aaaagccgat tcacatcacg 1080
gaaaacgggc tatectgtcg tgactggccg tcgctcgacg ggcacgtcca cgacgccgac 1140
cgcatcgact tcatggcccg gcacttgccg gcagcgcac gagccattcg cgatgggata 1200
ccgatcgaag gctacttcca ctggtctgcg atcgacaact tcgagtgggc agaaggctac 1260
aaggaacgct tcgggctcat ttacgtcgac tatacgagcg gcgagcgcac tccgaaggac 1320
tcgtaccact ggtaccagaa ggtcattgcc tccgaggggc gggcagcgcct cggcgcgccc 1380
agtgctgctc gcccataa 1398

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<210> 124

<211> 465

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (5)...(454)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (13)...(27)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<400> 124

Met Pro Met Ser Thr Glu Thr Thr Phe Pro Ser Asp Phe Thr Trp Gly

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Ala	Ala	Thr	Ala	Ala	Tyr	Gln	Ile	Glu	Gly	Gly	Asp	Arg	Ala	Gly	Gly
		20						25					30		
Arg	Gly	Arg	Ser	Val	Trp	Asp	Met	Phe	Cys	Glu	Lys	Arg	Gly	Ala	Ile
		35					40					45			
Trp	Glu	Gly	His	Thr	Gly	Gln	Arg	Ala	Ser	Leu	His	Leu	Gln	Arg	Trp
	50					55					60				
Arg	Glu	Asp	Val	Met	Leu	Met	Gln	Gln	Leu	Gly	Leu	Arg	Gly	Tyr	Arg
65					70					75					80
Phe	Ser	Val	Ser	Trp	Pro	Arg	Val	Phe	Pro	Thr	Gly	Val	Gly	Lys	Val
				85					90					95	
Asn	Arg	Glu	Gly	Leu	Ala	Phe	Tyr	Asp	Gln	Leu	Val	Asp	Ala	Leu	Leu
			100					105					110		
Glu	Ala	Gly	Ile	Thr	Pro	Phe	Ile	Thr	Leu	Phe	His	Trp	Asp	Phe	Pro
		115					120					125			
Leu	Asp	Leu	Tyr	His	Arg	Gly	Gly	Trp	Leu	Asn	Arg	Asp	Ser	Ala	Asp
	130					135					140				
Trp	Phe	Ala	Ser	Tyr	Ala	Glu	Cys	Leu	Gly	Lys	Ala	Leu	Gly	Asp	Arg
145					150					155					160
Val	Lys	His	Trp	Val	Thr	Leu	Asn	Glu	Pro	Gln	Val	Phe	Ile	Gly	Leu
				165					170					175	
Gly	His	Tyr	Glu	Gly	Arg	His	Ala	Pro	Gly	Leu	Lys	Leu	Ser	Ile	Ala
			180					185					190		
Glu	Met	Leu	Arg	Cys	Gly	His	His	Ala	Leu	Leu	Ala	His	Gly	Lys	Ala
		195					200					205			
Val	Gln	Ala	Leu	Arg	Ala	Ser	Val	Asp	Gly	Pro	Cys	Lys	Ile	Gly	Phe
	210					215					220				
Ala	Pro	Val	Gly	Ile	Pro	Lys	Leu	Pro	Ala	Ser	Glu	Ser	Ser	Glu	Asp
225					230					235					240
Ile	Ala	Ala	Ala	Arg	Lys	Ala	Gln	Phe	Ala	Ala	Gly	Ala	Pro	Pro	Tyr
				245					250					255	

Trp Thr Leu Ser Trp Trp Ala Asp Pro Val Phe Gln Gly Thr Tyr Pro
260 265 270

Ala Asp Ala Cys Gln Ala Leu Gly Ala Asp Ala Pro Gln Val Ala Asp
275 280 285

His Asp Met Ser Ile Ile Ser Glu Pro Thr Asp Phe Leu Gly Leu Asn
290 295 300

Leu Tyr Gln Gly Val Val Val Arg Ala Asp His Thr Gly Gln Pro Glu
305 310 315 320

Thr Val Pro Phe Pro Pro Gly Phe Pro Val Thr Ala Leu Asn Trp Ala
325 330 335

Val Thr Pro Glu Ala Leu Tyr Trp Gly Pro Arg Phe Ala Phe Glu Arg
340 345 350

Tyr Lys Lys Pro Ile His Ile Thr Glu Asn Gly Leu Ser Cys Arg Asp
355 360 365

Trp Pro Ser Leu Asp Gly His Val His Asp Ala Asp Arg Ile Asp Phe
370 375 380

Met Ala Arg His Leu Arg Ala Ala His Arg Ala Ile Arg Asp Gly Ile
385 390 395 400

Pro Ile Glu Gly Tyr Phe His Trp Ser Ala Ile Asp Asn Phe Glu Trp
405 410 415

Ala Glu Gly Tyr Lys Glu Arg Phe Gly Leu Ile Tyr Val Asp Tyr Thr
420 425 430

Ser Gly Glu Arg Ile Pro Lys Asp Ser Tyr His Trp Tyr Gln Lys Val
435 440 445

Ile Ala Ser Glu Gly Arg Ala Ala Leu Gly Ala Pro Ser Ala Ala Arg
450 455 460

Pro
465

<210> 125
<211> 1350
<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 125

atgtcagatg cgcggccgac tgatccgaaa tccgcaatgc ccagacgctc ggacttcccc	60
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ggcgcggggcc cctgccattg ggacagcttc gccgcaaccg ggcgtaacgt ggtcggcaat	180
gaggatggcg cgcgcgcctg cgagcattac acccgctggc cgcaggatct ggacctgatc	240
cgcgaggccg ggctcgacgc ctaccgcttc tcgacctcct gggcgcgggt gatgcccgat	300
ggcgtgacct tgaaccccga ggggctggat ttctacgacc gcctcgtcga tggcatgctc	360
gagcgcgggc taaagcccta tctcacctc taccattggg aattgccctc ggcgcttgcc	420
gacagggggcg gctggaccaa tcgcgacacg gccgagcgc ttgccgattt cgcagcggtg	480
gtgatggagc ggttgggcag ccgcgtcgcc cgcacggcca ccatcaacga gccatggtgc	540
gtgagctggc tctcgcatth cgaaggccat cagcgcggcg gcctgcgcga catccgtgcc	600
accgcacgcg ccatgcatca tgtgcaactg gcgcacggcc tcgcgctcgg gaagctgcgc	660
gcgcaggggc atggcaatct cggcatcgtg ctgaatttct cggaaatcat tcccgcgggg	720
cgagagcacg cgaaggcggc tgatctcggc gacgcaatct cgaaccgctg gttcatcgag	780
tcagtcgcgc gtggcaccta tcccgatgtg gtcctcgagg gtctgggcaa gcacatgccc	840
gagggctggc aggatgacat gaaaaccatc gcggccccgc tcgactggct ggggtgtgaac	900
tactacacce gcggcatcgt cgcgcatgac ccggacgcgt cctggccctc gacccgagcg	960
gaggaggggc ccctgcccga gacgcagatg ggctgggaga tctaccccga gggcttgccg	1020
aacctgctgg tgcgcatggc gcgcgactat gtgggcgacc ttcccatggt cgtgaccgaa	1080
aacgggatgg cctggggccga cgaggtcgcg gatggcgccg tcagagatac gatccgcacc	1140
gaatatgtcg cagcccatct caacgcgacc cgcgaggcgc tggccggcgg ggcgaaatc	1200
gaaggtttct tctattggtc gctgctcgac aattacgaat gggccttcgg ctatgccaa	1260
cgcttcggcc tcgtccatgt cgatttcgac acgatggcac gcacgcccga agcctcctac	1320
cacgcgctga gggccgcgct gcagggttga	1350

<210> 126

<211> 449

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (15)...(443)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (235)...(238)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (361)...(369)

<223> Glycosyl hydrolases family 1 active site. Prosite id = PS00572

<220>

<221> SITE

<222> (393)...(396)

<223> N-glycosylation site. Prosite id = PS00001

<400> 126

Met	Ser	Asp	Ala	Ala	Pro	Thr	Asp	Pro	Lys	Ser	Ala	Met	Pro	Arg	Arg
1				5					10					15	

Ser	Asp	Phe	Pro	Glu	Gly	Phe	Val	Phe	Gly	Ala	Ala	Thr	Ala	Ala	Tyr
			20					25					30		

Gln	Ile	Glu	Gly	His	Ala	Phe	Gly	Gly	Ala	Gly	Pro	Cys	His	Trp	Asp
		35					40					45			

Ser	Phe	Ala	Ala	Thr	Gly	Arg	Asn	Val	Val	Gly	Asn	Glu	Asp	Gly	Ala
	50					55					60				

Arg	Ala	Cys	Glu	His	Tyr	Thr	Arg	Trp	Pro	Gln	Asp	Leu	Asp	Leu	Ile
65					70					75					80

Arg	Glu	Ala	Gly	Leu	Asp	Ala	Tyr	Arg	Phe	Ser	Thr	Ser	Trp	Ala	Arg
				85					90					95	

Val	Met	Pro	Asp	Gly	Val	Thr	Leu	Asn	Pro	Glu	Gly	Leu	Asp	Phe	Tyr
			100					105					110		

Asp	Arg	Leu	Val	Asp	Gly	Met	Leu	Glu	Arg	Gly	Leu	Lys	Pro	Tyr	Leu
		115					120					125			

Thr	Leu	Tyr	His	Trp	Glu	Leu	Pro	Ser	Ala	Leu	Ala	Asp	Arg	Gly	Gly
	130					135					140				

Trp	Thr	Asn	Arg	Asp	Thr	Ala	Glu	Arg	Phe	Ala	Asp	Phe	Ala	Ala	Val
145					150					155					160

Val	Met	Glu	Arg	Leu	Gly	Ser	Arg	Val	Ala	Arg	Thr	Ala	Thr	Ile	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

165

170

175

Glu Pro Trp Cys Val Ser Trp Leu Ser His Phe Glu Gly His His Ala
 180 185 190

Pro Gly Leu Arg Asp Ile Arg Ala Thr Ala Arg Ala Met His His Val
 195 200 205

Gln Leu Ala His Gly Leu Ala Leu Gly Lys Leu Arg Ala Gln Gly His
 210 215 220

Gly Asn Leu Gly Ile Val Leu Asn Phe Ser Glu Ile Ile Pro Ala Gly
 225 230 235 240

Arg Glu His Ala Lys Ala Ala Asp Leu Gly Asp Ala Ile Ser Asn Arg
 245 250 255

Trp Phe Ile Glu Ser Val Ala Arg Gly Thr Tyr Pro Asp Val Val Leu
 260 265 270

Glu Gly Leu Gly Lys His Met Pro Glu Gly Trp Gln Asp Asp Met Lys
 275 280 285

Thr Ile Ala Ala Pro Leu Asp Trp Leu Gly Val Asn Tyr Tyr Thr Arg
 290 295 300

Gly Ile Val Ala His Asp Pro Asp Ala Ser Trp Pro Ser Thr Arg Ala
 305 310 315 320

Glu Glu Gly Pro Leu Pro Lys Thr Gln Met Gly Trp Glu Ile Tyr Pro
 325 330 335

Glu Gly Leu Arg Asn Leu Leu Val Arg Met Ala Arg Asp Tyr Val Gly
 340 345 350

Asp Leu Pro Met Val Val Thr Glu Asn Gly Met Ala Trp Ala Asp Glu
 355 360 365

Val Ala Asp Gly Ala Val Arg Asp Thr Ile Arg Thr Glu Tyr Val Ala
 370 375 380

Ala His Leu Asn Ala Thr Arg Glu Ala Leu Ala Gly Gly Ala Asn Ile
 385 390 395 400

Glu Gly Phe Phe Tyr Trp Ser Leu Leu Asp Asn Tyr Glu Trp Ala Phe
 405 410 415

Gly Tyr Ala Lys Arg Phe Gly Leu Val His Val Asp Phe Asp Thr Met
420 425 430

Ala Arg Thr Pro Lys Ala Ser Tyr His Ala Leu Arg Ala Ala Leu Gln
435 440 445

Gly

<210> 127
<211> 774
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 127
atggacttgc agctaggcgg aaagcgcgtg ctgatcacgg gtgcgtccaa aggcattcggc 60
ctggcctgcg ccgtcgcctt tgcgcgcgag ggtgccgacc cgattctggt ggcgcgcgat 120
gatgcggcgt tgcattcacgc cacgtccgcc atccgcgaac aaagcggccg cgcggcacat 180
gccattcacgc tggacctggc cctgcctggc gcggcgga aa agctggccaa ggaaaccggc 240
cccatcgaca tactgggtcaa caacgcgggc gcggtgcccg gcggcgcgct ggaccagggtg 300
caagacgaac gctggcgcgcg gggctgggaa ttgaaagtgc acggctacat cagcctggcg 360
cgctgctact acccgcacat gcgcgaagcg ggcgcgggcg tcatcgccaa catcatcggc 420
atggcgggcg cggcgccccg cgccgactac atctgcggcg cggcggccaa tgcctcactg 480
attgccttta ccgcgcgcgt ggggtggcgaa gcgccccgcc acggcgtgcg cgtctttggc 540
gtcaaccctt cgcgcacgcg gaccgaccgc gtgctgacct tggcccggca acgcgcgcag 600
gcgcgctggg gcgacgaaac gcgttggcag gaaacgctgt cggacctgcc cttcaaccgg 660
ctgatggaac ccgccgaagt ggccgacatg attgtgttcg gcgcctcgcc acgcgcgggt 720
tacctgagcg gcacgggtcat cgacctggac ggcgggcgaa agtacgcgaa atag 774

<210> 128
<211> 257
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (8)...(172)
<223> short chain dehydrogenase

<220>

<221> SITE

<222> (159)...(162)

<223> N-glycosylation site. Prosite id = PS00001

<400> 128

Met Asp Leu Gln Leu Gly Gly Lys Arg Val Leu Ile Thr Gly Ala Ser
 1 5 10 15

Lys Gly Ile Gly Leu Ala Cys Ala Val Ala Phe Ala Arg Glu Gly Ala
 20 25 30

Asp Pro Ile Leu Val Ala Arg Asp Asp Ala Ala Leu His His Ala Thr
 35 40 45

Ser Ala Ile Arg Glu Gln Ser Gly Arg Ala Ala His Ala Ile Thr Leu
 50 55 60

Asp Leu Ala Leu Pro Gly Ala Ala Glu Lys Leu Ala Lys Glu Thr Gly
 65 70 75 80

Pro Ile Asp Ile Leu Val Asn Asn Ala Gly Ala Val Pro Gly Gly Ala
 85 90 95

Leu Asp Gln Val Gln Asp Glu Arg Trp Arg Ala Gly Trp Glu Leu Lys
 100 105 110

Val His Gly Tyr Ile Ser Leu Ala Arg Cys Tyr Tyr Pro His Met Arg
 115 120 125

Glu Ala Gly Ala Gly Val Ile Ala Asn Ile Ile Gly Met Ala Gly Ala
 130 135 140

Ala Pro Arg Ala Asp Tyr Ile Cys Gly Ala Ala Ala Asn Ala Ser Leu
 145 150 155 160

Ile Ala Phe Thr Arg Ala Leu Gly Gly Glu Ala Pro Arg His Gly Val
 165 170 175

Arg Val Phe Gly Val Asn Pro Ser Arg Thr Arg Thr Asp Arg Val Leu
 180 185 190

Thr Leu Ala Arg Gln Arg Ala Gln Ala Arg Trp Gly Asp Glu Thr Arg
 195 200 205

Trp Gln Glu Thr Leu Ser Asp Leu Pro Phe Asn Arg Leu Met Glu Pro
 210 215 220

Ala Glu Val Ala Asp Met Ile Val Phe Gly Ala Ser Pro Arg Ala Gly
 225 230 235 240

Tyr Leu Ser Gly Thr Val Ile Asp Leu Asp Gly Gly Glu Gln Tyr Ala
 245 250 255

Lys

<210> 129
 <211> 747
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 129
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 ctggccgcgc gccgcggcta cgcggtcggc atcaactacc gcacccattc cgacgccgcc 120
 gacgccgtcg tggccgaaat ccagcaggcg ggccggcaccg cgctggccat ccaggccgac 180
 gtgtcgcagg aagacgatgt gctgcacatg ttccgcacgc tggacgagcg cctgggcccgc 240
 atcgacgcgc tgggtcaataa cgccggcatc ctggaaacgc agatgcgcct ggaccagatg 300
 gaagccgacc gcctgctgcg cgtgctgtcc accaacgtca tcggcgcttt cctatgtgcg 360
 cgcgaagccg tgcgcaggat gtcgacgcgc catggcgggcg tgggcggcgc catcgtcaac 420
 gtgtcttcgg cggcggcgcg cctgggctcg cccaatgaat acgtggatta cgcggcctcc 480
 aagggcgcgc tggacacgat gaccatcggc ctgtcgaaag aggtggcgcc cgaaggatc 540
 cgcgtgaatg gcgtgcgccc cggcaccatc tacaccgaca tgcacgcaag cggcggcgag 600
 ccgggcccggg tggatcgcct gaaaagcgtg atcccgtgc gccgcggcgg ctcggtggaa 660
 gaagtggcgg gcgccgtcat gtggctgttt tccgaagaag ccggctatac cagcggttcg 720
 ttcatcgacg tgtccggcgg tagttga 747

<210> 130
 <211> 248
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (3)...(176)
 <223> short chain dehydrogenase

<220>

<221> SITE

<222> (142)...(145)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (146)...(174)

<223> Short-chain dehydrogenases/reductases family signature. Prosite id = PS00061

<400> 130

Met Pro Lys Val Met Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Ala
 1 5 10 15

Ala Val Ala Lys Leu Ala Ala Arg Arg Gly Tyr Ala Val Gly Ile Asn
 20 25 30

Tyr Arg Thr His Ser Asp Ala Ala Asp Ala Val Val Ala Glu Ile Gln
 35 40 45

Gln Ala Gly Gly Thr Ala Leu Ala Ile Gln Ala Asp Val Ser Gln Glu
 50 55 60

Asp Asp Val Leu His Met Phe Arg Thr Leu Asp Glu Arg Leu Gly Arg
 65 70 75 80

Ile Asp Ala Leu Val Asn Asn Ala Gly Ile Leu Glu Thr Gln Met Arg
 85 90 95

Leu Asp Gln Met Glu Ala Asp Arg Leu Leu Arg Val Leu Ser Thr Asn
 100 105 110

Val Ile Gly Ala Phe Leu Cys Ala Arg Glu Ala Val Arg Arg Met Ser
 115 120 125

Thr Arg His Gly Gly Val Gly Gly Ala Ile Val Asn Val Ser Ser Ala
 130 135 140

Ala Ala Arg Leu Gly Ser Pro Asn Glu Tyr Val Asp Tyr Ala Ala Ser
 145 150 155 160

Lys Gly Ala Leu Asp Thr Met Thr Ile Gly Leu Ser Lys Glu Val Ala
 165 170 175

Pro Glu Gly Ile Arg Val Asn Gly Val Arg Pro Gly Thr Ile Tyr Thr
 180 185 190

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Asp Met His Ala Ser Gly Gly Glu Pro Gly Arg Val Asp Arg Leu Lys
 195 200 205

Ser Val Ile Pro Leu Arg Arg Gly Gly Ser Val Glu Glu Val Ala Gly
 210 215 220

Ala Val Met Trp Leu Phe Ser Glu Glu Ala Gly Tyr Thr Ser Gly Ser
 225 230 235 240

Phe Ile Asp Val Ser Gly Gly Ser
 245

<210> 131
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 131
 gtggaaacct attttcccct gcaccgcggg atcaacatga gccactggct ttcgcaagtg 60
 aatgaaaaca ttcccgaccg ttccacctat gtgacggagc gggacctgca atttttgcgg 120
 gcagcgggct tcgaccatgt gcgtctgccg atcgatgaga tcgaactctg ggatgaggag 180
 ggccatcaga tcgaggaggc ctggcaatac atgcacaact ttatgcgctg gagccgaaag 240
 aatgacctcc gggttattct cgacctgcac acggtattgt cccaccactt caacgcgatc 300
 aacatgggag aggtcaacac cctctttaat gatcccaagg aacaggaaaa attcctcaat 360
 ctctgggagc aaatcatgga tgccgtaggg caccacccca acgagtttct cgcttatgaa 420
 atgctcaatg aggcggtcgc ggaagatgat gaagactgga acctgctcct caaccgtgcg 480
 attgaacgca tccgggaacg tgagccgcat cgcgttctga ttgccggggc caactggtgg 540
 cagcatgccg cccgcgttcc caacctgagg cttccccctg gtgatcccaa catcatcatc 600
 agttttcact ttactcacc ctttctcttc acgcactatc gcagcagctg gactgccatg 660
 cgggcatacc agggtttcgt ccaatacccc ggcatocca ttcccgccat ccatctcgaa 720
 ggaatgaact atccggagtc ctttgtccaa atgtgggaag agcacaatca gtattacgac 780
 atccattcaa tgtatgccga aatgggtcccg gcggtgcgtt ttgccgaaaa gctgggcctt 840
 cggctctatt gcggcgaatt tggagccatg aagaccgttg atcgtgcccc aatgctgcag 900
 tggatatcggg atgtggtcag agtctttgaa atgttggaca ttccctacac tgcctgggat 960
 tatcagggaa cttttggaat ccgcgatgag ctgaccggtg agcctgatca tgaactgatc 1020
 gacattctcc tcggccgcta a 1041

<210> 132
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (14)...(325)
 <223> Cellulase (glycosyl hydrolase family 5)

<220>
 <221> SITE
 <222> (12)...(15)
 <223> N-glycosylation site. Prosite id = PS00001

<400> 132
 Met Glu Thr Tyr Phe Pro Leu His Arg Gly Ile Asn Met Ser His Trp
 1 5 10 15
 Leu Ser Gln Val Asn Glu Asn Ile Pro Asp Arg Ser Thr Tyr Val Thr
 20 25 30
 Glu Arg Asp Leu Gln Phe Leu Arg Ala Ala Gly Phe Asp His Val Arg
 35 40 45
 Leu Pro Ile Asp Glu Ile Glu Leu Trp Asp Glu Glu Gly His Gln Ile
 50 55 60
 Glu Glu Ala Trp Gln Tyr Met His Asn Phe Met Arg Trp Ser Arg Lys
 65 70 75 80
 Asn Asp Leu Arg Val Ile Leu Asp Leu His Thr Val Leu Ser His His
 85 90 95
 Phe Asn Ala Ile Asn Met Gly Glu Val Asn Thr Leu Phe Asn Asp Pro
 100 105 110
 Lys Glu Gln Glu Lys Phe Leu Asn Leu Trp Glu Gln Ile Met Asp Ala
 115 120 125
 Val Gly His His Pro Asn Glu Phe Leu Ala Tyr Glu Met Leu Asn Glu
 130 135 140
 Ala Val Ala Glu Asp Asp Glu Asp Trp Asn Leu Leu Leu Asn Arg Ala
 145 150 155 160
 Ile Glu Arg Ile Arg Glu Arg Glu Pro His Arg Val Leu Ile Ala Gly
 165 170 175

Ala Asn Trp Trp Gln His Ala Ala Arg Val Pro Asn Leu Arg Leu Pro
180 185 190

Pro Gly Asp Pro Asn Ile Ile Ile Ser Phe His Phe Tyr Ser Pro Phe
195 200 205

Leu Phe Thr His Tyr Arg Ser Ser Trp Thr Ala Met Arg Ala Tyr Gln
210 215 220

Gly Phe Val Gln Tyr Pro Gly Ile Thr Ile Pro Ala Ile His Leu Glu
225 230 235 240

Gly Met Asn Tyr Pro Glu Ser Phe Val Gln Met Trp Glu Glu His Asn
245 250 255

Gln Tyr Tyr Asp Ile His Ser Met Tyr Ala Glu Met Val Pro Ala Val
260 265 270

Arg Phe Ala Glu Lys Leu Gly Leu Arg Leu Tyr Cys Gly Glu Phe Gly
275 280 285

Ala Met Lys Thr Val Asp Arg Ala Gln Met Leu Gln Trp Tyr Arg Asp
290 295 300

Val Val Arg Val Phe Glu Met Leu Asp Ile Pro Tyr Thr Ala Trp Asp
305 310 315 320

Tyr Gln Gly Thr Phe Gly Ile Arg Asp Glu Leu Thr Gly Glu Pro Asp
325 330 335

His Glu Leu Ile Asp Ile Leu Leu Gly Arg
340 345

<210> 133

<211> 1377

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 133

atgacacaac tggctttttcc atctaacttc atctgggggaa cagctacttc cgcttaccaa 60

atcgaaggcg cctggaacgc agacggcaag ggcgaatcta tttgggatcg cttttcccat 120

acgcagggga agatcattga cggcagcaac ggcgatgtgg cctgcgatca ctaccaccgc 180

tggcgcgagg acgtggccct catgagagac ttgggtatgc aggcatatcg cttctccatc 240
tcctggccac gcatcctgcc caccggtcac ggacagatca atcaggctgg gctggacttt 300
tacaatcgcc tgggtggacgg gttgctggaa gctggcatca agccctttgc caccctctac 360
cactgggacc tgccgctggc gctacaggct gacggcggct ggccggagcg ctccacggcc 420
aaggcctttg tcgaatacgc cgacgtggtc agccgcgcgc tgggcgatcg ggtgaagagc 480
tggatcaccc ataacgaacc gtggtgcatc agcatgctga gccatcaa at tggggagcat 540
gcgcccggct ggccgggactg gcaggctgcg ttggcggccg cgcaccacgt cctcctttcg 600
catggttggg ccgtgccgga actgcgtcgc aacagccgcg atgcagaaat cggcatcacg 660
ttgaacttta ccccggcgga gccagcttcg aacagcgcag ccgatttcaa ggcctatcgc 720
cagttcgatg gctacttcaa ccgctggttc ctggacccgc tctatggccg ccactatccg 780
gcagatatgg tgcacgatta catcgcgcaa ggctacctgc catcacaggg tttgactttc 840
gtggaagctg gtgacctgga cgcgatcgcg acgcgcaccg atttcctggg tgtgaactat 900
tacacgcgcg aagtgggtccg tagccaggaa atcccagaga gtgagaacgc gccgcgcaca 960
gtcttgccgcg cgccacagga agagtggaca gagatgggct ggggaagtgt tcttgagggc 1020
ctctacaggt tgctcaatcg gttgcacttt gaataccagc cgcgcaagct ctacgtgacc 1080
gagagcgggt gcagctactc cgatggaccc ggccccaacg gtcggatacc ggaccaacgc 1140
cgtatcaact acctgcgcga tcacttcgca gcggcgcac atc aggcgataca atgcggcgtc 1200
ccgctggccg gctacttcgt ctggtcgttc atggacaact tcgagtgggc caaagggtac 1260
acccaacggt ttggtatcgt atgggtggat tatcaatcgc aacgacggat accgaaagac 1320
agcgcctact ggtatcgcga tgtcgtcgc gccaacgcgg tgcaagttcc tgattag 1377

<210> 134

<211> 458

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (2)...(454)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (10)...(24)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<400> 134

Met Thr Gln Leu Ala Phe Pro Ser Asn Phe Ile Trp Gly Thr Ala Thr

1	5	10	15
Ser	Ala	Tyr	Gln
20			
Ile	Glu	Gly	Ala
25			
Trp	Asn	Ala	Asp
30			
Gly	Lys	Gly	Glu
Ser	Ile	Trp	Asp
35			
Arg	Phe	Ser	His
40			
Thr	Gln	Gly	Lys
45			
Ile	Ile	Asp	Gly
Ser	Asn	Gly	Asp
50			
Val	Ala	Cys	Asp
55			
His	Tyr	His	Arg
60			
Trp	Arg	Glu	Asp
Val	Ala	Leu	Met
65			
Arg	Asp	Leu	Gly
70			
Met	Gln	Ala	Tyr
75			
Arg	Phe	Ser	Ile
80			
Ser	Trp	Pro	Arg
85			
Ile	Leu	Pro	Thr
90			
Gly	His	Gly	Gln
Ile	Asn	Gln	Ala
95			
Gly	Leu	Asp	Phe
100			
Tyr	Asn	Arg	Leu
105			
Val	Asp	Gly	Leu
110			
Leu	Glu	Ala	Gly
Ile	Lys	Pro	Phe
115			
Ala	Thr	Leu	Tyr
120			
His	Trp	Asp	Leu
125			
Pro	Leu	Ala	Leu
Gln	Ala	Asp	Gly
130			
Gly	Trp	Pro	Glu
135			
Arg	Ser	Thr	Ala
140			
Lys	Ala	Phe	Val
Glu	Tyr	Ala	Asp
145			
Val	Val	Ser	Arg
150			
Ala	Leu	Gly	Asp
155			
Arg	Val	Lys	Ser
160			
Trp	Ile	Thr	His
165			
Asn	Glu	Pro	Trp
170			
Cys	Ile	Ser	Met
175			
Leu	Ser	His	Gln
Ile	Gly	Glu	His
180			
Ala	Pro	Gly	Trp
185			
Arg	Asp	Trp	Gln
190			
Ala	Ala	Leu	Ala
Ala	Ala	His	His
195			
Val	Leu	Leu	Ser
200			
His	Gly	Trp	Ala
205			
Val	Pro	Glu	Leu
Arg	Arg	Asn	Ser
210			
Arg	Asp	Ala	Glu
215			
Ile	Gly	Ile	Thr
220			
Leu	Asn	Phe	Thr
Pro	Ala	Glu	Pro
225			
Ala	Ser	Asn	Ser
230			
Ala	Ala	Asp	Phe
235			
Lys	Ala	Tyr	Arg
240			
Gln	Phe	Asp	Gly
245			
Tyr	Phe	Asn	Arg
250			
Trp	Phe	Leu	Asp
255			
Pro	Leu	Tyr	Gly

Arg His Tyr Pro Ala Asp Met Val His Asp Tyr Ile Ala Gln Gly Tyr
260 265 270

Leu Pro Ser Gln Gly Leu Thr Phe Val Glu Ala Gly Asp Leu Asp Ala
275 280 285

Ile Ala Thr Arg Thr Asp Phe Leu Gly Val Asn Tyr Tyr Thr Arg Glu
290 295 300

Val Val Arg Ser Gln Glu Ile Pro Glu Ser Glu Asn Ala Pro Arg Thr
305 310 315 320

Val Leu Arg Ala Pro Gln Glu Glu Trp Thr Glu Met Gly Trp Glu Val
325 330 335

Tyr Pro Glu Gly Leu Tyr Arg Leu Leu Asn Arg Leu His Phe Glu Tyr
340 345 350

Gln Pro Arg Lys Leu Tyr Val Thr Glu Ser Gly Cys Ser Tyr Ser Asp
355 360 365

Gly Pro Gly Pro Asn Gly Arg Ile Pro Asp Gln Arg Arg Ile Asn Tyr
370 375 380

Leu Arg Asp His Phe Ala Ala Ala His Gln Ala Ile Gln Cys Gly Val
385 390 395 400

Pro Leu Ala Gly Tyr Phe Val Trp Ser Phe Met Asp Asn Phe Glu Trp
405 410 415

Ala Lys Gly Tyr Thr Gln Arg Phe Gly Ile Val Trp Val Asp Tyr Gln
420 425 430

Ser Gln Arg Arg Ile Pro Lys Asp Ser Ala Tyr Trp Tyr Arg Asp Val
435 440 445

Val Ala Ala Asn Ala Val Gln Val Pro Asp
450 455

<210> 135

<211> 987

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 135
atggttgagc ctgccgatca gagtcatttt tcagatgctt ttcaggtaaa tcgcactctt 60
ggaaaaggca tcaatcttgg taacacactg gaggctccaa atgaaggcga gtggggattg 120
acaattcgcg aggagtatth ttgatgaagt aaacaagccg gattttgaatc cgtgcgtatt 180
ccgatacgat ggaatgctca tgctctggaa ggttttccat atacgataga tgaatctttt 240
tttgaccggg ttgatgaagt tattggctgg gcttttgatc gtgatcttgc agtcatgatt 300
aacattcatc actacaacga attgatggag cagccacagg atcaccggga tcgctttttg 360
aaactttggg agcaaattgc tgcgcactat aaagagtacc cggaagaact ggtattcgag 420
attttaaacg aaccccacga taatctgacc ccggctatct ggaatagctt tttggctgat 480
gctctcggtt ttatacgcca aaccaatcca ggaagggtta ttgcagtcgg aacagctgaa 540
tggggcggtt tcgggagttt gcaggatctt gagctgcctg ataatgaccg ccagataatc 600
accaccgttc attactataa cccatttcat ttcacgcac agggggcaga ttgggttgga 660
gatgaagcgg atcagtggct tggaaccgaa tgggatggag cagatcatga aaaagctgaa 720
gttgacagcg attttgactc tgtggaacag tgggcccga atcatgaccg gccaatacac 780
gtgggagagt tcggagcttt cagcgccgca gatgatttgt cacgtgaaca gtggacggca 840
tacgtacgtg agtcttcgga gaaccggcag tttagctggg cgtattggga gtttgggtca 900
gggttcggtg cctatgatcc cggttccgga gaatggcgtg aatatttact ccgggcgtta 960
atccccgaca gtccggtgat tgattaa 987

<210> 136
<211> 328
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (27)...(306)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (17)...(20)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (139)...(148)
<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<400> 136.
Met Val Glu Pro Ala Asp Gln Ser His Phe Ser Asp Ala Phe Gln Val

1	5	10	15
Asn Arg Thr Leu Gly Lys Gly Ile Asn Leu Gly Asn Thr Leu Glu Ala	20	25	30
Pro Asn Glu Gly Glu Trp Gly Leu Thr Ile Arg Glu Glu Tyr Phe Asp	35	40	45
Glu Val Lys Gln Ala Gly Phe Glu Ser Val Arg Ile Pro Ile Arg Trp	50	55	60
Asn Ala His Ala Leu Glu Gly Phe Pro Tyr Thr Ile Asp Glu Ser Phe	65	70	75
Phe Asp Arg Val Asp Glu Val Ile Gly Trp Ala Phe Asp Arg Asp Leu	85	90	95
Ala Val Met Ile Asn Ile His His Tyr Asn Glu Leu Met Glu Gln Pro	100	105	110
Gln Asp His Arg Asp Arg Phe Leu Lys Leu Trp Glu Gln Ile Ala Ala	115	120	125
His Tyr Lys Glu Tyr Pro Glu Glu Leu Val Phe Glu Ile Leu Asn Glu	130	135	140
Pro His Asp Asn Leu Thr Pro Ala Ile Trp Asn Ser Phe Leu Ala Asp	145	150	155
Ala Leu Gly Ile Ile Arg Gln Thr Asn Pro Gly Arg Val Ile Ala Val	165	170	175
Gly Thr Ala Glu Trp Gly Gly Phe Gly Ser Leu Gln Asp Leu Glu Leu	180	185	190
Pro Asp Asn Asp Arg Gln Ile Ile Thr Thr Val His Tyr Tyr Asn Pro	195	200	205
Phe His Phe Thr His Gln Gly Ala Asp Trp Val Gly Asp Glu Ala Asp	210	215	220
Gln Trp Leu Gly Thr Glu Trp Asp Gly Ala Asp His Glu Lys Ala Glu	225	230	235
Val Asp Ser Asp Phe Asp Ser Val Glu Gln Trp Ala Arg Asn His Asp	245	250	255

Arg Pro Ile His Val Gly Glu Phe Gly Ala Phe Ser Ala Ala Asp Asp
260 265 270

Leu Ser Arg Glu Gln Trp Thr Ala Tyr Val Arg Glu Ser Ser Glu Asn
275 280 285

Arg Gln Phe Ser Trp Ala Tyr Trp Glu Phe Gly Ser Gly Phe Gly Ala
290 295 300

Tyr Asp Pro Gly Ser Gly Glu Trp Arg Glu Tyr Leu Leu Arg Ala Leu
305 310 315 320

Ile Pro Asp Ser Pro Val Ile Asp
325

<210> 137
<211> 702
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 137
atgagccacc gatcgagga attcaacggc cagccactga tgggtgtccga agacggccac 60
ttcgtgctcg gattcgggag cgacgacgag gccacccacc gactgcgcgt tcagctaccg 120
gatgagcgag tctgggagaa gaatctgcgt ccggaatcgc gcgagttcga tattcagcgg 180
atcgacggct tgccgcaaga ccagggtcacc ccacccact ccgtgctggc gagaatccga 240
gaggacgctt cgctgtcgcg ccgtgcccgc gaacgacgcg atccgcggac cgactggacc 300
gatggctgga tctggccggc cgagggccgc atttccggcg tgtacggcag ccagcgcac 360
ctcaacgggtg agcctcgcaa cccgcactgg gggctggata tcgccgcgcc aaccggcagc 420
ccggtcgtgg cgcctgccgg cggcatcgtc agcctgactc atccggacat gtatTTTTTcc 480
ggcggcaccc tgttaatcga ccacgggtcac ggcctgggtg ctgcgttcct ccacctgagt 540
gaaatcctgg tcgaggaagg gcagcgggtc gagcaggggg atctgatcgc acgcattggc 600
gccaccggtc gtgccaccgg gccgcacctg gactggcgga tcaatctcgg cgatgtacgc 660
gtggaccac agctgctgct gccgccgatg gacgcgcagt ga 702

<210> 138
<211> 233
<212> PRT
<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (127)...(223)

<223> Peptidase family M23

<400> 138

Met	Ser	His	Arg	Ser	Gln	Glu	Phe	Asn	Gly	Gln	Pro	Leu	Met	Val	Ser
1				5					10					15	

Glu	Asp	Gly	His	Phe	Val	Leu	Gly	Phe	Gly	Arg	Asp	Asp	Glu	Ala	Thr
			20					25					30		

His	Arg	Leu	Arg	Val	Gln	Leu	Pro	Asp	Glu	Arg	Val	Trp	Glu	Lys	Asn
		35					40					45			

Leu	Arg	Pro	Glu	Ser	Arg	Glu	Phe	Asp	Ile	Gln	Arg	Ile	Asp	Gly	Leu
	50					55					60				

Pro	Gln	Asp	Gln	Val	Thr	Pro	Pro	His	Ser	Val	Leu	Ala	Arg	Ile	Arg
65					70					75					80

Glu	Asp	Ala	Ser	Leu	Ser	Arg	Arg	Ala	Arg	Glu	Arg	Arg	Asp	Pro	Arg
				85					90					95	

Thr	Asp	Trp	Thr	Asp	Gly	Trp	Ile	Trp	Pro	Ala	Glu	Gly	Arg	Ile	Ser
			100					105						110	

Gly	Val	Tyr	Gly	Ser	Gln	Arg	Ile	Leu	Asn	Gly	Glu	Pro	Arg	Asn	Pro
		115					120					125			

His	Trp	Gly	Leu	Asp	Ile	Ala	Ala	Pro	Thr	Gly	Ser	Pro	Val	Val	Ala
	130					135					140				

Pro	Ala	Gly	Gly	Ile	Val	Ser	Leu	Thr	His	Pro	Asp	Met	Tyr	Phe	Ser
145					150					155					160

Gly	Gly	Thr	Leu	Leu	Ile	Asp	His	Gly	His	Gly	Leu	Val	Ser	Ala	Phe
				165					170						175

Leu	His	Leu	Ser	Glu	Ile	Leu	Val	Glu	Glu	Gly	Gln	Arg	Val	Glu	Gln
			180					185					190		

Gly	Asp	Leu	Ile	Ala	Arg	Ile	Gly	Ala	Thr	Gly	Arg	Ala	Thr	Gly	Pro
		195					200					205			

His	Leu	Asp	Trp	Arg	Ile	Asn	Leu	Gly	Asp	Val	Arg	Val	Asp	Pro	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210

215

220

Leu Leu Leu Pro Pro Met Asp Ala Gln
225 230

<210> 139
<211> 351
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 139
atggaaaaaa ttctcgttat cggatgcgcg ggccagatag gctcagagct tacgctcgaa 60
cttcgtaaga ttatggtga tgacaatgtg gtggctactg acattaagcc ggccagcaag 120
gaaattaccg agggcggccc ctttgaaatt cttgatgtgc tcgacacca ccggcttttt 180
ggcactgtaa gccgcaacaa gatcaccag atttatcacc ttgcagccat cctttcgggc 240
aatgccgaga aaaaaccact tgcaagctgg cacattaaca tggagagttt gctcaacgtg 300
cttgaactgg cccgtgaact gaagcttcat aaaattttct ggccaagctc a 351

<210> 140
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 140
Met Glu Lys Ile Leu Val Ile Gly Cys Ala Gly Gln Ile Gly Ser Glu
1 5 10 15

Leu Thr Leu Glu Leu Arg Lys Ile Tyr Gly Asp Asp Asn Val Val Ala
20 25 30

Thr Asp Ile Lys Pro Ala Ser Lys Glu Ile Thr Glu Gly Gly Pro Phe
35 40 45

Glu Ile Leu Asp Val Leu Asp Thr His Arg Leu Phe Gly Thr Val Ser
50 55 60

Arg Asn Lys Ile Thr Gln Ile Tyr His Leu Ala Ala Ile Leu Ser Gly
65 70 75 80

Asn Ala Glu Lys Lys Pro Leu Ala Ser Trp His Ile Asn Met Glu Ser
85 90 95

Leu Leu Asn Val Leu Glu Leu Ala Arg Glu Leu Lys Leu His Lys Ile
100 105 110

Phe Trp Pro Ser Ser
115

<210> 141
<211> 1350
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 141
atgctgtcct atacgagtcc gttcccaaag aactttgtct ggggtgtggc gacggcggcg 60
ccgcagatcg agggcgctgc gcgagaagac ggaaaggggcg aatcgatatg ggatcgcttt 120
tgccgcgtgc ccggaaaggt ccacaatggc gatactctcg atgttgcggtg cgaccactac 180
caccggttcc gggaggattt cgcgctcatg cgagacttgg gcgtgcgcca ctaccggctt 240
tcgcttgccct ggccccgcat attcccggac ggcgacggcg cattgaacca gcgcggagtg 300
gatttctacc accggctctt tgaggccatg atcgagcacg ggattacgcc ttgggtgacg 360
ctctttcact gggatttgcc gcaggcgctc gaggaccgcg gcggctgggtg tgagcgtctc 420
accgtcgatg cattcggggcg ctacgctgac accgtgggtga aggcgttttg cgatcgcggtg 480
aagaattgga tcaccctgaa cgaaatccgc tgcttcacgt tgctcgctta cgatctctgc 540
atcaaggccc cgggccgcaa ggtctcgcgg gcgcagctca accagacctt tcatcacgcg 600
ctgatctgcc atgggcatgg cgtccggggcg gtccgcgaac acggcggggcg aggcgctcgc 660
gtcgggctta ccgacaacag cgacgtatgc gtgcccgtca ccgagaccgc gcccgacatc 720
attgcggcca gatcctggta tgcgtcgcga aatattcatc tgctcgatcc gatctatcgc 780
ggcgagtatg cgccggaata cctcgaacgc tgcgggtgcgg acgcgccccca ggtggccgag 840
gacgatttcg cgctgatttc aatgcctgacg gattttctcg ggctgaatgt atatacggcg 900
acctttgtgc gtgccgacgc ggagggcagg ccggaggaga ttaaactgcc gcggaattac 960
ccgcgcgcgg atagcgcgtg gttgaatatt gtgccccagt cgatgtactg ggccacacgg 1020
ctggcgcggg aaacctacgg cgtgagatca atctacatca ccgaaaacgg ctgcggctac 1080
gacgacgagc ccgtcgacgg cggcgagggtg ctcgacctgc atcgacgcga ttttctgcgc 1140
aaccaccttc ggggaattgca tcgcgccata ggcgacggcg tgcccgttga cgggtatattt 1200
ctctggtcct tcatggacaa ctacgagtgg gaggacgggt atgcgcggcg gttcggcatc 1260
gttcacgtcg acttcgaaag ccagaaacgg actccaaaac tctcggcgcg ctattacgcg 1320

caggtaatga aagaaaaccg gatcctgtga

1350

<210> 142

<211> 449

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (4)...(448)

<223> Glycosyl hydrolase family 1

<400> 142

Met	Leu	Ser	Tyr	Thr	Ser	Pro	Phe	Pro	Lys	Asn	Phe	Val	Trp	Gly	Val
1				5					10					15	

Ala	Thr	Ala	Ala	Pro	Gln	Ile	Glu	Gly	Ala	Ala	Arg	Glu	Asp	Gly	Lys
			20					25					30		

Gly	Glu	Ser	Ile	Trp	Asp	Arg	Phe	Cys	Arg	Val	Pro	Gly	Lys	Val	His
		35					40					45			

Asn	Gly	Asp	Thr	Leu	Asp	Val	Ala	Cys	Asp	His	Tyr	His	Arg	Phe	Arg
	50					55					60				

Glu	Asp	Phe	Ala	Leu	Met	Arg	Asp	Leu	Gly	Val	Arg	His	Tyr	Arg	Leu
65					70					75					80

Ser	Leu	Ala	Trp	Pro	Arg	Ile	Phe	Pro	Asp	Gly	Asp	Gly	Ala	Leu	Asn
				85					90					95	

Gln	Arg	Gly	Val	Asp	Phe	Tyr	His	Arg	Leu	Phe	Glu	Ala	Met	Ile	Glu
			100					105					110		

His	Gly	Ile	Thr	Pro	Trp	Val	Thr	Leu	Phe	His	Trp	Asp	Leu	Pro	Gln
		115					120					125			

Ala	Leu	Glu	Asp	Arg	Gly	Gly	Trp	Cys	Glu	Arg	Leu	Thr	Val	Asp	Ala
	130					135					140				

Phe	Gly	Arg	Tyr	Ala	Asp	Thr	Val	Val	Lys	Ala	Phe	Gly	Asp	Arg	Val
145					150					155					160

Lys	Asn	Trp	Ile	Thr	Leu	Asn	Glu	Ile	Arg	Cys	Phe	Thr	Leu	Leu	Ala
				165					170					175	

Tyr	Asp	Leu	Cys	Ile	Lys	Ala	Pro	Gly	Arg	Lys	Val	Ser	Arg	Ala	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180	185	190
Leu Asn Gln Thr Tyr His His Ala Leu Ile Cys His Gly His Gly Val 195 200 205		
Arg Ala Val Arg Glu His Gly Gly Arg Gly Ala Arg Val Gly Leu Thr 210 215 220		
Asp Asn Ser Asp Val Cys Val Pro Val Thr Glu Thr Ala Pro Asp Ile 225 230 235 240		
Ile Ala Ala Arg Ser Trp Tyr Ala Ser Arg Asn Ile His Leu Leu Asp 245 250 255		
Pro Ile Tyr Arg Gly Glu Tyr Ala Pro Glu Tyr Leu Glu Arg Cys Gly 260 265 270		
Ala Asp Ala Pro Gln Val Ala Glu Asp Asp Phe Ala Leu Ile Ser Met 275 280 285		
Pro Thr Asp Phe Leu Gly Leu Asn Val Tyr Thr Ala Thr Phe Val Arg 290 295 300		
Ala Asp Ala Glu Gly Arg Pro Glu Glu Ile Lys Leu Pro Arg Asn Tyr 305 310 315 320		
Pro Arg Ala Asp Ser Ala Trp Leu Asn Ile Val Pro Gln Ser Met Tyr 325 330 335		
Trp Ala Thr Arg Leu Ala Arg Glu Thr Tyr Gly Val Arg Ser Ile Tyr 340 345 350		
Ile Thr Glu Asn Gly Cys Gly Tyr Asp Asp Glu Pro Val Asp Gly Gly 355 360 365		
Glu Val Leu Asp Leu His Arg Arg Asp Phe Leu Arg Asn His Leu Arg 370 375 380		
Glu Leu His Arg Ala Ile Gly Asp Gly Val Pro Val Asp Gly Tyr Phe 385 390 395 400		
Leu Trp Ser Phe Met Asp Asn Tyr Glu Trp Glu Asp Gly Tyr Ala Arg 405 410 415		
Arg Phe Gly Ile Val His Val Asp Phe Glu Ser Gln Lys Arg Thr Pro 420 425 430		

Lys Leu Ser Ala Arg Tyr Tyr Ala Gln Val Met Lys Glu Asn Arg Ile
 435 440 445

Leu

<210> 143
 <211> 1188
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 143
 atgaccatca ccttccccga cgggttctgg tgggggacgg cgacggccgc ccaccaggtg 60
 gagggcggca actggaacac cgactggtgg gcctacgagc acgccccggg caccgctgc 120
 gcggagccgt ccggcgatgc gtgcgaccac tggcaccgct acccggagga catcgccctc 180
 ctcgccgcgc tcgggttcag tgcctaccgc ttctcggtgg aatgggctcg catcgagccc 240
 gaggaagggc atttctcccg cgccaccctc gaccactacc ggcgcatgat cgcctgctgc 300
 cgcgaccacg ggctggcccc ggtggtgacc ttccaccact tcaccacccc ccgctggggc 360
 gcggccgggg gctgctggtc cgacccggtc accgccgagc gcttcgcccg ttactgcgag 420
 cgcaccgtgg ccgcccctcg cgacgagatc gcgatggcct gcacgatcaa cgagccgaac 480
 atcgtggcca ccctcgggta cttcctcggc gagttcccgc cggccgtcgc cgaccccgc 540
 cgctaccggc aggcgaacga cacgctgatc cgcgcccata gcctcgccta cgaggcgctg 600
 aaggccgggc ccggcgagtt ccccgctcggc ctcaccctgt cgatggccga gttcgctgcc 660
 gagcccggcg gcgaggccca cctcgcccag gtccggcaca cgatggagga catcttcctg 720
 gaggccgccc ggggcgacga cttcatcggg gtgcagacct acagccgcat gcgcttcggt 780
 cccgactcgc cgatcccgtc cgggcccggc gagggcgctc aggtcgtcca gatgggggtac 840
 gagtactggc cgtgggcgct cgaggcgacg atccggcgcg ccgcccaggt caccggcacg 900
 gcggtccacg tcaccgagaa cggcatcggg accgcccacg acacgcagcg ggtcgccctac 960
 gtcaccgagg ccctccgggg gctgcggcgc tgccctcgacg acggcatcga cgtccgcagc 1020
 tacttctact ggacgctgct cgacaacttc gagtggacgc gcggctacgt gccgacgttc 1080
 gggctcgtcg ccgtcgaccg caccacccag cgccggtcgg tgaagccgag cgcggtgtgg 1140
 ctcggcgagg tcgcccgcac gaaccgcctc gagctcccgg accgctga 1188

<210> 144
 <211> 395

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (1)...(390)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (9)...(23)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (188)...(191)

<223> N-glycosylation site. Prosite id = PS00001

<400> 144

Met	Thr	Ile	Thr	Phe	Pro	Asp	Gly	Phe	Trp	Trp	Gly	Thr	Ala	Thr	Ala
1				5					10					15	

Ala	His	Gln	Val	Glu	Gly	Gly	Asn	Trp	Asn	Thr	Asp	Trp	Trp	Ala	Tyr
			20					25					30		

Glu	His	Ala	Pro	Gly	Thr	Arg	Cys	Ala	Glu	Pro	Ser	Gly	Asp	Ala	Cys
		35					40					45			

Asp	His	Trp	His	Arg	Tyr	Pro	Glu	Asp	Ile	Ala	Leu	Leu	Ala	Ala	Leu
	50					55					60				

Gly	Phe	Ser	Ala	Tyr	Arg	Phe	Ser	Val	Glu	Trp	Ala	Arg	Ile	Glu	Pro
65					70					75				80	

Glu	Glu	Gly	His	Phe	Ser	Arg	Ala	Thr	Leu	Asp	His	Tyr	Arg	Arg	Met
			85						90					95	

Ile	Ala	Cys	Cys	Arg	Asp	His	Gly	Leu	Ala	Pro	Val	Val	Thr	Phe	His
			100					105						110	

His	Phe	Thr	Thr	Pro	Arg	Trp	Ala	Ala	Ala	Gly	Gly	Cys	Trp	Ser	Asp
		115					120					125			

Pro	Val	Thr	Ala	Glu	Arg	Phe	Ala	Arg	Tyr	Cys	Glu	Arg	Thr	Val	Ala
	130					135					140				

Ala	Leu	Gly	Asp	Glu	Ile	Ala	Met	Ala	Cys	Thr	Ile	Asn	Glu	Pro	Asn
145					150					155					160

Ile Val Ala Thr Leu Gly Tyr Phe Leu Gly Glu Phe Pro Pro Ala Val
 165 170 175

Ala Asp Pro Asp Arg Tyr Arg Gln Ala Asn Asp Thr Leu Ile Arg Ala
 180 185 190

His Arg Leu Ala Tyr Glu Ala Leu Lys Ala Gly Pro Gly Glu Phe Pro
 195 200 205

Val Gly Leu Thr Leu Ser Met Ala Glu Phe Val Ala Glu Pro Gly Gly
 210 215 220

Glu Ala His Leu Ala Gln Val Arg His Thr Met Glu Asp Ile Phe Leu
 225 230 235 240

Glu Ala Ala Arg Gly Asp Asp Phe Ile Gly Val Gln Thr Tyr Ser Arg
 245 250 255

Met Arg Phe Gly Pro Asp Ser Pro Ile Pro Leu Gly Pro Ala Glu Gly
 260 265 270

Val Glu Val Val Gln Met Gly Tyr Glu Tyr Trp Pro Trp Ala Leu Glu
 275 280 285

Ala Thr Ile Arg Arg Ala Ala Glu Val Thr Gly Thr Ala Val His Val
 290 295 300

Thr Glu Asn Gly Ile Gly Thr Ala Asp Asp Thr Gln Arg Val Ala Tyr
 305 310 315 320

Val Thr Glu Ala Leu Arg Gly Leu Arg Arg Cys Leu Asp Asp Gly Ile
 325 330 335

Asp Val Arg Ser Tyr Phe Tyr Trp Thr Leu Leu Asp Asn Phe Glu Trp
 340 345 350

Thr Arg Gly Tyr Val Pro Thr Phe Gly Leu Val Ala Val Asp Arg Thr
 355 360 365

Thr Gln Arg Arg Ser Val Lys Pro Ser Ala Val Trp Leu Gly Glu Val
 370 375 380

Ala Arg Thr Asn Arg Leu Glu Leu Pro Asp Arg
 385 390 395

<210> 145
<211> 1386
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 145
atgtcgtttc cgagaaattt cctgtgggga tcagccacct cctcctacca aatcgaaggc 60
gcctggcaag aagacggcaa aggcccaa atctgggacg tgttttcaca caccgccggg 120
aaagtcgcca atggcgacac cgggtgatat gccatcgacc actaccaccg ataccgagac 180
gacgttgccc tgatggctga gcttggactt caggcatacc gtttctcgtt ctccctgggccc 240
agaataatgc cggaaggagc aggccccatc gagcaacggg gtctggactt ctacgaccgc 300
ctcattgatg cactgctgga gaaaaacatc caacccatgg ccaccctcta ccactgggat 360
ttaccagccg cactgcaaga cagagggggg tggactaacc gcgacagcgc gtcctgggtt 420
gctgactact cagccgttgt tcacgacgct ttttctgacc ggggtgggaat gtgggcaacg 480
ttgaacgagc cgtgggtgtc tgcatttttg ggccacggaa ctggcatcca cgcacctggc 540
atcacaagcc cccacgcggc gtccgcgcgc gggcatcacc tgcttctggg gcatggcaag 600
gccatccaag cgatgcgcgc tcaatcgtct agcaccacaac tgggaattgt tttgaacctc 660
gccccgtgt atctcgaagg tgacaccctt gctgaccacc cggctcacac ctccgtggca 720
ctacacgatg ccattttgaa tgggttgtgg acagagccgc ttctgcgctc cagatacccc 780
gacctgcttc ttcaactagg cgacatggtg aaaaaaaca tccacgacgg tgacctcgcc 840
atcatggccg agccgattga ctggatgggc atcaactact accaggacat tagatttgtg 900
gccactgatg ttgccccac ggctaaccgc atggcccctc cgggtaacga cctgcggggc 960
accgtcgggg tggagcctgc gccagcaatc ggaaacatca ccagctttgg ctgggtccacc 1020
accccgacg gactgcgagt actgttgggtg ggcctggatg aggaatacga caacctcccg 1080
ccgatattca ttaccgaaaa cgggtgtgct tacgattacc ccgtcgagga cgggtgtcgtc 1140
aacgacaccc ttcgtgtcac atacatgcga gaacacctca ccgcgttgtc gcaggccatt 1200
gaggcgggtg tgaatgtccg gggctatatg cactggtctc tgttcgacaa ctctcgagtgg 1260
gccgaagggc atcgccaacg ctttggcatg gtgcacgtcg actttgagac cttggagcgg 1320
actcccaaag cctcagctca ctactattca cgtgtcatca caaataacgc cctctctgac 1380
gactga 1386

<210> 146
<211> 461
<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (1)...(458)

<223> Glycosyl hydrolase family 1

<220>

<221> SITE

<222> (7)...(21)

<223> Glycosyl hydrolases family 1 N-terminal signature. Prosite id = PS00653

<220>

<221> SITE

<222> (337)...(340)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (386)...(389)

<223> N-glycosylation site. Prosite id = PS00001

<400> 146

Met	Ser	Phe	Pro	Arg	Asn	Phe	Leu	Trp	Gly	Ser	Ala	Thr	Ser	Ser	Tyr
1				5					10					15	

Gln	Ile	Glu	Gly	Ala	Trp	Gln	Glu	Asp	Gly	Lys	Gly	Pro	Asn	Ile	Trp
		20						25					30		

Asp	Val	Phe	Ser	His	Thr	Pro	Gly	Lys	Val	Ala	Asn	Gly	Asp	Thr	Gly
		35					40					45			

Asp	Ile	Ala	Ile	Asp	His	Tyr	His	Arg	Tyr	Arg	Asp	Asp	Val	Ala	Leu
	50					55					60				

Met	Ala	Glu	Leu	Gly	Leu	Gln	Ala	Tyr	Arg	Phe	Ser	Phe	Ser	Trp	Ala
65					70					75					80

Arg	Ile	Met	Pro	Glu	Gly	Ala	Gly	Pro	Ile	Glu	Gln	Arg	Gly	Leu	Asp
				85					90					95	

Phe	Tyr	Asp	Arg	Leu	Ile	Asp	Ala	Leu	Leu	Glu	Lys	Asn	Ile	Gln	Pro
			100					105					110		

Met	Ala	Thr	Leu	Tyr	His	Trp	Asp	Leu	Pro	Ala	Ala	Leu	Gln	Asp	Arg
		115					120					125			

Gly	Gly	Trp	Thr	Asn	Arg	Asp	Ser	Ala	Ser	Trp	Phe	Ala	Asp	Tyr	Ser
	130					135					140				

Ala Val Val His Asp Ala Phe Ser Asp Arg Val Gly Met Trp Ala Thr
 145 150 155 160

Leu Asn Glu Pro Trp Val Ser Ala Phe Leu Gly His Gly Thr Gly Ile
 165 170 175

His Ala Pro Gly Ile Thr Ser Pro His Ala Ala Phe Ala Ala Gly His
 180 185 190

His Leu Leu Leu Gly His Gly Lys Ala Ile Gln Ala Met Arg Ala Gln
 195 200 205

Ser Ser Ser Thr Gln Leu Gly Ile Val Leu Asn Leu Ala Pro Val Tyr
 210 215 220

Leu Glu Gly Asp Thr Pro Ala Asp His Pro Ala His Thr Ser Val Ala
 225 230 235 240

Leu His Asp Ala Ile Leu Asn Gly Leu Trp Thr Glu Pro Leu Leu Arg
 245 250 255

Ser Arg Tyr Pro Asp Leu Leu Leu Gln Leu Gly Asp Met Val Thr Lys
 260 265 270

Asn Ile His Asp Gly Asp Leu Ala Ile Met Ala Glu Pro Ile Asp Trp
 275 280 285

Met Gly Ile Asn Tyr Tyr Gln Asp Ile Arg Phe Val Ala Thr Asp Val
 290 295 300

Ala Pro Thr Ala Asn Pro Met Ala Pro Pro Gly Asn Asp Leu Pro Gly
 305 310 315 320

Thr Val Gly Val Glu Pro Ala Pro Ala Ile Gly Asn Ile Thr Ser Phe
 325 330 335

Gly Trp Ser Thr Thr Pro Asp Gly Leu Arg Val Leu Leu Val Gly Leu
 340 345 350

Asp Glu Glu Tyr Asp Asn Leu Pro Pro Ile Phe Ile Thr Glu Asn Gly
 355 360 365

Cys Ala Tyr Asp Tyr Pro Val Glu Asp Gly Val Val Asn Asp Thr Leu
 370 375 380

Arg Val Thr Tyr Met Arg Glu His Leu Thr Ala Leu Ser Gln Ala Ile
 385 390 395 400

Glu Ala Gly Val Asn Val Arg Gly Tyr Met His Trp Ser Leu Phe Asp
 405 410 415

Asn Phe Glu Trp Ala Glu Gly Tyr Arg Gln Arg Phe Gly Met Val His
 420 425 430

Val Asp Phe Glu Thr Leu Glu Arg Thr Pro Lys Ala Ser Ala His Tyr
 435 440 445

Tyr Ser Arg Val Ile Thr Asn Asn Ala Leu Ser Asp Asp
 450 455 460

<210> 147
 <211> 1242
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 147
 atgctaaaag ttttacgtaa acctattatt tctggattag ctttagctct attattgccg 60
 gcaggggagc ctggtgccga aactaatatt tcaaagaagc caaatataag tggattaacc 120
 gcgccgcaat tagaccaaag atataaagat tctttcacca ttggtgctgc ggttgagccg 180
 tatcaattat tagatgcaaa agattcacaa atgctaaagc ggcattttta tagtatcgta 240
 gcagagaaatg tcatgaagcc tagtagttta cagccagtag aaggacaatt caactgggag 300
 ccggctgata aacttggttca gtttgccaag gaaaatggaa tggacatgcg aggtcatacg 360
 cttgtctggc atagccaggt accggattgg ttctttgaag atgcggcagg aaatccaatg 420
 gttgtttggg aaaatggcag gcaagtgggt gccgatccat caaagcttca ggaaaacaaa 480
 gagctcttac ttagccgatt acaaaatcat attcaggcag tcgtaacgcg ttataaagat 540
 gatataaaat cttgggatgt tgtcaatgaa gtaatcgatg aatggggcgg acattctgaa 600
 gggctgcgtc aatctccatg gttcctcatc accggaacgg actatattaa agttgctttt 660
 gaaactgcaa gagaatatgc agctccagac gctaagctgt atatcaatga ttacaataca 720
 gaagtagaac caaaaaggac gcacctttat aacttagtaa aaagtttaaa agaagaacag 780
 aacgttccga ttgatgggtg tgggcatcag tctcacattc aaattggctg gccttcagaa 840
 aaagaaattg aagatactat taatatgttt gcagatcttg gtttagataa ccaaaccacc 900
 gagcttgatg ttagtatgta tggctggccg gtaaggctcg atccaactta tgatgcgatc 960

ccagaactta aattcatgga tcaagcagct cgttatgatc gtttatTTaa gttatatgag 1020
aaattaggag ataaaatcag taatgtgaca ttctggggta ttgcggataa ccatacatgg 1080
ctgaatgacc gcgcagatgt ttactatgat gaaaatggaa atgttgtatt agatagagaa 1140
acaccaagag tagaaagagg agcaggaaaa gatgcgccat ttgtatttga tcctgaatac 1200
aatgtaaaac cagcttattg ggcaattatc gatcacaaat aa 1242

<210> 148
<211> 413
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(26)

<220>
<221> DOMAIN
<222> (43)...(413)
<223> Glycosyl hydrolase family 10

<220>
<221> SITE
<222> (29)...(32)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (35)...(38)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (298)...(308)
<223> Glycosyl hydrolases family 10 active site. Prosite id = PS00591

<220>
<221> SITE
<222> (353)...(356)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (362)...(365)
<223> N-glycosylation site. Prosite id = PS00001

<400> 148
Met Leu Lys Val Leu Arg Lys Pro Ile Ile Ser Gly Leu Ala Leu Ala
1 5 10 15

Leu Leu Leu Pro Ala Gly Ala Ala Gly Ala Glu Thr Asn Ile Ser Lys
20 25 30

Lys Pro Asn Ile Ser Gly Leu Thr Ala Pro Gln Leu Asp Gln Arg Tyr
 35 40 45
 Lys Asp Ser Phe Thr Ile Gly Ala Ala Val Glu Pro Tyr Gln Leu Leu
 50 55 60
 Asp Ala Lys Asp Ser Gln Met Leu Lys Arg His Phe Asn Ser Ile Val
 65 70 75 80
 Ala Glu Asn Val Met Lys Pro Ser Ser Leu Gln Pro Val Glu Gly Gln
 85 90 95
 Phe Asn Trp Glu Pro Ala Asp Lys Leu Val Gln Phe Ala Lys Glu Asn
 100 105 110
 Gly Met Asp Met Arg Gly His Thr Leu Val Trp His Ser Gln Val Pro
 115 120 125
 Asp Trp Phe Phe Glu Asp Ala Ala Gly Asn Pro Met Val Val Trp Glu
 130 135 140
 Asn Gly Arg Gln Val Val Ala Asp Pro Ser Lys Leu Gln Glu Asn Lys
 145 150 155 160
 Glu Leu Leu Leu Ser Arg Leu Gln Asn His Ile Gln Ala Val Val Thr
 165 170 175
 Arg Tyr Lys Asp Asp Ile Lys Ser Trp Asp Val Val Asn Glu Val Ile
 180 185 190
 Asp Glu Trp Gly Gly His Ser Glu Gly Leu Arg Gln Ser Pro Trp Phe
 195 200 205
 Leu Ile Thr Gly Thr Asp Tyr Ile Lys Val Ala Phe Glu Thr Ala Arg
 210 215 220
 Glu Tyr Ala Ala Pro Asp Ala Lys Leu Tyr Ile Asn Asp Tyr Asn Thr
 225 230 235 240
 Glu Val Glu Pro Lys Arg Thr His Leu Tyr Asn Leu Val Lys Ser Leu
 245 250 255
 Lys Glu Glu Gln Asn Val Pro Ile Asp Gly Val Gly His Gln Ser His
 260 265 270

Ile Gln Ile Gly Trp Pro Ser Glu Lys Glu Ile Glu Asp Thr Ile Asn
275 280 285

Met Phe Ala Asp Leu Gly Leu Asp Asn Gln Ile Thr Glu Leu Asp Val
290 295 300

Ser Met Tyr Gly Trp Pro Val Arg Ser Tyr Pro Thr Tyr Asp Ala Ile
305 310 315 320

Pro Glu Leu Lys Phe Met Asp Gln Ala Ala Arg Tyr Asp Arg Leu Phe
325 330 335

Lys Leu Tyr Glu Lys Leu Gly Asp Lys Ile Ser Asn Val Thr Phe Trp
340 345 350

Gly Ile Ala Asp Asn His Thr Trp Leu Asn Asp Arg Ala Asp Val Tyr
355 360 365

Tyr Asp Glu Asn Gly Asn Val Val Leu Asp Arg Glu Thr Pro Arg Val
370 375 380

Glu Arg Gly Ala Gly Lys Asp Ala Pro Phe Val Phe Asp Pro Glu Tyr
385 390 395 400

Asn Val Lys Pro Ala Tyr Trp Ala Ile Ile Asp His Lys
405 410

<210> 149
<211> 1068
<212> DNA
<213> Unknown

<220>
<223> Obtained from environmental sample

<400> 149
atgacccgaa tgcgcgggat aaacatgggc ggctggctca gccaaattga cgccatacag 60
gaaaaagacc ctgatacatt tcccgggaaca gacaaacata tggaaacttt tatccagcag 120
aaggattttg ccaatgtcag gagatggggt ttcgatcatg tgcgaattcc aattgacgcg 180
tatctgttct ttaccgaaaa aggagagccg attgaaaaca ggcttgccaa tcttgaccgc 240
gccgtagagt atgcgctgcc cgccggcctc aacatgatat tggacctcca cgagtgtccg 300
gggcacgatt tttcgggaagc agtaaaaagc cctgtccaaa aacttttctc gggagatgac 360
acctggataa ggaaaactga aaaaatatgg gcttgccttg ccgagcgta ttctcaaaag 420
ggccacgtcc tttttgagac gctcaatgag cctgtcgctc ccaccgcgga gatttggaac 480

aatgttaagg acaggctctg ccgcgaaata cggctccacg cccctgggtc gactataatc 540
accgggtcca acatgtggaa ctcagcggca accttcgaca gcctcacgcc ctttgacgac 600
gacaacatga tctacagcgt acatttttac gagccgctgc ttttcacgca ccagaacgca 660
ttgtggatcg acaatccgga aatcaggatc gcaaggccgt atccggggcg ttacgggtccc 720
ggctttgtcc ccaaagacgg ttgacgctg tcggacggcg tctggaacag ggatcgtctc 780
gccggcgcac tagcgcccgt gaacgcgttc aggaaaaagt acaatgcgaa gattatctgt 840
aacgagttcg gcgttttacgc gcccgtagac cttcaatcgc agctgcgctg gtatgaagat 900
ctgctctcaa tcctcaatga gacgggggatc ggtttcacgt actggaacta taaaaatctc 960
gacttcggga taatttccat aggggagaag ctgcacgaag cccttccgca gtacgacaat 1020
agcgatcgaa taaataaatc ggttcttgaa gtgttaaaaa agtattag 1068

<210> 150
<211> 355
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (24)...(325)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (145)...(154)
<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<220>
<221> SITE
<222> (310)...(313)
<223> N-glycosylation site. Prosite id = PS00001

<220>
<221> SITE
<222> (350)...(353)
<223> N-glycosylation site. Prosite id = PS00001

<400> 150
Met Thr Arg Met Arg Gly Ile Asn Met Gly Gly Trp Leu Ser Gln Ile
1 5 10 15

Asp Ala Ile Gln Glu Lys Asp Pro Asp Thr Phe Pro Gly Thr Asp Lys
20 25 30

His Met Glu Thr Phe Ile Gln Gln Lys Asp Phe Ala Asn Val Arg Arg
35 40 45

Trp Gly Phe Asp His Val Arg Ile Pro Ile Asp Ala Tyr Leu Phe Phe
 50 55 60

Thr Glu Lys Gly Glu Pro Ile Glu Asn Arg Leu Ala Asn Leu Asp Arg
 65 70 75 80

Ala Val Glu Tyr Ala Leu Pro Ala Gly Leu Asn Met Ile Leu Asp Leu
 85 90 95

His Glu Cys Pro Gly His Asp Phe Ser Glu Ala Val Lys Ser Pro Val
 100 105 110

Gln Lys Leu Phe Ser Gly Asp Asp Thr Trp Ile Arg Lys Thr Glu Lys
 115 120 125

Ile Trp Ala Cys Leu Ala Glu Arg Tyr Ser Gln Lys Gly His Val Leu
 130 135 140

Phe Glu Thr Leu Asn Glu Pro Val Ala Pro Thr Ala Glu Ile Trp Asn
 145 150 155 160

Asn Val Lys Asp Arg Leu Cys Arg Glu Ile Arg Leu His Ala Pro Trp
 165 170 175

Ser Thr Ile Ile Thr Gly Ser Asn Met Trp Asn Ser Ala Ala Thr Phe
 180 185 190

Asp Ser Leu Thr Pro Phe Asp Asp Asp Asn Met Ile Tyr Ser Val His
 195 200 205

Phe Tyr Glu Pro Leu Leu Phe Thr His Gln Asn Ala Leu Trp Ile Asp
 210 215 220

Asn Pro Glu Ile Arg Ile Ala Arg Pro Tyr Pro Gly Asp Tyr Gly Pro
 225 230 235 240

Gly Phe Val Pro Lys Asp Gly Leu Thr Leu Ser Asp Gly Val Trp Asn
 245 250 255

Arg Asp Arg Leu Ala Gly Ala Leu Ala Pro Val Asn Ala Phe Arg Lys
 260 265 270

Lys Tyr Asn Ala Lys Ile Ile Cys Asn Glu Phe Gly Val Tyr Ala Pro
 275 280 285

Val Asp Leu Gln Ser Gln Leu Arg Trp Tyr Glu Asp Leu Leu Ser Ile

290

295

300

Leu Asn Glu Thr Gly Ile Gly Phe Thr Tyr Trp Asn Tyr Lys Asn Leu
 305 310 315 320

Asp Phe Gly Ile Ile Ser Ile Gly Glu Lys Leu His Glu Ala Leu Pro
 325 330 335

Gln Tyr Asp Asn Ser Asp Arg Ile Asn Lys Ser Val Leu Glu Val Leu
 340 345 350

Lys Lys Tyr
 355

<210> 151
 <211> 1068
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 151
 atgaccagaa tgcgcggaat aaacatgggc ggctggctca gccagattga cgccatacag 60
 gaaaaagacc ccgataaatt tcccgggaata gacaaacaca tggaaacatt tatcggttcc 120
 aatgatttttt ccaatgtcag gaaatgggggt ttcgatcatg tgcgaatccc gattgacgcg 180
 taccttttttt ttaccgatca ggaagccccg attgaaaaca ggcttgtcca tattgacaac 240
 gccgtaaaat acgcgcggag caacggcctc aaggtgatat tggacctcca cgagtgtccg 300
 gggcatgatt ttctggacgc ggcaaaaaggc cctgtccaga aacttttctc cggagatgac 360
 acttatataa aaaagaccga aaaaatatgg gcatgtctgg ccgagcgtta ttcgaaaaac 420
 gacaacgtcc tctatgagac tctcaacgag cctgtcgccc ccacgcctga gatttggaac 480
 actgttaagg acaggctctg ccgggaaata cgctgcacg cccctggggc gacgataatc 540
 accggttcca atatgtggaa ttggccgagc acctttgaca gcctgacgcc ctttgacgac 600
 gacaacgtga tctacagcgt gcattttttac gagccgctgc tttttacgca ccagaacgcg 660
 ccctggatca acaattctga aatcaggatc acaaggccgt atccggggcg ttacggcccc 720
 ggctttgtcc gcaaatacgg ctttaactctg tcagccggcg tctggaacag ggacaggctg 780
 gcgaaggaat tcgcgcccgt gaacgcgttc aggaaaaaat acaaggcgca ggttatatgc 840
 gacgaattcg gcgtttacgc gcctgtcgag attgaatcgc agcttcgatg gtatgaggat 900
 ttgctctcga tcctcaggga gatgggtata gggttttcgt actggaacta taaaaacctg 960
 gactttggga taatttccat aggggagaag ctgcacgaaa gccttctgca gtacggcaac 1020

ggcgacagga taaatcatat gggtcttgac ttgctaaaga agtactaa

1068

<210> 152
<211> 355
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (19)...(325)
<223> Cellulase (glycosyl hydrolase family 5)

<220>
<221> SITE
<222> (145)...(154)
<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<220>
<221> SITE
<222> (227)...(230)
<223> N-glycosylation site. Prosite id = PS00001

<400> 152
Met Thr Arg Met Arg Gly Ile Asn Met Gly Gly Trp Leu Ser Gln Ile
1 5 10 15

Asp Ala Ile Gln Glu Lys Asp Pro Asp Lys Phe Pro Gly Ile Asp Lys
20 25 30

His Met Glu Thr Phe Ile Gly Ser Asn Asp Phe Ser Asn Val Arg Lys
35 40 45

Trp Gly Phe Asp His Val Arg Ile Pro Ile Asp Ala Tyr Leu Phe Phe
50 55 60

Thr Asp Gln Glu Ala Pro Ile Glu Asn Arg Leu Val His Ile Asp Asn
65 70 75 80

Ala Val Lys Tyr Ala Arg Ser Asn Gly Leu Lys Val Ile Leu Asp Leu
85 90 95

His Glu Cys Pro Gly His Asp Phe Ser Asp Ala Ala Lys Gly Pro Val
100 105 110

Gln Lys Leu Phe Ser Gly Asp Asp Thr Tyr Ile Lys Lys Thr Glu Lys
115 120 125

Ile Trp Ala Cys Leu Ala Glu Arg Tyr Ser Lys Asn Asp Asn Val Leu
130 135 140

Tyr Glu Thr Leu Asn Glu Pro Val Ala Pro Thr Pro Glu Ile Trp Asn
 145 150 155 160

Thr Val Lys Asp Arg Leu Cys Arg Glu Ile Arg Leu His Ala Pro Trp
 165 170 175

Ala Thr Ile Ile Thr Gly Ser Asn Met Trp Asn Trp Pro Ser Thr Phe
 180 185 190

Asp Ser Leu Thr Pro Phe Asp Asp Asp Asn Val Ile Tyr Ser Val His
 195 200 205

Phe Tyr Glu Pro Leu Leu Phe Thr His Gln Asn Ala Pro Trp Ile Asn
 210 215 220

Asn Ser Glu Ile Arg Ile Thr Arg Pro Tyr Pro Gly Asp Tyr Gly Pro
 225 230 235 240

Gly Phe Val Arg Lys Tyr Gly Leu Thr Leu Ser Ala Gly Val Trp Asn
 245 250 255

Arg Asp Arg Leu Ala Lys Glu Phe Ala Pro Val Asn Ala Phe Arg Lys
 260 265 270

Lys Tyr Lys Ala Gln Val Ile Cys Asp Glu Phe Gly Val Tyr Ala Pro
 275 280 285

Val Glu Ile Glu Ser Gln Leu Arg Trp Tyr Glu Asp Leu Leu Ser Ile
 290 295 300

Leu Arg Glu Met Gly Ile Gly Phe Ser Tyr Trp Asn Tyr Lys Asn Leu
 305 310 315 320

Asp Phe Gly Ile Ile Ser Ile Gly Glu Lys Leu His Glu Ser Leu Leu
 325 330 335

Gln Tyr Gly Asn Gly Asp Arg Ile Asn His Met Val Leu Asp Leu Leu
 340 345 350

Lys Lys Tyr
 355

<210> 153
 <211> 1068
 <212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 153

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atgcaaagaa tgcgaggctt aaatattggc ggctggctca gccagattga cgccatacag      60
gaaaaggacc ctgaggggctt tcccgggaata gacaaacaca tggaaacatt cattgtttcc      120
ggagatTTTTT acaatatcag gaaatgggggt ttcgaccatg tgcgggcttcc cattgactcg      180
tacctgttct ttacggaaga cgatgcccc attgagaaca ggtttgcccc tcttgaccgc      240
gccgtacaat tcgcgaagag caacagcctc aagctgatat tggacctcca cgagtgtccg      300
ggacacgatt tttccgaagc cgcgaaagga cccgtccaga aacttttttc gggagatgac      360
gtttacataa aaaaaaccga gaaaatctgg gcctgcctcg ccgagcgtta ttcgaaaaac      420
gaccatgtac tctttgagac tctcaacgaa cctgtcgctc ccaactgccga aatttggaac      480
aaggttaagg acaggctctg cagagtaatc cgcattccacg cgccctggtc gaccataatc      540
accggctcca atatgtggaa ctgcgcgtcc gccttcgacg gtcttacgcc ctttgacgat      600
ggcaacgtga tctacagcgt gcattttttac gagccgctgc tttttacgca tcagaacgcg      660
ccgtggatcg acaatccgga gatcaggacg gcaaggccct atccggggcg ttacggcccc      720
ggccttgctc gcaaatacgg tatggcgcag tcggccggca tctggaacaa gaaacggctt      780
gcaaaagaat ttgagcccgt ggacgcgttc aggaaaaaat acaaggcgcg cgttatctgt      840
aacgagtttg gcgtgtacgc ccccgccgat ctggaatcgc agcttcgctg gtatgaggat      900
ctgctctcaa tcctcaacgg gatgcagata ggttactcgt actggaacta caaaaatctg      960
gatttcggaa taatttccat aggggagaaa ctgcacgaaa gactttcgca gtatgacaac     1020
gacgagcgga taaaccaccc ggtgctgaat gtgctgaaga aatattaa                       1068
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<210> 154

<211> 355

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (19)...(325)

<223> Cellulase (glycosyl hydrolase family 5)

<220>

<221> SITE

<222> (145)...(154)

<223> Glycosyl hydrolases family 5 signature. Prosite id = PS00659

<400> 154

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Met Gln Arg Met Arg Gly Leu Asn Ile Gly Gly Trp Leu Ser Gln Ile
 1 5 10 15
 Asp Ala Ile Gln Glu Lys Asp Pro Glu Gly Phe Pro Gly Ile Asp Lys
 20 25 30
 His Met Glu Thr Phe Ile Val Ser Gly Asp Phe Tyr Asn Ile Arg Lys
 35 40 45
 Trp Gly Phe Asp His Val Arg Leu Pro Ile Asp Ser Tyr Leu Phe Phe
 50 55 60
 Thr Glu Asp Asp Ala Pro Ile Glu Asn Arg Phe Ala His Leu Asp Arg
 65 70 75 80
 Ala Val Gln Phe Ala Lys Ser Asn Ser Leu Lys Leu Ile Leu Asp Leu
 85 90 95
 His Glu Cys Pro Gly His Asp Phe Ser Glu Ala Ala Lys Gly Pro Val
 100 105 110
 Gln Lys Leu Phe Ser Gly Asp Asp Val Tyr Ile Lys Lys Thr Glu Lys
 115 120 125
 Ile Trp Ala Cys Leu Ala Glu Arg Tyr Ser Lys Asn Asp His Val Leu
 130 135 140
 Phe Glu Thr Leu Asn Glu Pro Val Ala Pro Thr Ala Glu Ile Trp Asn
 145 150 155 160
 Lys Val Lys Asp Arg Leu Cys Arg Val Ile Arg Ile His Ala Pro Trp
 165 170 175
 Ser Thr Ile Ile Thr Gly Ser Asn Met Trp Asn Ser Pro Ser Ala Phe
 180 185 190
 Asp Gly Leu Thr Pro Phe Asp Asp Gly Asn Val Ile Tyr Ser Val His
 195 200 205
 Phe Tyr Glu Pro Leu Leu Phe Thr His Gln Asn Ala Pro Trp Ile Asp
 210 215 220
 Asn Pro Glu Ile Arg Thr Ala Arg Pro Tyr Pro Gly Asp Tyr Gly Pro
 225 230 235 240
 Gly Leu Val Arg Lys Tyr Gly Met Ala Gln Ser Ala Gly Ile Trp Asn

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245

250

255

Lys Lys Arg Leu Ala Lys Glu Phe Glu Pro Val Asp Ala Phe Arg Lys
 260 265 270

Lys Tyr Lys Ala Arg Val Ile Cys Asn Glu Phe Gly Val Tyr Ala Pro
 275 280 285

Ala Asp Leu Glu Ser Gln Leu Arg Trp Tyr Glu Asp Leu Leu Ser Ile
 290 295 300

Leu Asn Gly Met Gln Ile Gly Tyr Ser Tyr Trp Asn Tyr Lys Asn Leu
 305 310 315 320

Asp Phe Gly Ile Ile Ser Ile Gly Glu Lys Leu His Glu Arg Leu Ser
 325 330 335

Gln Tyr Asp Asn Asp Glu Arg Ile Asn His Pro Val Leu Asn Val Leu
 340 345 350

Lys Lys Tyr
 355

<210> 155
 <211> 954
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 155
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 gactacagcg aggagcgcct gaacagcttc atcaccgaaa aggactttga ggtgatcgcc 120
 tcctgggggtt ttgaccacgt ccgcctcccg gtggactata atgtcatcca ggatgcggaa 180
 ggccgcatga tggagaaagg ccttgacgc atcgacgccg cgcttcgggtt ttgtgagaag 240
 accgggcttc acatggttct cgacctgcat aagacaccgg gcttttcctt cgaccgcag 300
 gagcaggaga tgggattctt ccggtcggcg cccgaccagc agctcttcta cacgatctgg 360
 gagagccttg ctgcccggta tgcagacaaa tcggagatac tcatgttcga tcttctgaac 420
 gagatcacgg agccggcgta tctggaggac tggaaccgga tttccgcgga atgcatccgc 480
 cgcacccggc gtacgatgcc ggacgtccga attctggctc gaagctatca ccacaatgcc 540
 gtcagcgcg taaaggacct gcctgcgccg gcagacgata aggtttttta cagctttcac 600
 tgttacgacc ctcacaccta taccaccag ggcgcttact ggatgccgga tgactttgac 660

atcgatgcaa gagtttcctt ccgcgacacc ggcgttaccc ccgtcttctt cgaaaagctg 720
tttgcctccg ccgttgaaaa ggcgcaggcg gaagggacgg aactgtactg cggagaatac 780
ggcgtcatcg acattgttcc gccggaggat gccgttctct gggtccggac cattcatgag 840
gtctttgaag cattcgggat tgcaagaagc gtctggagct ataaggaaat ggatttcggt 900
ctcgccgacc cccgcatgga tgcgggtccgg gcagagctgc tgacctgtct ctga 954

<210> 156
<211> 317
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> DOMAIN
<222> (14)...(302)
<223> Cellulase (glycosyl hydrolase family 5)

<400> 156
Met Leu Lys Asp Ser Gly Phe Tyr Lys Gly Ile Asn Leu Gly Gly Trp
1 5 10 15

Leu Ser Gln Cys Asp Tyr Ser Glu Glu Arg Leu Asn Ser Phe Ile Thr
20 25 30

Glu Lys Asp Phe Glu Val Ile Ala Ser Trp Gly Phe Asp His Val Arg
35 40 45

Leu Pro Val Asp Tyr Asn Val Ile Gln Asp Ala Glu Gly Arg Met Met
50 55 60

Glu Lys Gly Leu Ala Arg Ile Asp Ala Ala Leu Arg Phe Cys Glu Lys
65 70 75 80

Thr Gly Leu His Met Val Leu Asp Leu His Lys Thr Pro Gly Phe Ser
85 90 95

Phe Asp Pro Gln Glu Gln Glu Met Gly Phe Phe Arg Ser Ala Pro Asp
100 105 110

Gln Gln Leu Phe Tyr Thr Ile Trp Glu Ser Leu Ala Ala Arg Tyr Ala
115 120 125

Asp Lys Ser Glu Ile Leu Met Phe Asp Leu Leu Asn Glu Ile Thr Glu
130 135 140

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Pro Ala Tyr Leu Glu Asp Trp Asn Arg Ile Ser Ala Glu Cys Ile Arg
 145 150 155 160

Arg Ile Arg Arg Thr Met Pro Asp Val Arg Ile Leu Val Gly Ser Tyr
 165 170 175

His His Asn Ala Val Ser Ala Val Lys Asp Leu Pro Ala Pro Ala Asp
 180 185 190

Asp Lys Val Phe Tyr Ser Phe His Cys Tyr Asp Pro His Thr Tyr Thr
 195 200 205

His Gln Gly Ala Tyr Trp Met Pro Asp Asp Phe Asp Ile Asp Ala Arg
 210 215 220

Val Ser Phe Arg Asp Thr Gly Val Thr Pro Val Phe Phe Glu Lys Leu
 225 230 235 240

Phe Ala Ser Ala Val Glu Lys Ala Gln Ala Glu Gly Thr Glu Leu Tyr
 245 250 255

Cys Gly Glu Tyr Gly Val Ile Asp Ile Val Pro Pro Glu Asp Ala Val
 260 265 270

Leu Trp Phe Arg Thr Ile His Glu Val Phe Glu Ala Phe Gly Ile Ala
 275 280 285

Arg Ser Val Trp Ser Tyr Lys Glu Met Asp Phe Gly Leu Ala Asp Pro
 290 295 300

Arg Met Asp Ala Val Arg Ala Glu Leu Leu Thr Cys Leu
 305 310 315

<210> 157
 <211> 954
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 157
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 gactacagcg aggagcgcct gaacagcttc atcaccgaaa aagactttga ggtgatcgcc 120
 tcctgggggtt ttgaccacgt ccgtctgccg gtggactata atgtcatcca ggatgcggaa 180
 ggccgcatga tggaggaagg cctcgcacgc atcgacgccg cgcttcgggtt ttgtgaaaag 240


```

accgggcttc acatgggttct cgacctgcat aagacaccgg gcttttcctt cgacccgcag      300
gagcaggaga tgggattctt ccggtcggcg cccgaccagc agcgcttcta cacgatctgg      360
gagagccttg ctgcccggta tgcagacaaa tcggagatgc tcatgttcga tcttctgaac      420
gagatcacgg agccggcgta tctgaaggac tggaaccgga tttccgcgga atgcatccgc      480
cgcatccggc gtacgatgcc ggacgtccgg attctggtcg gaagctatca ccacaatgcc      540
gtcagcgcgg taaaggacct gcctgcgccg gcggacgacc gggtttttta cagctttcac      600
tgttacgacc ctcacaccta taccaccag ggcgcttact ggatgccgga tgactttgac      660
atcgatgcaa gagtttcctt ccgcgacatc ggcgtcacc cgccttctt cgaagagctg      720
tttgcattctg ccgttgaaaa ggcgaagggt gaagggacgg aactgtactg cggagaatac      780
ggcgtcatcg acattgttcc gccggaggat gccgttctct ggttccggac cattcatgag      840
gtctttgaga aatacgggat tgcaagaagc gtctggagct ataaggaaat ggatttcggt      900
ctctccgacc cccgcatgga cgcggtccgg gcagagctgc tgacctgtct ctga          954

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<210> 158

<211> 317

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (14)...(302)

<223> Cellulase (glycosyl hydrolase family 5)

<400> 158

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Met Leu Lys Asp Ser Gly Phe Tyr Lys Gly Ile Asn Leu Gly Gly Trp
1           5           10          15

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```

Leu Ser Gln Cys Asp Tyr Ser Glu Glu Arg Leu Asn Ser Phe Ile Thr
          20          25          30

```

```

Glu Lys Asp Phe Glu Val Ile Ala Ser Trp Gly Phe Asp His Val Arg
          35          40          45

```

```

Leu Pro Val Asp Tyr Asn Val Ile Gln Asp Ala Glu Gly Arg Met Met
          50          55          60

```

```

Glu Glu Gly Leu Ala Arg Ile Asp Ala Ala Leu Arg Phe Cys Glu Lys
          65          70          75          80

```

```

Thr Gly Leu His Met Val Leu Asp Leu His Lys Thr Pro Gly Phe Ser
          85          90          95

```

Phe Asp Pro Gln Glu Gln Glu Met Gly Phe Phe Arg Ser Ala Pro Asp
100 105 110

Gln Gln Arg Phe Tyr Thr Ile Trp Glu Ser Leu Ala Ala Arg Tyr Ala
115 120 125

Asp Lys Ser Glu Met Leu Met Phe Asp Leu Leu Asn Glu Ile Thr Glu
130 135 140

Pro Ala Tyr Leu Lys Asp Trp Asn Arg Ile Ser Ala Glu Cys Ile Arg
145 150 155 160

Arg Ile Arg Arg Thr Met Pro Asp Val Arg Ile Leu Val Gly Ser Tyr
165 170 175

His His Asn Ala Val Ser Ala Val Lys Asp Leu Pro Ala Pro Ala Asp
180 185 190

Asp Arg Val Phe Tyr Ser Phe His Cys Tyr Asp Pro His Thr Tyr Thr
195 200 205

His Gln Gly Ala Tyr Trp Met Pro Asp Asp Phe Asp Ile Asp Ala Arg
210 215 220

Val Ser Phe Arg Asp Ile Gly Val Thr Pro Ala Phe Phe Glu Glu Leu
225 230 235 240

Phe Ala Ser Ala Val Glu Lys Ala Lys Val Glu Gly Thr Glu Leu Tyr
245 250 255

Cys Gly Glu Tyr Gly Val Ile Asp Ile Val Pro Pro Glu Asp Ala Val
260 265 270

Leu Trp Phe Arg Thr Ile His Glu Val Phe Glu Lys Tyr Gly Ile Ala
275 280 285

Arg Ser Val Trp Ser Tyr Lys Glu Met Asp Phe Gly Leu Ser Asp Pro
290 295 300

Arg Met Asp Ala Val Arg Ala Glu Leu Leu Thr Cys Leu
305 310 315

<210> 159

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 159

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atgaatccaa cattcagttc cgtaccggca ttaaaggagc tgtttgcggc ggacttcaac      60
atcggggcgcg cggtgaatcc gacgacgac cggacgcagg aggcgttgct ggcttatcat      120
tttaacagcc tgactgcgga gaacgagatg aagttcgtca gcgtgcatcc ggaggagcag      180
acctatacct tcgaggcggc ggaccggctg gtcgaattcg cccgagagca cggcatggcc      240
atgcgggggac acacgctcgt atggcataac cagacgtccg attggctggt ccaggatcgc      300
caaggcgggga gggtaagcaa ggaggtgctg ctcggaaggc tccgggagca tattcatacc      360
atagtaggcc ggtacaagaa cgagatctac gcctgggacg tcgtcaacga ggtcatcgcg      420
gacgaagggg aggcgctgct gcgcacttcc aaatggacgg aaatcgcggg acctgaattt      480
atcgctaaag cgttcgagta tgcacatgag gcggatccac aggcgctggt gttttataac      540
gactacaacg aatcgaatcc tctgaaacgc gataaaattt acacactcgt tcattcgctg      600
ctggagcaag gggtgccgat ccatggcatc ggattacaag cgcactggaa cctgtacgat      660
ccatcgttgg atgagattaa ggcagcgatt gagaagtatg cttcgctggg ttgacagctg      720
cagctgacgg agctggatct ctcgatgttc cgcttcgatg accggcgaac cgatttgacc      780
gcgccagagc cggggatgct ggagcaacag gccgagcgtt atgaagccgt gttccggctg      840
ttgctggagt atcgtgacgt catcagcggc gttaccttct ggggagcggc ggatgattat      900
acctggctgg acaattttcc ggtgcgcggc cggaagaact ggccgtttct gttcgatgcc      960
cagcaccagc cgaaggcagc ttatcacctg gtggcggcat tggctgcgga gcaacgagca     1020
taa                                                                    1023
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<210> 160

<211> 340

<212> PRT

<213> Unknown

<220>

<223> Obtained from environmental sample

<220>

<221> DOMAIN

<222> (10)...(335)

<223> Glycosyl hydrolase family 10

<220>

<221> SITE

<222> (91)...(94)

<223> N-glycosylation site. Prosite id = PS00001

<220>

<221> SITE

<222> (185)...(188)

<223> N-glycosylation site. Prosite id = PS00001

<400> 160

Met Asn Pro Thr Phe Ser Ser Val Pro Ala Leu Lys Glu Leu Phe Ala
 1 5 10 15

Ala Asp Phe Asn Ile Gly Ala Ala Val Asn Pro Thr Thr Ile Arg Thr
 20 25 30

Gln Glu Ala Leu Leu Ala Tyr His Phe Asn Ser Leu Thr Ala Glu Asn
 35 40 45

Glu Met Lys Phe Val Ser Val His Pro Glu Glu Gln Thr Tyr Thr Phe
 50 55 60

Glu Ala Ala Asp Arg Leu Val Glu Phe Ala Arg Glu His Gly Met Ala
 65 70 75 80

Met Arg Gly His Thr Leu Val Trp His Asn Gln Thr Ser Asp Trp Leu
 85 90 95

Phe Gln Asp Arg Gln Gly Gly Arg Val Ser Lys Glu Val Leu Leu Gly
 100 105 110

Arg Leu Arg Glu His Ile His Thr Ile Val Gly Arg Tyr Lys Asn Glu
 115 120 125

Ile Tyr Ala Trp Asp Val Val Asn Glu Val Ile Ala Asp Glu Gly Glu
 130 135 140

Ala Leu Leu Arg Thr Ser Lys Trp Thr Glu Ile Ala Gly Pro Glu Phe
 145 150 155 160

Ile Ala Lys Ala Phe Glu Tyr Ala His Glu Ala Asp Pro Gln Ala Leu
 165 170 175

Leu Phe Tyr Asn Asp Tyr Asn Glu Ser Asn Pro Leu Lys Arg Asp Lys
 180 185 190

Ile Tyr Thr Leu Val His Ser Leu Leu Glu Gln Gly Val Pro Ile His
 195 200 205

Gly Ile Gly Leu Gln Ala His Trp Asn Leu Tyr Asp Pro Ser Leu Asp
 210 215 220

Glu Ile Lys Ala Ala Ile Glu Lys Tyr Ala Ser Leu Gly Leu Gln Leu

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225		230		235		240
Gln Leu Thr Glu Leu Asp Leu Ser Met Phe Arg Phe Asp Asp Arg Arg						
		245		250		255
Thr Asp Leu Thr Ala Pro Glu Pro Gly Met Leu Glu Gln Gln Ala Glu						
		260		265		270
Arg Tyr Glu Ala Val Phe Arg Leu Leu Leu Glu Tyr Arg Asp Val Ile						
		275		280		285
Ser Gly Val Thr Phe Trp Gly Ala Ala Asp Asp Tyr Thr Trp Leu Asp						
		290		295		300
Asn Phe Pro Val Arg Gly Arg Lys Asn Trp Pro Phe Leu Phe Asp Ala						
305		310		315		320
Gln His Gln Pro Lys Ala Ala Tyr His Arg Val Ala Ala Leu Ala Ala						
		325		330		335
Glu Gln Arg Ala						
		340				

<210> 161
 <211> 2820
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<400> 161
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 ttattcctca gaaccggttc gggtacagga caaacttaca attatgccga agtcctgcag 120
 aaatctatgt ttttctacga atgtcaggag tctaaaattg ccccgggcaa tcgggtgaca 180
 tggcgagcta atgcagccat gaacgatggg agcgatgttg gaaaagacct gacaggagga 240
 tggtttgatg cagggtgacca tgtgaaattt aattttccca tggcgtttac cgctacggcg 300
 ctggcggtggg gagctattga ctttgctcag ggatacatta gttccgggca aatgcaatac 360
 ctgaaacgta atctgcgcta cgtcaatgac tattttcatta aatgtcacac agcccccaac 420
 gaattgtatg gtcagggtggg taatggaggg cttgaccatg cctttttgggg accacccgaa 480
 gtcatgcgca tggctaggcc tgcctataaa attgatgcgt caaaaccggg atcagatctg 540
 gctgccgaaa cagctgctgc aatggctgcc gccagcattg ttttcaaata cgacgatcct 600
 acctatagcg ctacttttgct gaatcatgca aaacagctgt tttctttttgc cgaaacctat 660

aaaggaaaat attccgacgc tattaccgat gctgcaggat attataactc ctggagcggc	720
tataacgatg aactggtatg gggagctata tggctttacc gggctaccgg cgatgcaacc	780
tatctatcta aggcagaatc ctattacgac aatctgggta atcaggggtca ggaacccggt	840
aaagcctaca aatggaccat tgcattgggat gacaaatcct atggctgtta tgccctactg	900
gccaaattga caggtaagga aaaatacaaaa attgacgccg aacgttttct cgactattgg	960
accgatgggtt ataatgggttc ccggattact tataccccgg gaggactcgc tttcctcgat	1020
atatggggat cgttgcgcta tgctatgaat actgcctttg ttgctgccta ctatgccgat	1080
gcagccactt cagctgctaa aaccacaaaa tatctcaact ttgctaaaca acaactgcat	1140
tatgctcttg gatccaatcc gagcaacaga agctatgtct gtggcttttg caataatcct	1200
cccgtaaata ctcaccatag aggtgcacac ggagcatggg ctaataatgt tcaaggacct	1260
cctaccgaaa cagcacatat cctctacggc gcattagtgg gtggaccagg cagtaatgac	1320
tcctatactg acgaccgatc caattacacc aataacgaag tagcatgtga ctacaatgct	1380
cttttctccg gactgcttgc aaagtctgct attgattatg gaggcacacc gttagccaac	1440
ttccctgttc gtgaaacccc aaaagatgaa tatttcgttg aagcaaaagc aaacgctaca	1500
ggaaccaatt tctccgaatg gacgggatgg gtatacaacc aactgcatg gccagcccgt	1560
gaaggttctg aatataaatt cagattatac gtaaataatt cggaaggact ggctgcaggc	1620
tatactgcct caaattatgt tgtgcaaacc aataatgccg gtgtggtaaa ctttacccaa	1680
cttttagctg ctgatgcagc taacggcatc tattataccg aagtaacctt taaacctggg	1740
accgaaattt atcctggcgg gcaacagtat gacaagaagg aagctcagat gcgtattagt	1800
ttgcccattg ctccggcttc tgcattggat ccgactaacg acccgatcat ggccgggaatc	1860
acctctacct tgaaacaaat gccgggtata cccatgtatg tagatgggtg aaaggatatt	1920
ggtaatgagc ctgtcccagg tcagacagtt cccgtcaccg gagtaaccgt atcgccctacc	1980
accctgagtc tgactgtagg acagaccagt acactcaccg ctaccgtatc gccggcta	2040
gctaccaaca aaaacgtcac ctggagcagc agcaatacca gcgtagccac ggtaagctca	2100
acaggcggtg tcacagccgt agcagccggt tcggccacca tcaccgtaac cacagtcgat	2160
ggcgctaaaa cagccacctg cgccgtaacg gtaacaggca gcaccaacgt tcccgtcacc	2220
ggagtaaccg tatcgccac cacgctgagt ctgaccgtag ggcagaccgc taccctcacc	2280
gctaccgtat cgccggctaa tgctaccaac aagaacgtta cctggagcag cagcaatacc	2340
agcgtagcca cggtaagttc aacaggcgta gttactgccg tagcggccgg ttcggccacc	2400
atcaccgtaa ccaccgtcga tggagctaaa accgctacct gcaccgtaac ggtaacgggc	2460
agcactaccg taccggtcac cggcgtaact gtatcgcta ccaccctgag tctgaccgtt	2520

ggacaaaccg ctaccctgac cgctaccgta tcgccagctg atgctaccaa caagaacgtc 2580
acctggagca gcagcaatac cagcgtagcc acggtaagct caacaggcgt agtcactgcc 2640
gtagcggccg gttcagctac catcaccgtg accacagtcg atggggctaa aactgctacc 2700
tgtgccgtga ccgtaaccgc cggagggttc accaccccct gcagtaatcc ggtaagcaaa 2760
accctacctc tggtacagga tggtgccggc gaattcaggt tgagtaatag ttttaattaa 2820

<210> 162
<211> 939
<212> PRT
<213> Unknown

<220>
<223> Obtained from environmental sample

<220>
<221> SIGNAL
<222> (1)...(30)

<220>
<221> DOMAIN
<222> (34)...(469)
<223> Glycosyl hydrolase family 9

<220>
<221> DOMAIN
<222> (491)...(576)
<223> Cellulose binding domain

<220>
<221> DOMAIN
<222> (738)...(816)
<223> Bacterial Ig-like domain (group 2)

<220>
<221> DOMAIN
<222> (825)...(903)
<223> Bacterial Ig-like domain (group 2)

<220>
<221> DOMAIN
<222> (651)...(729)
<223> Bacterial Ig-like domain (group 2)

<400> 162
Met Ser Cys Arg Thr Leu Met Ser Arg Arg Val Gly Trp Gly Leu Leu
1 5 10 15

Leu Trp Gly Gly Leu Phe Leu Arg Thr Gly Ser Val Thr Gly Gln Thr
20 25 30

Tyr Asn Tyr Ala Glu Val Leu Gln Lys Ser Met Phe Phe Tyr Glu Cys
35 40 45

Gln Glu Ser Lys Ile Ala Pro Gly Asn Arg Val Thr Trp Arg Ala Asn
 50 55 60

Ala Ala Met Asn Asp Gly Ser Asp Val Gly Lys Asp Leu Thr Gly Gly
 65 70 75 80

Trp Phe Asp Ala Gly Asp His Val Lys Phe Asn Phe Pro Met Ala Phe
 85 90 95

Thr Ala Thr Ala Leu Ala Trp Gly Ala Ile Asp Phe Ala Gln Gly Tyr
 100 105 110

Ile Ser Ser Gly Gln Met Gln Tyr Leu Lys Arg Asn Leu Arg Tyr Val
 115 120 125

Asn Asp Tyr Phe Ile Lys Cys His Thr Ala Pro Asn Glu Leu Tyr Gly
 130 135 140

Gln Val Gly Asn Gly Gly Leu Asp His Ala Phe Trp Gly Pro Pro Glu
 145 150 155 160

Val Met Arg Met Ala Arg Pro Ala Tyr Lys Ile Asp Ala Ser Lys Pro
 165 170 175

Gly Ser Asp Leu Ala Ala Glu Thr Ala Ala Ala Met Ala Ala Ala Ser
 180 185 190

Ile Val Phe Lys Ser Asp Asp Pro Thr Tyr Ser Ala Thr Leu Leu Asn
 195 200 205

His Ala Lys Gln Leu Phe Ser Phe Ala Glu Thr Tyr Lys Gly Lys Tyr
 210 215 220

Ser Asp Ala Ile Thr Asp Ala Ala Gly Tyr Tyr Asn Ser Trp Ser Gly
 225 230 235 240

Tyr Asn Asp Glu Leu Val Trp Gly Ala Ile Trp Leu Tyr Arg Ala Thr
 245 250 255

Gly Asp Ala Thr Tyr Leu Ser Lys Ala Glu Ser Tyr Tyr Asp Asn Leu
 260 265 270

Gly Asn Gln Gly Gln Glu Pro Val Lys Ala Tyr Lys Trp Thr Ile Ala
 275 280 285

Trp	Asp	Asp	Lys	Ser	Tyr	Gly	Cys	Tyr	Ala	Leu	Leu	Ala	Lys	Leu	Thr
	290					295					300				
Gly	Lys	Glu	Lys	Tyr	Lys	Ile	Asp	Ala	Glu	Arg	Phe	Leu	Asp	Tyr	Trp
305					310					315					320
Thr	Asp	Gly	Tyr	Asn	Gly	Ser	Arg	Ile	Thr	Tyr	Thr	Pro	Gly	Gly	Leu
				325					330					335	
Ala	Phe	Leu	Asp	Ile	Trp	Gly	Ser	Leu	Arg	Tyr	Ala	Met	Asn	Thr	Ala
			340					345					350		
Phe	Val	Ala	Ala	Tyr	Tyr	Ala	Asp	Ala	Ala	Thr	Ser	Ala	Ala	Lys	Thr
		355					360					365			
Thr	Lys	Tyr	Leu	Asn	Phe	Ala	Lys	Gln	Gln	Leu	His	Tyr	Ala	Leu	Gly
	370					375					380				
Ser	Asn	Pro	Ser	Asn	Arg	Ser	Tyr	Val	Cys	Gly	Phe	Gly	Asn	Asn	Pro
385					390					395					400
Pro	Val	Asn	Pro	His	His	Arg	Gly	Ala	His	Gly	Ala	Trp	Ser	Asn	Asn
				405					410					415	
Val	Gln	Gly	Pro	Pro	Thr	Glu	Thr	Arg	His	Ile	Leu	Tyr	Gly	Ala	Leu
			420					425					430		
Val	Gly	Gly	Pro	Gly	Ser	Asn	Asp	Ser	Tyr	Thr	Asp	Asp	Arg	Ser	Asn
		435					440					445			
Tyr	Thr	Asn	Asn	Glu	Val	Ala	Cys	Asp	Tyr	Asn	Ala	Leu	Phe	Ser	Gly
	450					455					460				
Leu	Leu	Ala	Lys	Phe	Val	Ile	Asp	Tyr	Gly	Gly	Thr	Pro	Leu	Ala	Asn
465					470					475					480
Phe	Pro	Val	Arg	Glu	Thr	Pro	Lys	Asp	Glu	Tyr	Phe	Val	Glu	Ala	Lys
				485					490					495	
Ala	Asn	Ala	Thr	Gly	Thr	Asn	Phe	Ser	Glu	Trp	Thr	Val	Trp	Val	Tyr
			500					505					510		
Asn	His	Thr	Ala	Trp	Pro	Ala	Arg	Glu	Gly	Ser	Glu	Tyr	Lys	Phe	Arg
		515					520					525			
Leu	Tyr	Val	Asn	Ile	Ser	Glu	Gly	Leu	Ala	Ala	Gly	Tyr	Thr	Ala	Ser

530		535		540
Asn Tyr Val Val Gln Thr Asn Asn Ala Gly Val Val Asn Phe Thr Gln 545 550 555 560				
Leu Leu Ala Ala Asp Ala Ala Asn Gly Ile Tyr Tyr Thr Glu Val Thr 565 570 575				
Phe Lys Pro Gly Thr Glu Ile Tyr Pro Gly Gly Gln Gln Tyr Asp Lys 580 585 590				
Lys Glu Ala Gln Met Arg Ile Ser Leu Pro Asn Ala Pro Ala Ser Ala 595 600 605				
Trp Asp Pro Thr Asn Asp Pro Ser Trp Ala Gly Ile Thr Ser Thr Leu 610 615 620				
Lys Gln Met Pro Gly Ile Pro Met Tyr Val Asp Gly Val Lys Val Phe 625 630 635 640				
Gly Asn Glu Pro Val Pro Gly Gln Thr Val Pro Val Thr Gly Val Thr 645 650 655				
Val Ser Pro Thr Thr Leu Ser Leu Thr Val Gly Gln Thr Ser Thr Leu 660 665 670				
Thr Ala Thr Val Ser Pro Ala Asn Ala Thr Asn Lys Asn Val Thr Trp 675 680 685				
Ser Ser Ser Asn Thr Ser Val Ala Thr Val Ser Ser Thr Gly Val Val 690 695 700				
Thr Ala Val Ala Ala Gly Ser Ala Thr Ile Thr Val Thr Thr Val Asp 705 710 715 720				
Gly Ala Lys Thr Ala Thr Cys Ala Val Thr Val Thr Gly Ser Thr Asn 725 730 735				
Val Pro Val Thr Gly Val Thr Val Ser Pro Thr Thr Leu Ser Leu Thr 740 745 750				
Val Gly Gln Thr Ala Thr Leu Thr Ala Thr Val Ser Pro Ala Asn Ala 755 760 765				
Thr Asn Lys Asn Val Thr Trp Ser Ser Ser Asn Thr Ser Val Ala Thr 770 775 780				

Val Ser Ser Thr Gly Val Val Thr Ala Val Ala Ala Gly Ser Ala Thr
785 790 795 800

Ile Thr Val Thr Thr Val Asp Gly Ala Lys Thr Ala Thr Cys Thr Val
805 810 815

Thr Val Thr Gly Ser Thr Thr Val Pro Val Thr Gly Val Thr Val Ser
820 825 830

Pro Thr Thr Leu Ser Leu Thr Val Gly Gln Thr Ala Thr Leu Thr Ala
835 840 845

Thr Val Ser Pro Ala Asp Ala Thr Asn Lys Asn Val Thr Trp Ser Ser
850 855 860

Ser Asn Thr Ser Val Ala Thr Val Ser Ser Thr Gly Val Val Thr Ala
865 870 875 880

Val Ala Ala Gly Ser Ala Thr Ile Thr Val Thr Thr Val Asp Gly Ala
885 890 895

Lys Thr Ala Thr Cys Ala Val Thr Val Thr Ala Gly Gly Ser Thr Thr
900 905 910

Pro Cys Ser Asn Pro Val Ser Lys Thr Leu Pro Leu Val Gln Asp Gly
915 920 925

Ala Gly Glu Phe Arg Leu Ser Asn Ser Phe Asn
930 935

<210> 163

<211> 2733

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 163

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gagtctaaaa ttgccccggg caatcgggtg acatggcgag ctaatgcagc catgaacgat 120

gggagcgatg ttggaaaaga cctgacagga ggatgggtttg atgcagggtga ccatgtgaaa 180

tttaattttc ccatggcggtt taccgctacg gcgctggcgt ggggagctat tgactttgct 240

cagggataca ttagttccgg gcaaagtcaa tacctgaaac gtaatctgcg ctacgtcaat 300

gactatttca ttaaagtgtca cacagcccc aacgaattgt atggtcaggt gggtaatgga 360

ggccttgacc atgccttttg gggaccaccc gaagtcatgc gcatggctag gcctgcctat	420
aaaattgatg cgtcaaaacc cggatcagat ctggctgccg aaacagctgc tgcaatggct	480
gccgccagca ttgttttcaa atccgacgat cctacctata gcgctacttt gctgaatcat	540
gcaaaacagc tgtttttcttt tgccgaaacc tataaaggaa aatattccga cgctattacc	600
gatgctgcag gatattataa ctcttgagc ggctataacg atgaactggc atggggagct	660
atatggcttt accgggctac cggcgatgca acctatctat ctaaggcaga atcctattac	720
gacaatctgg gtaatcaggg tcaggaaccc gttaaagcct acaaattggc cattgcatgg	780
gatgacaaat cctatggctg ttatgcccta ctggccaaat tgacaggtaa ggaaaaatac	840
aaaattgacg ccgaacgttt tctcgactat tggaccgatg gttataatgg ttcccggatt	900
acttataccc cgggaggact cgctttcttc gatatatggg gatcgttgcg ctatgctatg	960
aatactgcct ttgttgctgc ctactatgcc gatgcagcca cttcagctgc taaaaccaca	1020
aaatatctca actttgctaa acaacaactg cattatgctc ttggatccaa tccgagcaac	1080
agaagctatg tctgtggctt tggcaataat cctcccgtta atcctcacca tagagggtgca	1140
cacggagcat ggtctaataa tgttcaagga cctcctaccg aaacacgaca tatcctctac	1200
ggcgcattag tgggtggacc aggcagtaat gactcctata ctgacgaccg atccaattac	1260
accaataacg aagtagcatg tgactacaat gctcttttct ccggactgct tgcaaagttc	1320
gtcattgatt atggaggcac accgttagcc aacttccttg ttcgtgaaac cccaaaagat	1380
gaatatctcg ttgaagcaaa agcaaacgct acaggaacca atttctccga atggacggta	1440
tgggtataca accacactgc atggccagcc cgtgaagggt ctgaatataa attcagatta	1500
tacgtaaata tttcgggaagg actggctgca ggctatactg cctcaaatta tgttgtgcaa	1560
accaataatg ccggtgtggt aaactttacc caacttttag ctgctgatgc agctaacggc	1620
atctattata ccgaagtaac ctttaaacct ggtaccgaaa tttatcctgg cgggcaacag	1680
tatgacaaga aggaagctca gatgcgtatt agtttgccca atgctccggc ttctgcatgg	1740
gatccgacta acgaccctgc atgggcccga atcacctcta ccttgaaaca aatgccgggt	1800
atacccatgt atgtagatgg tgtaaaggta tttggtaatg agcctgtccc aggtcagaca	1860
gttcccgtca ccggagtaac cgtatcgctt accaccctga gtctgactgt aggacagacc	1920
agtacactca ccgctaccgt atcgccggct aatgctacca aaaaaaacgt cacctggagc	1980
agcagcaata ccagcgtagc cacggtaagc tcaacaggcg ttgtcacagc cgtagcagcc	2040
ggttcggcca ccatcacctg aaccacagtc gatggcgcta aaacagccac ctgcgccgta	2100
acggtaacag gcagcaccaa cgttcccgtc accggagtaa ccgtatcgcc caccacgctg	2160

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agtctgaccg tagggcagac cgctaccctc accgctaccg tatcgccggc taatgctacc 2220
aacaagaacg ttacctggag cagcagcaat accagcgtag ccacggtaag ttcaacaggc 2280
gtagttactg ccgtagcggc cggttcggcc accatcaccg taaccaccgt cgatggagct 2340
aaaaccgcta cctgcaccgt aacggtaacg ggcagcacta ccgtaccctg caccggcgta 2400
actgtatcgc ctaccaccct gagtctgacc gttggacaaa ccgctaccct gaccgctacc 2460
gtatcgccag ctgatgctac caacaagaac gtcacctgga gcagcagcaa taccagcgta 2520
gccacggtaa gctcaacagg cgtagtcact gccgtagcgg ccggttcagc taccatcacc 2580
gtgaccacag tcgatggggc taaaactgct acctgtgccg tgaccgtaac cgccggaggt 2640
tccaccaccc cctgcagtaa tccggtaagc aaaaccctac ctctggtaca ggatggtgcc 2700
ggcgaattca gggtgagtaa tagttttaat taa 2733

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<210> 164
 <211> 910
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> DOMAIN
 <222> (5)...(440)
 <223> Glycosyl hydrolase family 9

<220>
 <221> DOMAIN
 <222> (462)...(547)
 <223> Cellulose binding domain

<220>
 <221> DOMAIN
 <222> (709)...(787)
 <223> Bacterial Ig-like domain (group 2)

<220>
 <221> DOMAIN
 <222> (796)...(874)
 <223> Bacterial Ig-like domain (group 2)

<220>
 <221> DOMAIN
 <222> (622)...(700)
 <223> Bacterial Ig-like domain (group 2)

<400> 164
 Met Gln Thr Tyr Asn Tyr Ala Glu Val Leu Gln Lys Ser Met Phe Phe
 1 5 10 15
 Tyr Glu Cys Gln Glu Ser Lys Ile Ala Pro Gly Asn Arg Val Thr Trp
 20 25 30

Arg	Ala	Asn	Ala	Ala	Met	Asn	Asp	Gly	Ser	Asp	Val	Gly	Lys	Asp	Leu	35	40	45
Thr	Gly	Gly	Trp	Phe	Asp	Ala	Gly	Asp	His	Val	Lys	Phe	Asn	Phe	Pro	50	55	60
Met	Ala	Phe	Thr	Ala	Thr	Ala	Leu	Ala	Trp	Gly	Ala	Ile	Asp	Phe	Ala	65	70	75
Gln	Gly	Tyr	Ile	Ser	Ser	Gly	Gln	Met	Gln	Tyr	Leu	Lys	Arg	Asn	Leu	85	90	95
Arg	Tyr	Val	Asn	Asp	Tyr	Phe	Ile	Lys	Cys	His	Thr	Ala	Pro	Asn	Glu	100	105	110
Leu	Tyr	Gly	Gln	Val	Gly	Asn	Gly	Gly	Leu	Asp	His	Ala	Phe	Trp	Gly	115	120	125
Pro	Pro	Glu	Val	Met	Arg	Met	Ala	Arg	Pro	Ala	Tyr	Lys	Ile	Asp	Ala	130	135	140
Ser	Lys	Pro	Gly	Ser	Asp	Leu	Ala	Ala	Glu	Thr	Ala	Ala	Ala	Met	Ala	145	150	155
Ala	Ala	Ser	Ile	Val	Phe	Lys	Ser	Asp	Asp	Pro	Thr	Tyr	Ser	Ala	Thr	165	170	175
Leu	Leu	Asn	His	Ala	Lys	Gln	Leu	Phe	Ser	Phe	Ala	Glu	Thr	Tyr	Lys	180	185	190
Gly	Lys	Tyr	Ser	Asp	Ala	Ile	Thr	Asp	Ala	Ala	Gly	Tyr	Tyr	Asn	Ser	195	200	205
Trp	Ser	Gly	Tyr	Asn	Asp	Glu	Leu	Val	Trp	Gly	Ala	Ile	Trp	Leu	Tyr	210	215	220
Arg	Ala	Thr	Gly	Asp	Ala	Thr	Tyr	Leu	Ser	Lys	Ala	Glu	Ser	Tyr	Tyr	225	230	235
Asp	Asn	Leu	Gly	Asn	Gln	Gly	Gln	Glu	Pro	Val	Lys	Ala	Tyr	Lys	Trp	245	250	255
Thr	Ile	Ala	Trp	Asp	Asp	Lys	Ser	Tyr	Gly	Cys	Tyr	Ala	Leu	Leu	Ala	260	265	270
Lys	Leu	Thr	Gly	Lys	Glu	Lys	Tyr	Lys	Ile	Asp	Ala	Glu	Arg	Phe	Leu	275	280	285
Asp	Tyr	Trp	Thr	Asp	Gly	Tyr	Asn	Gly	Ser	Arg	Ile	Thr	Tyr	Thr	Pro	290	295	300
Gly	Gly	Leu	Ala	Phe	Leu	Asp	Ile	Trp	Gly	Ser	Leu	Arg	Tyr	Ala	Met	305	310	315
Asn	Thr	Ala	Phe	Val	Ala	Ala	Tyr	Tyr	Ala	Asp	Ala	Ala	Thr	Ser	Ala	325	330	335
Ala	Lys	Thr	Thr	Lys	Tyr	Leu	Asn	Phe	Ala	Lys	Gln	Gln	Leu	His	Tyr	340	345	350
Ala	Leu	Gly	Ser	Asn	Pro	Ser	Asn	Arg	Ser	Tyr	Val	Cys	Gly	Phe	Gly			

355	360	365
Asn 370	Asn 375	Ala 380
Ser 385	Gly 390	Arg 395
Gly 405	Pro 410	Ser 415
Arg 420	Glu 425	Asp 430
Phe 435	Phe 440	Tyr 445
Leu 450	Arg 455	Asp 460
Glu 465	Thr 470	Phe 475
Trp 485	Ala 490	Arg 495
Lys 500	Ile 505	Gly 510
Thr 515	Gln 520	Ala 525
Phe 530	Asp 535	Gly 540
Glu 545	Thr 550	Tyr 555
Tyr 565	Met 570	Ser 575
Ala 580	Asn 585	Pro 590
Ser 595	Gly 600	Tyr 605
Lys 610	Val 615	Thr 620
Gly 625	Thr 630	Leu 635
Ser 645	Val 650	Ala 655
Val 660	Thr 665	Val 670
Gly 675	Ala 680	Ile 685

Thr Val Asp Gly Ala Lys Thr Ala Thr Cys Ala Val Thr Val Thr Gly
 690 695 700
 Ser Thr Asn Val Pro Val Thr Gly Val Thr Val Ser Pro Thr Thr Leu
 705 710 715 720
 Ser Leu Thr Val Gly Gln Thr Ala Thr Leu Thr Ala Thr Val Ser Pro
 725 730 735
 Ala Asn Ala Thr Asn Lys Asn Val Thr Trp Ser Ser Ser Asn Thr Ser
 740 745 750
 Val Ala Thr Val Ser Ser Thr Gly Val Val Thr Ala Val Ala Ala Gly
 755 760 765
 Ser Ala Thr Ile Thr Val Thr Thr Val Asp Gly Ala Lys Thr Ala Thr
 770 775 780
 Cys Thr Val Thr Val Thr Gly Ser Thr Thr Val Pro Val Thr Gly Val
 785 790 795 800
 Thr Val Ser Pro Thr Thr Leu Ser Leu Thr Val Gly Gln Thr Ala Thr
 805 810 815
 Leu Thr Ala Thr Val Ser Pro Ala Asp Ala Thr Asn Lys Asn Val Thr
 820 825 830
 Trp Ser Ser Ser Asn Thr Ser Val Ala Thr Val Ser Ser Thr Gly Val
 835 840 845
 Val Thr Ala Val Ala Ala Gly Ser Ala Thr Ile Thr Val Thr Thr Val
 850 855 860
 Asp Gly Ala Lys Thr Ala Thr Cys Ala Val Thr Val Thr Ala Gly Gly
 865 870 875 880
 Ser Thr Thr Pro Cys Ser Asn Pro Val Ser Lys Thr Leu Pro Leu Val
 885 890 895
 Gln Asp Gly Ala Gly Glu Phe Arg Leu Ser Asn Ser Phe Asn
 900 905 910

<210> 165

<211> 1347

<212> DNA

<213> Unknown

<220>

<223> Obtained from environmental sample

<400> 165

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ggttcttcca gcagcgacaa ggacccttca agctccagct ccagtgaatc atcaagttcc 180

agcgaatcct cgagctcagc ttccagcgaa tcctcgagca gtgagtccag cagtagctct 240

tccgcggggc atttctccat cgagccggac ttccagctct acagcctggc caacttcccg 300

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gtgggctggtg cggtctccgc cgccaacgag aacgacagca tcttcaacag tccggatgcc      360
gccgaacgtc aggccgttat tattgagcac ttctctcagc tcaccgccgg caacatcatg      420
aaaatgagct acctgcagcc gagtcaaggc aacttcacct tcgatgacgc cgacgagttg      480
gttaacttcg cccaagccaa tggcatgacc gtacacggcc actccaccat ctggcacgcg      540
gactaccaag taccgaactt catgagaaac tttgaagggtg accaggagga atgggcagaa      600
attctgaccg atcacgtcac taccatcatc gagcacttcc ccgacgatgt ggtcatcagc      660
tgggacgtgg tgaacgaggc tgtcgatcaa ggcacggcga acggctggcg ccattcgggtg      720
ttctacaatg cattcgacgc cccggaagaa ggcgacattc ccgaatacat caaagtcgct      780
ttccgcgccg cgcgcgaggc tgacgccaac gtagacctct actacaacga ctacgacaat      840
accgccaatg ccagcgccct ggccaaaaca ctgcaaattg ccgaggtact ggacgccgaa      900
ggcaccattg acggcgctcg tttccagatg cacgcctaca tggattaccc gagcctgacc      960
cattttgaaa acgccttccg gcaagtcgtc gacctggggc tcaaagtga agttaccgag     1020
ctggacgtat ccgtagtcaa ccctacggc ggcgaagcac ctccacaacc ggaatacgac     1080
aaagaactgg ccggcgcgca aaaactgcgc ttctgccaaa tcgccgaagt ttacatgaac     1140
actgtacccg aggagttacg cgggtggcttc accgtctggg gcctgaccga tgatgaaagt     1200
tggctgatgc aacagttcag aaacgccacc ggcgcgcgact acgacgacgt ctggccgtta     1260
ctgttcaatg ccgacaaatc cgccaaaccg gcactgcaag gcgtggccga cgcctttacc     1320
ggacaaacct gcacctccga gttctaa                                     1347

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<210> 166
 <211> 448
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from environmental sample

<220>
 <221> SIGNAL
 <222> (1)...(45)

<400> 166
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 His Asn Ser Leu Pro Ser Leu Arg Thr Leu Phe Thr Thr Ser Leu Leu
 20 25 30
 Thr Leu Ala Leu Thr Ala Cys Gly Gly Ser Ser Ser Ser Asp Lys Asp
 35 40 45
 Pro Ser Ser Ser Ser Ser Ser Glu Ser Ser Ser Ser Ser Glu Ser Ser
 50 55 60

Ser 65	Ser	Ala	Ser	Ser	Glu 70	Ser	Ser	Ser	Ser	Glu 75	Ser	Ser	Ser	Ser	Ser	80
Ser	Ala	Gly	His	Phe 85	Ser	Ile	Glu	Pro	Asp 90	Phe	Gln	Leu	Tyr	Ser 95	Leu	
Ala	Asn	Phe	Pro 100	Val	Gly	Val	Ala	Val 105	Ser	Ala	Ala	Asn	Glu 110	Asn	Asp	
Ser	Ile	Phe 115	Asn	Ser	Pro	Asp	Ala 120	Ala	Glu	Arg	Gln	Ala 125	Val	Ile	Ile	
Glu 130	His	Phe	Ser	Gln	Leu	Thr 135	Ala	Gly	Asn	Ile	Met 140	Lys	Met	Ser	Tyr	
Leu 145	Gln	Pro	Ser	Gln	Gly 150	Asn	Phe	Thr	Phe	Asp 155	Asp	Ala	Asp	Glu	Leu 160	
Val	Asn	Phe	Ala	Gln 165	Ala	Asn	Gly	Met	Thr 170	Val	His	Gly	His	Ser 175	Thr	
Ile	Trp	His	Ala 180	Asp	Tyr	Gln	Val	Pro 185	Asn	Phe	Met	Arg	Asn 190	Phe	Glu	
Gly	Asp	Gln 195	Glu	Glu	Trp	Ala	Glu 200	Ile	Leu	Thr	Asp	His 205	Val	Thr	Thr	
Ile 210	Ile	Glu	His	Phe	Pro	Asp 215	Asp	Val	Val	Ile	Ser 220	Trp	Asp	Val	Val	
Asn 225	Glu	Ala	Val	Asp	Gln 230	Gly	Thr	Ala	Asn	Gly 235	Trp	Arg	His	Ser	Val 240	
Phe	Tyr	Asn	Ala	Phe 245	Asp	Ala	Pro	Glu	Glu 250	Gly	Asp	Ile	Pro	Glu 255	Tyr	
Ile	Lys	Val	Ala 260	Phe	Arg	Ala	Ala	Arg 265	Glu	Ala	Asp	Ala 270	Asn	Val	Asp	
Leu	Tyr 275	Tyr	Asn	Asp	Tyr	Asp	Asn 280	Thr	Ala	Asn	Ala	Gln 285	Arg	Leu	Ala	
Lys 290	Thr	Leu	Gln	Ile	Ala	Glu 295	Val	Leu	Asp	Ala	Glu 300	Gly	Thr	Ile	Asp	
Gly 305	Val	Gly	Phe	Gln 310	Met	His	Ala	Tyr	Met	Asp 315	Tyr	Pro	Ser	Leu	Thr 320	
His	Phe	Glu	Asn	Ala 325	Phe	Arg	Gln	Val	Val 330	Asp	Leu	Gly	Leu	Lys 335	Val	
Lys	Val	Thr 340	Glu	Leu	Asp	Val	Ser	Val 345	Val	Asn	Pro	Tyr	Gly 350	Gly	Glu	
Ala	Pro 355	Pro	Gln	Pro	Glu	Tyr	Asp 360	Lys	Glu	Leu	Ala	Gly 365	Ala	Gln	Lys	
Leu 370	Arg	Phe	Cys	Gln	Ile	Ala 375	Glu	Val	Tyr	Met	Asn 380	Thr	Val	Pro	Glu	

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Glu	Leu	Arg	Gly	Gly	Phe	Thr	Val	Trp	Gly	Leu	Thr	Asp	Asp	Glu	Ser
385					390					395					400
Trp	Leu	Met	Gln	Gln	Phe	Arg	Asn	Ala	Thr	Gly	Ala	Asp	Tyr	Asp	Asp
				405					410					415	
Val	Trp	Pro	Leu	Leu	Phe	Asn	Ala	Asp	Lys	Ser	Ala	Lys	Pro	Ala	Leu
			420					425					430		
Gln	Gly	Val	Ala	Asp	Ala	Phe	Thr	Gly	Gln	Thr	Cys	Thr	Ser	Glu	Phe
		435					440					445			